3 ugen Ltd. c 1	0	<pre>; Search time 3588.29 Seconds [without alignments) 19096.316 Million cell updates/sec</pre>	1 1 1tcatttgaatatttctccc 4231		2 2 2	32308132	3 2 2 3	ом т м п	м m m
GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.	OM nucleic - nucleic search, using sw model	<pre>Run on: December 18, 2002, 07:04:25; Search time 3588.29 Seconds (Without alignments) 19096.316 Million cell updates,</pre>	Title: US-09-647-140A-1 Perfect score: 4231 Sequence: 1 ggacaggcgtggcggccggatt	Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0	Searched: 16154066 seqs, 8097743376 residues	Total number of hits satisfying chosen parameters:	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Database : EST:* 1: em_estba:*

3: em_estin:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	BM462073 AGENCOURT BQ069612 AGENCOURT BQ889997 AGENCOURT BE879353 601484613 BE879718 601491617 BI771442 603059489
SUMMARIES	. OI	BM462073 BQ069612 BQ889997 BE879353 BE879718
	DB	113
	Query ore Match Length DB I	1084 1139 896 682 727 689
ф	Query	17.3 16.7 15.7 15.0 14.5
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EST 02-APR-2002

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mRNA

dq 1139

BQ069612

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cloned into EocNI/XhOI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8bb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
14 a 259 c 280 g 285 t 1 others ä sapiens cDNA clone IMAGE:5812052 Homo sapiens
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleoston
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1139)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Onpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC ğ 131 142 191 202 251 262 311 322 AAGAAGTTTTAAGAGCTGAGAATGACGCACAGAAGCCTTCTTTAACAAGAGCAATCATAA 371 Gaps 71 82 CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC Clone distribution information or found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov n column: 21
High quality sequence start: 10
High quality sequence start: 10
Location/Qualifiers 23 GGGCCGGAGCCCCAGCATCCTGCTTGAGGTCCAGGAGCGGAGCCCGCGGCCACCGCCG CCTGATCAGCGCGGCCCGGCCCGGCCCGGCCGGCAAGATGCTGCCCGTGTACC GCGGCCGGAGCCCCAGCATCCCTGCTTGAGGTCCAGGAGCGGAGCCCGCGGCCACCGCCG 132 AGGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACATCTGCTCACGCGTGTTCTTCTGGT GGCTCAATCCCTTGTTTAAAATTGGCCATAAACGGAGATTAGAGGAAGATGATATGTATT CAGTGCTGCCAGAAGACCGCTCACAGCACCTTGGAGAGGAGTTGCAAGGGTTCTGGGATA 3; Length 1139; Indels Score 706.6; DB 14 Pred. No. 1.8e-188; 0; Mismatches 9;

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AGENCOURT_8730208 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:6339494
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Emall: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
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       AAGTAATCCAGCCCATATTTTGGGAAAAATTATTAATTTTTTGAAAATTATGATCCCA
                                                              612 TACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGTCTTAGTAACATGGCCA
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Plate: LLCM2534 row: g column:
High quality sequence stop: 599.
Location/Qualifiers
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BQ889997
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EST 20-0CT-2000
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                      435 TAATCCAGCCCATATTTTGGGAAAAATTATTAATTATTTGAAAATTATGG
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                                                  Score 664.8; DB 14
Pred. No. 1.2e-176;
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Best Local Similarity 97.1%;
Matches 699; Conservative
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/clone_lib="NIH_MGC_69"
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/tab_host="large cell carcinoma, undifferentiated"
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/tab_host="large ling; Vector: pCMV-SPORT6; Site_l: NotI;
/tab_host="large ling; Vector: large li
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can lfound through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
http://image.llnl.gov
tolumn: 03
Plate: LLAM9665 row: 1 column: 03
Plate: LLAM9665 row: 1
Location/Qualifiers
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Pred. No. 1.2e-168;
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (Dases 1 to 727)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
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/tissue_type="large cell carcinoma, undifferentiated"
/lab_host="DH10B (phage-resistant)"
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                                                                                                                                                                                     601491617F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3893669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapDS-remail.nih.gov
Tissue Procurement: DGTD/DTP/Gazdar
Tissue Procurement: DGTD/DTP/Gazdar
TONA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9682 row. b column: 06
High quality sequence stop: 571.
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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603059489F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5208502 5',
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/db_xref="taxon:9606"
/clone="IMAGE:5208502"
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AUTHORS
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NIH-MGC http://mgc.ncl.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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 DB 13;
Score 582.8; DB 13;
Pred. No. 1.9e-153;
0; Mismatches 12;
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Tissue Procurement: ATCC
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BE885514.1 GI:10334290
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                                                                                                                                                                                                                                                          /tissue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/hote="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sali; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 2.1 kb. cl
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                                      DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2197 AAAAGTTGGTTTTCAGGCCTATAAGAATTACTTCA--GAGCTGGTGCTCACTGGATTGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 926;
cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                        found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9725 row: m column: 02
High quality sequence stop: 590.
Location/Qualifiers
1. .926
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Pred. No. 5.8e-143;
0; Mismatches 55;
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                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3910441"
/clone_lib="NIH_MGC_71"
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                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 12.9%;
Best Local Similarity 90.0%;
Matches 657; Conservative
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EST 22-MAR-2002
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I (bases I to 497)

Wambutt, R., Heubner, D., Mewes, W., Weil, B. and Wiemann, S.

EST (Wambutt, R., Heubner, D., Mewes, H.W., Weil, B. and Wiemann, S.)

Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB; cDNA-collection"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2); Email s.wiemann@dkfz- heidelberg.de;
sequenced by AGOWA (Berlin/Germany) within the CDNA sequencing
consortium of the German Genome Project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This clone (DKFZp686F08149) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1581 TGAGGAGTAATATTTTATTTGGGAAGAAATATGAAAAGGAACGATATGAAAAGGTCATAA 1640
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                                                                                                                                                                  AL701816

AL701816

DKFZp686F08149_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone DKFZp686F08149 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="DKF2p686F08149"
/clone_lib="686 (synonym: hlcc3)"
/tissue_type="human skeletal muscle"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 No s1 sequence available.
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                           Homo sapiens
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LiNL, send email to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: lung; Vector: pT713D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized mid-library NCI_GGAP_Lu5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The diver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonelDs 1414920-1417991 and 1520904-1522439). Subtraction by Bento
                                                                                                                                                                                                                                                                                                            EST 08-SEP-2000
                                                                                                                                                                                                                                                                                                                     7d76g07.x1 NCI_CGAP_Lu24 Homo Sapiens CDNA clone INAGE:3778940 3/
similar to TR:075555 075555 ABC TRANSPORTER MOAT-B ISOFORM ;, mRNA
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Mammalia; Eutheria; Primates; Catarrhlni; Hominidae; Homo.
1 (bases 1 to 478)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                  Gaps
CCCTTTTAAAGAAGGATAATGAGGAAAGTGAACAACCTCCAGTTCCAGGAA-CTCCCACA
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Pred. No. 8.5e-121;
0; Mismatches 7;
                                                                                                                                                                                                                                                                                                            mRNA
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/clone_lib="NCI_CGAP_Lu24"
/tissue_type="carcinoid"
/lab_host="DH108"
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/db_xref="taxon:9606"
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Seq primer: -40UP from Gibco
High quality sequence stop: 446.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                           478 bp
                                                                                                                                                                                                                                                                                                                                                                            BE674208
BE674208.1 GI:10034749
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98.5%;
                                                                                                                                                                                     CTAAGGAATCGTACCTT 2076
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Unpublished (1997)
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TITLE
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COMMENT
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Louse muscaulus.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Musmuslala; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Eukaryota; Lo 639)

Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Saito,F., Saito,F., Sakai,K., Sakai,K., Sakai,K., Sakai,K., Sakai,K., Sakai,K., Sakai,K., Sakai,K., Takahashi,F., Takeda,Y., Tanaka,T., Muramatsu,M. and Hayashizaki,Y., et al. 2001)

On Jul 3, 2000 this sequence version replaced gi:8896327.

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute of Physical and Chemical Research (RIKEN)

To 2 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel. 81-45-503-9022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BB225682 RIKEN full-length enriched, adult male aorta and vein Mus musculus cDNA clone A530093119 3' similar to U83660 Human multidrug resistance-associated protein homolog (MRP4) mRNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
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wagi.K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura Hayashizaki,Y.
3466
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                                                                                                                                                                                                                                                            TCAATCATACCTCAGGAACCTGTTTTGTTCACTGGAACAATGAGGAAAAACCTGGATCCC 3526
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                                                                                                                              9407 ATTIGGATTGATAAGATCTTGACAACTGAAATIGGACTICACCATTTAAGGAAGAAAATG 3466
                                                                                                                                                                                                                                                                                      298 TCAATCATACCTCAGGAACCTGTTTTGTTCACTGGAACAATGAGGAAAAACCTGGATCCC 239
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RIKEN integrated sequence analysis (RISA) system--384-format

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sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara , Y. and Hayashizaki, Y. Computer-based methods for the mouse full-length cDNA
                                                                                                                        encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa ,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.
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                                                                                                                                                                                                                                                                                                                                 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
/clone="A530093119"
/clone_lib="RIKEN full-length enriched, adult male aorta
                                                                                                                                                                                                                                      Computational Analysis of Full-Length Mouse cDNAs Compared with
                                                                                                                                                                                                                                                              Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for
further details.
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Pred. No. 3.6e-117
0; Mismatches 77
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/dev_stage="adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
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86.7%;
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Best Local Similarity 86.79
Matches 501; Conservative
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BE327296 435 bp mRNA linear EST 14-JUL-2000 hw10b05.xl NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182481 3' similar to TR:075555 075555 ABC TRANSPORTER MOAT-B ISOFORM ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                  421
                                                                                                                                                                                                                                                   481
3575 CAACTTAAAGAAACCATTGAAGATCTTCCTGGTAAAATGGATACTGAATTAGCAGAATCA
                           1902 CAACTTAAAGAGGCCATTGAAGATCTTCCTGGAAAAATGGATACTGAATTAGCAGAAACT
                                                                                                                         3695 AAAAATCAGATATTGATTATTGATGAAGCGACGGCAAATGTGGATCCAAGAACTGATGAG
                                                                                                                                                                                                                       TTAATACAAAAAAAAATCCGGGAGAAATTTGCCCACTGCACCGTGCTAACCATTGCACAC
                                                                                                                                                                                                                                                                                                                    3635 GGATCCAATTTTAGTGTTGGACAAAGACAACTGGTGTGCCTTGCCAGGGCAATTCTCAGG
                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3182481"
/clone=lib="NoI_CGAP_Lu24"
/tissue_type="carcinoid"
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High quality sequence stop: 424.
Location/Qualifiers
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BE327296.1 GI:9201072
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Unpublished (1997)
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Length 435;

Score 433.4; DB 10;

10.2%;

Query Match

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Ota,T., Nishikawa,T., Suzuki,Y., Kawai,Y., Ishii,S., Saito,K.,
Nakamura,Y., Nagai,T., Suzuki,Y., Sugano,S. and Isogai,T.
Ishii,S., Saito,K., Nakamura,Y., Nishikawa,T., Sugano,Y., Kawai,Y.,
Ishii,S., Saito,K., Nakamura,Y., Nagai,T., Sugano,S., Isogai,T.)
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Fel: 81-438-52-3975
Fex: 81-438-52-3986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                        3626 GCAGAATCAGGATCCAATTTTAGTGTTGGACAAAGACAACTGGTGTGTCTTGCCAGGGCA 3685
                                                                                                                                                                                                                                                                                                                                                                ATGAGGAAAAACCTGGATCCCTTTAAGGAGCACACGGATGAGGAACTGTGGAATGCCTTA 3565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: genomics@hrl.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                      3446 CACGATTTAAGGAAGAAATGTCAATCATACCTCAGGAACCTGTTTTGTTCACTGGAACA
                                        GTTGGCATTGTGGGAAGAACCGGAGCTGGAAAAAGTTCCCTCATCTCAGCCCTTTTTAGA
                                                                                            TTGTCAGAACCCGAAGGTAAAATTTGGATTGATAAGATCTTGACAACTGAAATTGGACTT
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 Pred. No. 3.6e-111;
0; Mismatches 1;
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/clone_lb="NT2RP1001350"
/cell_type="teratocarcinoma"
/cell_line="NT2"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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AU126646.1 GI:10951362
 larity 99.8%;
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House mouse.

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.

1 (bases 1 to 734)

Rakawa_T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Muramatsu, M. and Hayashizaki, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.

Inpublished (2001)

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Fax: 81-45-503-9216
                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BB643073 RIKEN full-length enriched, 9.5 days embryo parthenogenote Mus musculus cDNA clone B130008G09 5', mRNA sequence.
    NT2 neuronal precursor (RA) induction"
                                                                                                                                                                              3540 CGGATGAGGAACTGTGGAATGCCTTACAAGAGGTACAACTTAAAGAAACCATTGAAGATC 3599
                                                                                                                                                                                                                                                                                                                                                                                                                                   3719
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0
                                                                                                         Length 465;
                                              3 others
                                                                                                                                             6; Indels
/note="Vector: pUC19FL3; mRNA from cells after 48-hours retinoic acid 80 c 106 g 115 t 3
                                                                                                     Score 433; DB 9; I
Pred. No. 4.8e-111;
O; Mismatches 6;
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URL:http://genome.gsc.riken.go.jp/
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BB643073.1 GI:16477826
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98.6%;
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house mouse.
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Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo,S., Shinaqawa,A., Saito,T., Kiyosawa, H., Yamanaka,I., Aizawa
,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
Hayashizaki,Y.
                                                                                                                                                                                                    RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. CDNA went through one round of subtraction to
Rot = 229.0 Second strand cDNA was prepared with the
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Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh, M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNas to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togwa,Y., Izawa,M., Ohara,E., Watshiki,M., Yooneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was GAGAGGAGGAGGAGGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     haydshizakl,r.
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="B13000609"
/clone_lib="RIKEN full-length enriched, 9.5 days embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87 CCCGGCCCGCCCCCCCCCCCGCCAAGATGCTGCCCGTGTACCAGGAGGTGAAGCCCA 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="parthenogenote"
/dev_stage="9.5 days embryo"
/lab_host="DH10B"
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llarity 74.6%;
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Arakawa, T. Carninci, P. Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda Limamoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda K., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, J., Shibara, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Muramatsu, M. and Hayashizaki, F., Takeda, Y., Tanaka, T., Toya, T., RIKEN Mouse ESTS (Arakawa, T., et al. 2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: genome-res@gsc.riken.go.jp,
URL.http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
.M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNas to
prepare full-length cDNA libraries for rapid discovery of new
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BB623281 RIKEN full-length enriched, 12 days embryo male wolffian duct Mus musculus cDNA clone 6720455A17 5', mRNA sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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The Institute of Physical and Chemical Research (RIKEN)
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                                246 ATCGCTCAAAGCACCTCGGAGAGGTTCAACGGTACTGGGATAAAGAACTTCTGCGAG 305
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                                                                                                                                                                                                     encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,H., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI"
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genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Trogawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="wolffian duct includes surrounding region"
/dev_stage="12 days embryo"
/lab_host="DH10B"
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Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
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/clone_lib="RIKEN full-length enriched, 12 days embryo
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                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
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/db_xref="taxon:10090"
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Matches 494; Conservative
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Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
Location/Qualifiers
                                                                                                     2805 GGAGTCCAGTGTTTCCCACTTGTCATCTTCTCTCCAGGGGCTCTGGACCATCCGGGGAT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute.
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 777)
Buerstedde J.M.
Gallus agllus bursal lymphocyte EST
Unpublished (2002)
Contact: Buerstedde JM
Cellular Immunology
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Pred. No. 5.9e-103;
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/dev_stage="2-3 weeks old"
/note="CB inbred strain"
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/db_xref="taxon:9031"
/clone="3i1r1"
/clone_lib="riken1"
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description		CDNA encoding a hu	Human differential	Human prostate on	Human prostato-spo	Human prostate-spe	Human P510S CDNA s	Human prostate exp	Human prostate exp	Human prostate exp
SUMMARIES			ΙD		AAZ30078	AAH81778	AAS63921	AAH93828	AAH85142	ABL95292	ABV20669	ABV22410	ABV24188
•			DB	1	20	22	22	22	22	24	23	23	23
		Query	Length	1	4231	4231	6082	6082	6082	6082	4515	4515	4515
	dР	Query	Match	1	100.0	100.0	99.5	99.2	99.5	99.5	99.2	99.2	99.2
			Score		4231	4231	4211	4211	4211	4211	4196.6	4196.6	4196.6
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Human prostate exp	ď	prostate	ate cancer	Human prostate cDN	prostate-	Human prostate-spe	Human P510S CDNA S		Human cDNA encodin	1	E3	Human prostate exp		- (17	Multi-drug resista	Human prostate exp	hila mela	Human prostate evn				Drosophila melanog		hila mela			ø	틀	Rat sequence diffe	canalicular m	ophila melan	Multidrug-resistan	Human multidrug re	Human MRP-beta cDN	CDNA encoding a hu
ABV24580	ABV26511	22	213	AAS63922	38	514	59	17	AAS64134	AAH93898	ABL95505	ABV24259	ABV12837	ABL02707	AAC63519	ABV33965	ABL02706	ABV03668	ABL25801	ABL18886	ABL18887	ABL13149	ABV42833	ABL07889	ABL09969	ABL04815	ABL25800	AAT94053	ABK63671	AAT94024	ABL18273	AAC85287 ·	AAV65682	AAA40481	AAZ30079
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ALIGNMENTS

AAZ30078 standard; cDNA; 4231 BP.

RESULT 1 .

AAZ30078

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cDNA encoding a human MPR-related ABC transporter designated MOAT-B.
                                                                                                                                                                           /transl_except= (pos: 1715..1717, aa: Pro)
/transl_except= (pos: 3566..3568, aa: Arg)
/note= "MPR-related ABC transporter"
                                                              Human; MPR-related ABC transporter; MOAT protein; MOAT-B;
MOAT mediated transport; anticancer drug sensitivity;
transporter mediated cellular efflux; anticancer; ss.
                                                                                                                                Location/Qualifiers
116..4093
                                                                                                                                                        /*tag= a
/product= "MOAT-B"
                                                                                                                                                                                                                                                                                     98US-0079759.
                                                                                                                                                                                                                                                                  99WO-US06644.
                  26-JAN-2000 (first entry)
                                                                                                          Homo sapiens
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03-AUG-1998;
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AAZ30078;
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                                                                                                                                     The present sequence encodes a human MPR-related ABC transporter (MOAT) protein, designated MOAT-B. The protein comprises a multi-domain structure including a tandem repeat of nucleotide binding folds appended C-terminal to a hydrophobic domain, having Walker A and B ATP binding sites and several potential membrane spanning domains. The MOAT nucleic acids are useful for screening a test compound for inhibition of MOAT mediated transport, indicated by restoration of anticancer drug sensitivity, which in turn causes a reduction of transporter mediated cellular efflux of anticancer agents. MOAT DNA or RNA may be used as probes to detect the presence or expression of genes encoding MOAT proteins. Anti-MOAT antibodies are useful for detecting and quantitating
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; Mismatches
                                                                                           New transporter gene useful for screening
                                                                                                                 Claim 1; Page 130-131; 153pp; English
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Qy Dp	88	GTGTCAGGAACTGTTTGATGCACACGGATTTACATTCAGAGGCTTGGTTCTTTTT 294
QY	2941	GACAACGTCCGCTGGTTCGCCGTCCGTCTGGATGCCATCTGTGCCATGTTTGTCATCAT 300
Qy	3001	CGTTGCCTTTGGGTCCCTGATTCTGGCAAAACTCTGGATGCCGGGCAGGTTGGTT
Qy Db	3061	CTATGCCCTCACGCTCATGGGGATGTTTCAGTGGTGTGTTCGACAAAGTGCTGA 312
QV Dp	3121	IGAGAATATGATGATCTCAGTAGAAAGGGTCATTGAATACACAGACCTTGAAAAGA 318
Oy Dp	3181	RATCAGAAACGCCCACCAGCCTGGCCCCATGAAGGGGTGATAAT 3
Qy	3241	ITGACAANGTGAACTICATGTACAGTCCAGGTGGGCCTCTGGTACTGAAGCATCTGAC 330
Qy	3301	atcacaagaaaaggttggcattgtgggaagaaccggagctggaaaag 336
Qy Db	3361 3361	TCAGCCCTTTTTAGATTGTCAGAACCGGAAGGTAAAATTTGGATTGATAA 342
Q _Y	3421	JEGAAATIGGACITCACGAITTAAGGAAGAAAATGICAATCAIACCICA 34:
do do	3481	AATGAGGAAAAACCTGGATCCCTTTAAGGAGCACAC 354
QY DP	3541	GAACTGTGGAATGCCTTACAAGAGGTACAACTTAAAGAAACCATTGAAGATCT 360
Qy	3601	TAGCAGAATCAGGATCCAATTTTAGTGT
Qy	3661 3661	CAATTCTCAGGAAAATCAGATATTGATTATTGATGA 372.
Qy Db	3721 3721	TGTGGATCCAAGAACTGATGAGTTAATACAAAAAAAATCCGGGAGAA 378
Oy Dp	3781 3781	ACTGCACCGTGCTAACCATTGCACACAGATTGAACACCATTATT
oy Og	3841	SATAATGGTTTTAGATTCAGGAAGACTGAAAGAATATGATGAGCGGTATG
QY	3901	FATTTTACAAGATGGTGCAACA

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between tumour and normal cells and which has cytostatic activity. (I) work as modulators of Ras activity by inducing expression of tumour suppressor genes. (I), and polypetides encoded by them, are useful as targets for diagnosis or therapy and in screening to determine the effects of an active compound (potential pharmaceutical) on a cell line, particularly for diagnosis and treatment of tumors, especially by modulating expression of (I) (by gene therapy, antisense RNA or ribozyme methods) or by modulating the amount and/or location of (I)-encoded notibody (Optionally as a conjugate) or inhibitor). The method allows identification of many Class II tumour suppressor genes (i.e. genes that are not primary targets for tumour-initiating mutations).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes a nucleic acid (I) with differential expression
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             GCAAAATAAAGAGCCTATTTACAAGATGGTGCAACAACTGGGCAAGGCAGAAGCCGC
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                                          TGCCCTCACTGAAACAGCAAAACAGGTATACTTCAAAAGAAATTATCCACATATTGGTCA
Differential transcription; human; rat; tumour cell; cytostatic;
Ras modulator; Class II tumour suppressor gene; gene therapy; ss
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                                                                                                                                                                                                                                                                      Disclosure; Page 442-443; 579pp; German
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polynucleotides, polypeptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides (or antigenic epitopes derived from them) and antigen-presenting cells expressing the polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polynucleotides and the antigen-presenting cells are useful for stimulating and/or expanding T cells specific for a tumour protein, and for inhibiting the development polynucleotide and/or polypeptide are useful for stimulating an immune response, and for treating cancer. The oligonucleotide is useful for detecting cancer. The present sequence is a prostate specific polynucleotide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              useful for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human prostate-specific polypeptides and polynucleotides usefu diagnosis and treatment of cancer, especially prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGACAGGCGTGGCGGCCGGAGCCCCAGCATCCCTGCTTGAGGTCCAGGAGCGGAGCCCGC
                                                                                                                                                                                                                                                                                                                                                                                                    Kalos M
Carter
                                                                                         Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 6082;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6082 BP; 1721 A; 1249 C; 1357 G; 1755 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention relates to isolated prostate-specific
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Pred. No. 0;
0; Mismatches
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                                                                sequence #438
                                                                                                                                                                                                                                    2000us-0568100.
2000us-0570737.
2000us-0693793.
2000us-0605783.
2000us-0651236.
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99.9%;
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2000US-0685166
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                                      entry)
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Best Local Similarity 99.9
Matches 4225; Conservative
                                                               Human prostate cDNA
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12-MAY-2000; 2
13-JUN-2000; 2
17-JUN-2000; 2
27-JUN-2000; 2
29-AUG-2000; 2
06-SEP-2000; 2
10-OCT-2000; 2
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QQ	191	GCCCGTGTACCAGGAGGTGAAGCCCAACCGCTGCAGGACCCCAACCTCTGCTCACGGT 250	qa		GCTGAC
λo 4	181	24	Qy Db	1261 (CATCCG
3 3	707		ΔO	_	GCGGTC
o o	311	TGATATTCATTCCATCCAGAAGACCGCTCACACACACCTTGGAAGAGTTGCAAGG 300	q q		GCCGTC
οy	301	36	oy a		ATCAGA
Dp	371	GTTCTGGGATAAAGAAGTTTTAAGAGCTGAGAATGACGCACAGAAGCCTTCTTTAACAAG 430	an .		ATCAGA
Qy	361	AGCAATCATAAAGTGTTACTGGAAATCTTATTTAGGAATTTTTTACGTTAATTGA 420 	oy Oy	1511	TGTGGT TGTGGT
Qy	421	4	Qy Db	1501 (222225 11111 26CCCC
οy		TTATGATCCCATGGATTCTGTGGCTTTGAACACAGGGTACGCTATACCACGGGGGTATACACACAC	Qy	1561	TEGGT
qq			QO	1631	CTGGGT
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Qy Dp	1201	GCTGACGGTTACCCTCTTCTTCCTCAGCCATTGAGAGGGTGTCAGAGGCAATCGTCAG 1260
QY	1261 1331	ITTTGCTACTTGATGAGATATCACAGCGCAACCGTCAGCT 13:
Qy Db	1321	GATAAGGC 138 GATAAGGC 145
Qy	1381	TTTACTGTCAGACCTGGCGAATTGTTAGC 144
Qy	1441	AGGGAAGTCATCACTGTTAAGTGCCGTGCTCGGGGAATT 1.
Qy	1501	rGGTCAGCGTGCATGGAAGAATTGCCTATGTGTCTCAGCAGC 156
Qy Dp	1561	PGGGAACTCTGAGGAGTAATATTTATTTGGAAGAATATGAAAAGA 10
Q _Y	1621 1691	*AAAGGCTTGTGCAAAAAGGATTTACAGCTGTTGGAGGA 16
QY	1681 1751	AGATCGGGGAACCACGCTGAGTGGAGGGCAGAAAGCACG 17
Qy Dp	1741	AGAGCAGIGIAICAAGAIGCIGACAICIAICICCIGGACGAICCICI 1
Qy	1801 1871	3ACACTTGTTCGAACTGTGTATTTGTCAAATTTT 16
Qy	1861 1931	BATCACAATTTTAGTGACTCATCAGTTGCAGTACCTCAAAGCTGCAAGTCA 19
Qy	1921	ATGGTGCAGAAGGGACTTACACTGAGTTCCTAAA 19
Qy	1981	AAGAAGGATAATGAGGAAAGTGAACAACCTCC 20
Qy	2041	CCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGGTCTCA 21
Qy	2101	CCCTCCTTGAAAGATGGTGCTCTGGAGAGCCAAGATACAGAGAATGT 21
QY Db	2161 (2231 (A - A
. da	2221 (TTGTCTTCATTTTCCTTATTC

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TGCAGCTCAGGTTGCCTATGTGCTTCAAGATTGGTGGCTTTCATACTGGGCAAACAAC		TITICALCCAGACATTGCTACAAGTGGTTGGTGTGTGTTGTGGCTGTGGCCGTGATTC TTGGATCGCAATACCCTTGGTTCCCCTTGGAATCATTTTCATTTTCTTCGGCGGTATAT TTGGATCGCAATACCCTTGGTTCCCCTTGGAATCATTTTTCTTTC	CCACTTGTCATCTTCTCCAGGGGCTCTGGACCATCCGGGCATACAAGCAGAAGCAGAG [GACAACGICCCGCTGGTTCGCCGTCTGGATGCCATCTGTGCCATGTTTGTCAT GACAACGTTCCGCTGGTTCGCCGTCTGGATGCCCATCTGTGCCATGTTTGTCAT CGTTGCCTTTGGGTCCCTGATTCTGGCAAAACTCTGGATGCCGGGCAGGTTGGTT	AGCACCTTGGGAATATCAGAAACGCCCACCAGCCTGGCCCCATGAAGGAGTGATAAT [
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3540 3670 3660 3720 3790 3780 3849 3840 4020 3900 4089 4080 3969 3960 4029 4149 4140 4209 4200 4210 TTTGGACTATGTAAACCACATGTACTTTTTTTTACTTTGGCAACAAATATTTAACATA 4269 4090 CACTGACCACATGGTTACAAACACTTCCAATGGACAGCCCTCGACCTTAACTATTTTCGA 3661 ACAACTGGTGTGCCTTGCCAGGGCAATTCTCAGGAAAAATCAGATATTGATTATTGATGA 3781 ATTIGCCCACTGCACCGTGCTAACCATTGCACACAGATTGAACACCATTATTGACAGCGA 3850 ATTIGCCCACTGCACCTGCTAACCATTGCACAGAATTGAACACCATATTAACAGA 3970 GCAAAATAAAGAGGCCTATTTTACAAGATGGTGCAACAACTGGGCAAGGCAGGAAGCCGC 4030 TGCCCTCACTGAAACAGCAAAACAGGTATACTTCAAAAGAAATTATCCACATATTGGTCA 4021 CACTGACCACATGGTTACAAACACTTCCAATGGACAGCCCTCGACCTTAACTATTTTCGA 3601 TCCTGGTAAAATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGGACAAAG 3961 TGCCCTCACTGAAACAGCAAAACAGTATACTTCAAAAGAAATTATCCACATATTGGTCA GACAGCACTGTGAATCCAACCAAAATGTCAAGTCCGTTCCGAAGGCATTTTCCACTAGTT TITGGACTATGTAAACCACATTGTACTTTTTTTTTTTGGCAACAAATATTTATACATA prostate-specific 1st full length cDNA sequence for P510S. vaccine; Human; prostate cancer; prostate-specific; diagnosis; cytostatic; gene therapy; metastasis; ss. ВР AAH93828 standard; cDNA; 6082 (first entry) 04-OCT-2001 AAH93828; Нишап 3431 3551 3481 4081 4141 3901 4201 4270 RESULT 4 AAH93828 Db οy qq ά QQ δy Qγ Db Qy DD οğ 임 οy ΩD g g Db g a Qγ δ οy ò QQ g QΥ Qγ δy

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The present invention describes polynucleotide sequences (I) which encode prostate-specific proteins (II). (I) and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. (I), (II), and can be used in vaccine production and gene therapy. (I), (II), and can be used in proteins comprising (II), and isolated (II), the antibodies are also used in the detection of cancer in a patient. The cancer that is diagnosed or treated is particularly prostate cancer. (I) and (II) can be used in vaccines. The antibodies or (I) can be used for monitoring the progression of cancer in a patient. (I) and (II) can also be used to improve diagnostic and therapeutic methods for prostate cancer. They can indicate the level of metastasis as well as the prostate volume. AAM93357 to AAM93944 and AAM01115 to AAM01318 represent polynucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                            New polynucleotide encoding a prostate-specific protein, diagnosing, monitoring and treating prostate cancer in a
                                                                                                                                                                                                                       SL, Jiang Y
Stolk JA,
                                                                                                                                                                                                                     Harlocker S
Retter MW,
                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 411-412; 543pp; English.
                                                                                                                                                                                                                  Dillon DC, Mitcham JL, 4D, Fanger GR, Day CH,
                                                                                                                                              14-JAN-2000; 2000US-0483672.
                                                                                                          16-JAN-2001; 2001WO-US01574
                                                                                                                                                                                                                                                      Meagher MJ;
                                                                                                                                                                                                                                                                                          WPI; 2001-425873/45.
                                                                                                                                                                                                                                                                                                                                                                  use in vaccines
                                                                                                                                                                                (CORI-) CORIXA CORP
                                  WO200151633-A2
Homo sapiens
                                                                      19-JUL-2001
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patient

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encode

Sequence 6082 BP; 1721 A; 1249 C; 1357 G; 1755 T; 0 other;

99.58;

Query Match

Length

ij 120 180 250 240 310 300 370 360 430 420 490 Gaps 9 GGACAGGCGTGGCGGCGCGGAGCCCCAGCATCCCTGCTTGAGGTCCAGGAGCGGAGCCCGC GCCCGTGTACCAGGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACATCTGCTCACGCGT GTTCTTCTGGTGGCTCAATCCCTTGTTTAAAATTGGCCATAAACGGAGATTAGAGGAAGA TGATATGTATTCAGTGCTGCCAGAAGACCGCTCACAGCACCTTGGAGAGGAGTTGCAAGG GTTCTGGGATAAAGAAGTTTTAAGAGCTGAGAATGACGCACAGAAGCCTTCTTTAACAAG **AGCAATCATAAAGTGTTACTGGAAATCTTATTTAGTTTTTGGGAATTTTTACGTTAATTGA** Indels Score 4211; DB 22; Pred. No. 0; 0; Mismatches 5; Best Local Similarity 99.9 Matches 4225; Conservative Н 131 191 431 61 121 311 251 241 181 371 361 301 ò g qq g ò òγ δ g δ g op qq δ ò

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               491 GGAAAGTGCCAAAGTAATCCAGCCCATATTTTGGGAAAAATTATTATTTTGAAAA
                                        TGGGATGAGGTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGTCTTAG
                                                                                                                                       TTATGATCCCATGGATTCTGTGGCTTTGAACACAGGGTACGCCTATGCCACGGTGCTGAC
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157	156	162	168	174	180	186	192	198	204	210	216	222	228	234	240	246	252	ω
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chromosome 22q11.2; prostate-specific protein; chromosome
prostate specific antigen; PSA; ss.
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18-NOV-1999;
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                                     at least an immunogenic portion of a prostate-specific protein, or its variant. Also described are polynucleotides (N1) encoding (P1). (P1) and (N1) have eytostatic activity and can be used in vaccine production. The polypeptides, nucleic acids and antibodies from the present invention are useful in the diagnosis and therapy of prostate cancer. Prostate specific genes P704P, P712P, P774P, P75P and B305D are located in a genomic region on chromosome 22q11.2 known as the Cat Eye Syndrome region. Prostate specific antigen (PSA) P501S was located on chromosome 1. AAH84671 to AAH85143 and AAG99000 to AAG99077 represent polynucleotide and polypeptide sequences used in the exemplification
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                              present invention describes an isolated polypeptide (P1)
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                                                                                                                                            the present invention.
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Matches 4225; Conservative
          Page 310-312;
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Db 4090 CACTGACCACATGCTACAAACACTTCCAATGGACAGCCTTCGACTTTTCGA 1149 Qy 4081 GACAGCACTGTGAATCCAACAAAATGTCAAGTCGTTCCGAAGCATTTCCACTAGTT 4140	RESULT 6 ABL95292 ID ABL95292 ID ABL95292 ID ABL95292; XX AC ABL95292; XX DT 19-JUL-2002 (first entry) XX DE Human P510S cDNA sequence SEQ ID NO 535. XX KW Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant; XX	Homo sapiens US200202248 21 FEB-2002 12-JAN-2001; 25-FEB-1997; 01-AUG-1997; 05-FEB-1998; 25-FEB-1998; 14-JUL-1998; 23-SEP-1998; 23-SEP-1998;	PR 13-JAN-1999; 99US-0232149. PR 13-JUL-1999; 99US-0352616. PR 13-JUL-1999; 99US-0352616. PR 12-NOV-1999; 99US-0352616. PR 14-JAN-2000; 2000US-0433613. PR 27-MAR-2000; 2000US-0536857. PR 27-MAR-2000; 2000US-0536877. PR 12-MAY-2000; 2000US-05507737. PR 13-JUN-2000; 2000US-05507393. PR 13-JUN-2000; 2000US-05507393. PR 13-JUN-2000; 2000US-0636215. PR 27-JUN-2000; 2000US-0636215. PR 29-AUG-2000; 2000US-0636215. PR 02-CCT-2000; 2000US-0651236. PR 10-OCT-2000; 2000US-0665126.	PA (XUJJ/) XU J. PA (XUJJ/) XU J. PA (DILL/) DILLON D C. PA (MITC/) MITCHAM J L. PA (HARL/) HARLOCKER S L. PA (JIAN/) JANG Y. PA (KALO/) KALOS M D. PA (FANG) RG R. PA (FANG) STOLK J A. PA (STOL/) STOLK J A. PA (STOL/) STOLK J S. PA (VEDV/) VEDVICK T S. PA (VEDV/) VEDVICK T S. PA (CART/) CARTER D. PA (LISX/) LI S X. PA (WANG/) WANG A.
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                             Kalos M
Carter
                                                                                                           The present invention provides prostate-specific coding sequence their encoded proteins. These can be used in the diagnosis and of cancers, particularly prostate cancer. The present sequence described in the invention.
                                                                                                                                                                        ;;
                                                                                                                                                          Length 6082;
                                                                           for
                                                                                                                                             0 other;
                                                                     and
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                            Harlocker SL, Jiang Y,
1, Day CH, Vedvick TS,
Pler WT, Henderson RA;
                                                                    -specific polynucleotides for diagnosing
particular prostate cancer, and as marke
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                                                                                                                                                         99.5%; Score 4211; 99.9%; Pred. No. 0;
                                                                                                                                            BP; 1721 A; 1249 C; 1357
                                                                                               English
                                    JA, Da
Hepler
                            on DC, Mitcham JL,
Retter MW, Stolk J
J A, Skeiky YAW, F
                                                                                             535; 87pp;
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SKEIKY Y A W. HEPLER W T. HENDERSON R A.
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                                                      2002-255649/30
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                                         Wang A,
                                                                                              Claim 1; SEQ ID
                                                                                progression of
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01 CAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTGTTTTGCAAATTTT 1860 		11 GATICTGATATTGAAAGTGGTAAAATGGTGCAGAAGGGGACTTACACTGAGTTCCTAAA 1980 	~ ~	11 AGTTCCAGGAACTCCCACACTAAGGAATCGTACTTCTCAGAGTCTTCGGTTTGGTCTCA 2100)] ACAATCTTCTAGACCCTCCTTGAAAGATGGTGCTCTGGAGAGCCAAGATACAGAATGT 2160 	1 CCCAGTTACACTATCAGAGGAGAACCGTTCTGAAGGAAAAGTTGGTTTTCAGGCCTATAA 2220 	11 GAATTACTTCAGAGCTGGTGCTCACTGGATTGTCTTCATTTTCCTTATTCTCCTAAACAC 2280 	11 TGCAGCTCAGGTTGCCTATGTGCTTCAAGATTGGTGGCTTTCATACTGGGCAAACAACA 2340 	1. AAGTATGCTAAATGTCACTGTAAATGGAGGAGGAATGTAACCGAGAAGCTAGATCTTAA 2400 	1 CTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCGTTCTTTTTGGCATAGCAAG 2460 	1. ATCTCTATTGGTATTCTACGTCCTTGTTAACTCTTCACAACTTTGCACAAAAATGTT 2520 	1 TGAGTCAATTCTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGATTT 2580 	1 AAATCGTTTCTCCAAAGACATTGGACACTTGGATGATTTGCTGCCGCTGACGTTTTTAGA 2640 	1 TITCATCCAGACATIGCTACAAGTGGTTGGTGTGTCTGTGGCTGTGGCCGTGATTCC 2700 	1 TIGGATCGCAATACCCTIGGITCCCCTIGGAATCAITITICAITITITCTICGGCGATAIT 2760 	1 TITGGAAACGTCAAGAGAIGTGAAGCGCCTGGAAICTACAACTCGGAĞTCCAGIGITITC 2820 	1 CCACTIGICAICTICICCAGGGGCTCTGGACCAICCGGGCATACAAAGCAGAAGAGAG 2880
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δγ	2881	GTGTCAGGAACTGTTTGATGCACACCAGGATTTACATTCAGAGGCTTGGTTCTTGTTTTT 2940
Oy Dp	2941 3011	GACAACGTCCCGCTGGTTCGCCGTCCGGATGCCATCTGTGCCATGTTTGTCATCAT 3000
Qy Db	3001	CGTTGCCTTTGGGTCCCTGATTCTGGCAAAACTCTGGATGCCGGGCAGGTTGGTT
, go da	3061	ACTGTCCTATGCCCTCACGCTCATGGGGATGTTTCAGTGGTGTGTTCGACAAAGTGCTGA 3120
oy O	3121	AGTTGAGAATATGATGATCTCAGTAGAAAGGGTCATTGAATACACAGACCTTGAAAAGA 3180
Qy Db	3181	AGCACCTIGGGAATATCAGAAACGCCCACCACCAGCCTGGCCCCATGAAGGAGTGATAAT 3240
oy Op	3241	CITTGACAATGTGAACTTCATGTACAGTCCAGGTGGGCCTCTGGTACTGAAGCATCTGAC 3300
Qy Db	3301	AGCACTCATTAAATCACAAGAAAAGGTTGGCATTGTGGGAAGAACCGGAGCTGGAAAAAG 3360
Qy Dp	3361	TTCCCTCATCTCAGCCCTTTTTAGATTGTCAGAACCCGAAGGTAAAATTTGGATTGATAA 3420
Qy Db	3421	GATCTTGACAACTGAAATTGGACTTCACGATTTAAGGAAGAAATGTCAATCATACCTCA 3480
. Q3	3481 3551	54
Qy	3541	r 36 l 36
Qy Dp	3601	CARTITAGEGETGGACAAG 3
QY	3661	ACAACTIGGTGCCTTGCCAGGGCAATTCTCAGGAAAATCAGATATTGATTATTGATGA 3720
Qy	3721 3791	AGCGACGGCAAATGTGGATCCAAGAACTGATGAGTTAATACAAAAAAAA
oy da	3781 3850	ATTIGCCCACTGCACCGTGCTAACCATTGCACAGATTGAACACCATTATTGACAGCGA 3840
oy.	3841	CAAGATAATGGTTTTAGATTCAGGAAGACTGAAAGAATATGATGAGCCGFATGTTTGCT 3900
Qy Db	3901	GCAAAATAAAGAGCCTATTTACAAGATGGTGCAACAACTGGGCAAGGCAGAAGCCGC 3960
Qy	3961	STATACTTCAAAAAAATTATCCACATATTGGTCA 402

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        selecting a composition for inhibiting prostate cancer in a patient; assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastasized in a patient, assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytostatic; carcinogen; pharmacodyanamic marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                         4140
                                                                                                                      4150 GACAGCACTGTGAATCCAAAAATGTCAAGTCCGTTCCGAAGGCATTTGCCACTAGTT 4209
                                                                                                                                                                               TITGGACTATGTAAACCACATTGTACTTTTTTTACTTTGGCAACAAATATTTATACATA 4200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer
4030 TGCCCTCACTGAAACAGCAAAACAGGTATACTTCAAAAAGAAATTATCCACATATTGGTCA
                                                            CACTGACCACATGGTTACAAACACTTCCAATGGACAGCCCTCGACCTTAACTATTTTCGA
                                                                                                      GACAGCACTGTGAATCCAACCAAATGTCAAGTCCGTTCCGAAGGCATTTTCCACTAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                          expression marker cDNA 20660
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                                                                                                                                                                                                                       Claim 1; Page 3388; 11750pp; English
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2000US-189862P.
2000US-207454P.
2000US-211314P.
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2000US-255281P.
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pharmacogenomic
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25-MAY-2000;
09-JUN-2000;
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13-DEC-2000;
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RESULT 7 ABV20669

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(I) is also useful as a pharmacodyanamic or pharmacogenomic
                              Sequence 4515 BP; 1253 A; 942 C; 1059 G; 1261 T; 0 other;
                                                                                      4; Indels
                                                                        Pred. No. 0;
0; Mismatches
                                                            Score 4196.6;
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2041 CACTAAGGA 2118 CCTTGAAAC 2101 CCTTGAAAG 2178 AGGAGAACC 111111111111111111111111111111	2221 GTGCTCACT 2229 AÄGTGCTTC 2291 ATGTGCTTC 2281 ATGTGCTTC 2358 CTGTAAATG 1111111111111111111111111111111	2418 ATTCAGGTT 2401 ATTCAGGTT 2478 ACGTCCTTG 2461 ACGTCTTG 2538 CTCCGTAT 2521 CTCCGGTAT	2598 ACATTGGAC 2581 ACATTGGAC 2658 TACAAGTGG 2641 TACAAGTGG 2718 TGGTTCCCC 2701 MCGTTCCCC		2957 TTCGCCGTC 2941 TTCGCCGTC 3017 CTGATTCTG 3001 CTGATTCTG 3001 CTGATTCTG 3001 ACGCTCATG 3061 ACGCTCATG 3061 ACGCTCATG
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CCGTCTGGATGCCATCTGTGCCATGTTTGTCATCATCGTTCCCTTTGGGTCC 3016 GGGGALGTTTCAGTGGTGTTCGACAAAGTGCTGAAGTTGAGAATATGATG 3136 AGAAAGGGTCATTGAATACACAGACCTTGAAAAAGAAGCACCTTGGGAATAT 3196 CGTTCTGAAGGAAAGTTGGTTTTCAGGCCTATAAGAATTACTTCAGAGCTG TGGATTGTCTTCATTTTCCTTATTCTCCTAAACACTGCAGGTCAGGTTGCCT GTTGGTGTGTCTCTGTGGCTGTGGCCGTGATTCCTTGGATCGCAATACCCT NGATGGTGCTCTGGAGGGCCAAGATACAGAGAATGTCCCCAGTTACACTATCAG GTTAACTCTTCACAAACTTTGCACAACAAAATGTTTGAGTCAATTCTGAAAG CACTIGGATGATTTGCTGCCGCTGACGTTTTTAGATTTCATCCAGACATTGC GCAGGATTTACATTCAGAGGCTTGGTTCTTGTTTTTGACAACGTCCCGCTGG CTCTGGACCATCCGGGCATACAAAGCAGAAGAGAGGTGTCAGGAACTGTTTG SGCAAAAACTCTGGATGCCGGGCAGGTTGGTTTGGCACTGTCCTATGCCCTC -CAGGATITIACATICAGAGGCTIGGTICTIGITITIGACAACGICCCGCTGG

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comprising of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated nucleic acid molecule (I) comprisis a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate call carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120
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                                                                                                                                                                                                    Human prostate expression marker cDNA 22401
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                                                                                                                                                                                                                                                           cytostatic;
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Matches 4210; Conservative
                                                                                                                                                                                                                                                           Human; prostate cancer;
pharmacogenomic marker;
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25-MAY-2000;
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CATGGAAGAATTGCCTATGTGTCTCAGCAGCCCTGGGTGTTCTCGGGAA SCCATTGAGAGGGTGTCAGAGGCAATCGTCAGCATCCGAAGAATCCAGA CTTGATGAGATATCACAGCGCAACCGTCAGCTGCCGTCAGATGGTAAAA STGCAGGATTTTACTGCTTTTTGGGATAAGGCATCAGAGACCCCAACTC | CCTTTACTGTCAGACCTGGCGAATTGTTAGCTGTGGTCGGCCCCGTGG GTACCTTCTCAGAGTCTTCGGTTTGGTCTCAACAATCTTCTAGACCCT ATGCTGACATCTATCTCCTGGACGATCCTCTCAGTGCAGTAGATGCGG ACTIGITCGAACTGTGTATTTGTCAAATTTTGCATGAGAAGATCACAA **ATCAGTTGCAGTACCTCAAAGCTGCAAGTCAGATTCTGATATTGAAAG** TGCAGAAGGGGACTTACACTGAGTTCCTAAAAATCTGGTATAGATTTTG GTGCTCTGGAGAGCCAAGATACAGAGAATGTCCCAGTTACACTATCAG CTGAAGGAAAAGTTGGTTTTCAGGCCTATAAGAATTACTTCAGAGCTG TTGTCTTCATTTTCCTTATTCTCCTAAACACTGCAGCTCAGGTTGCCT ATTGGTGCCTTTCATACTGGGCAAACAAACAAAGTATGCTAAATGTCA

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CTGTAA CTGTAA	ATTCAG ATTCAG	ACGTCC ACGTCC	CTCCGG' CTCCGG'	ACATTG	7 - 7	TGGTT TGGTT	ATGT ATGT	TCCAG 	ATGCACA(TTCGCC	CTGATT CTGATT	ACGCTC 	ATCTCAGTZ ATCTCAGTZ	CAGAAACGCC	TTCATG TTCATG	CAAGAAAAGO	CTTTTTAC CTTTTTAC
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cancer; cytostatic; carcinogen; pharmacodyanamic marker;
marker; gene; ss.
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pharmacogenomic marker;
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                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                          tate of
useful
                                                                                                                                                                                                                                                                                                                     a patient;
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cer in a
                                                                                                                                                                                                                                                                                     cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer
                                                                                                                                                                                                                                                                                                                 (e) selecting a composition for inhibiting prostate cancer in a patien(f) assessing the prostate cell carcinogenic potential of a compound;(g) determining whether prostate cancer has metastasized in a patient.(h) assessing the aggressiveness or indolence of prostate cancer in a
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                                                                                                                                                                                                                                                                                                                                                                                   0 other;
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13-DEC-2000;
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CC The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABW00010-ABW62213) of the specification or its complement. (I) is useful for:

CC (a) assessing whether a patient is afflicted with prostate cancer;

CC (b) monitoring the progression of prostate cancer in a patient;

CC (c) assessing the efficacy of a test compound to inhibit prostate

CC cancer in a patient;

CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer

CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer

CC (d) assessing the prostate cell carcinomatic contexts assessing the prostate cancer

CC (f) assessing the prostate cell carcinomatic contexts as a context cell carcinomatic context cancer context cancer context cancer context cancer context cancer context cancer cancer context cancer context cancer context cancer context cancer context cancer c
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        with cancerous state of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid molecule (I) comprisis a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient, is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
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qq	QQ QD	Qy Db	Qy	Qy	Qy Bp	O _Y	Qy Dp	Qy	QY Dp	Oy QO	Qy	Qy	oy Ob	Oy da	Q _Y	Oy Dp	Qy	δy
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  TGCCAGAAGACCGCTCACAGCACCTTGGAGAGGGGTTGCAAGGGTTCTGGGATAAAGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV001010-ABV62213) of the specification or its complement. (I) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer;

(b) monitoring the progression of prostate cancer in a patient;

(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate cell carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (d) assessing the efficacy of a therapy for inhibiting prostate cancer
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                                                                                                                                                          carcinogen; pharmacodyanamic
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nilarity 99.9%; Pred. No. 0;
Conservative 0; Mismatches
                                                                                                                                  prostate expression marker cDNA 28215
                                                                                                                                                                                                                                                                                                                                                                              (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 5861-5862; 11750pp; English.
                                                                                                                                                         Human; prostate cancer; cytostatic;
pharmacogenomic marker; gene; ss.
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                                                            CDNA; 4515
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4201 TTGAATATTTCTCCC
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                                                            standard;
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Matches 4210; Conserv
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25-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                        13-DEC-2000;
                                                                                                                                                                                                                                                                                           17-FEB-2000;
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                                                                                                          16-SEP-2002
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                                                                                                                                                                                                                                           23-AUG-2001
                                                           ABV28224
                                                                                  ABV28224;
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                                                                                                                                 Human
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                                    RESULT 12
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	TTCCCCTCAGCCATTGAGAGGGTGTCAGAGGCAATCGTCAGCATCCGAAGAATCCAGA 1260	CCTTTTTGCTACTTGATGAGATATCACAGCGCAACCGTCAGCTGCCGTCAGATGGTAAAA 1337 	13	TACAAGGCCTTTCCTTTACTGTCAGACCTGGCGAATTGTTAGCTGTGGTCGCCCCGTGG 1457 	+ ~ ,	15	TGAGGAGTAATATTTATTTGGGAAGAAATATGAAAGGAACGATATGAAAAGGCA 1550 TGAGGAGTAATATTTATTTGGGAAGAAATATGAAAAGGAACGATATGAAAAGGTCA 1637 TGAGGAGTAATATTTTTTTTTTTTTTTTTTTTTTTTTT	SCTTGTGCTCTGAAAAAGGATTTACAGCTGTTGGAGGATGGTGATCTGACTGTGATGTGATGTGACTGTGAGTGA	CTTGCAAGAG 175 	TCCTGGACGATCCTCAGTGCAGTAGATGCGG 181	PAAATTTTGCATGAGAAGATCACAA 18 	19	199	CAGGAACTCCCA 205	211	217	22	229.	23
	I I	1278 CC 	1338 AG 1321 AG	1398 TAC 1381 TAC			0-0		1698 TAG 1681 TAG	1758 CAG 1741 CAG	1818 AAG 1801 AAG	1878 TTT 	1938 ATG 1921 ATG	1998 GCT 1981 GCT	2058 CAC 2041 CAC	0-0	2178 AGG 2161 AGG	2238 GTG 2221 GTG	2298 ATG
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        GTGCTAACCATTGCACACAGATTGAACACCATTATTGACAGCGACAAGATAATGGTTTTA
                                                                                                                                                                                                                        CTATTTTACAAGATGGTGCAACAACTGGGCAAGGCCGCAGAGCCGCTGCTCACTGAAACA
                                   ACTGGAACAATGAGGAAAAACCTGGATCCCTTTAAGGAGCACACGGATGAGGAACTGTGG
                                                                      AATGCCTTACAAGAGGTACAACTTAAAGAAACCATTGAAGATCTTCCTGGTAAAATGGAT
                                                                                                        ACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGGACAAAGACAACTGGTGTGCCTT
                                                                                                                                           GCCAGGGCAATTCTCAGGAAAAATCAGATATTGATTATTGATGAAGCGACGGCAAATGTG
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                                                                                                                                                                                                                                                                                                     CTATTTTACAAGATGGTGCAACAACTGGGCAAGGCCAGAAGCCGCTGCCTCACTGAAACA
                                                                                                                                                                            GATCCAAGAACTGATGAGTTAATACAAAAAAAAATCCGGGAGAAATTTGCCCACTGCACC
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Detecting a prostate cancer-associated transcript in a cell in a patient, useful for diagnosing prostate cancer (PC) or screening modulators of PC, by determining if prostate cancer-associated genes are expressed in a prostate tissue

Claim 22; Page 316; 436pp; English

The

P, Hevezi

Ď, Afar

Wilson KE,

Gish KC, Mack DH, WPI; 2002-471335/50. P-PSDB; ABG61820

(EOSB-) EOS BIOTECHNOLOGY INC

2001US-288589P

04-MAY-2001;

08-DEC-2000; 20000S-0733288 08-DEC-2000; 20000S-0733742. 24-JAN-2001; 20010S-05357P. 16-MAR-2001; 2001US-276791P. 16-MAR-2001; 2001US-276888P. 06-APR-2001; 2001US-281922P. 24-APR-2001; 2001US-281922P. 30-APR-2001; 2001US-26514P.

2001WO-US32045 2000US-0687576 2000US-0733288

12-OCT-2001;

18-APR-2002

WO200230268-A2.

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                                                                                                                                                                                                                                                                                                                                                                                                                                   concer-associated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with prostate cancer-associated polynucleotides (designated PC genes) that selectively hybridise to a sequence that is at least 80% identical to them. The prostate cancer-associated polynucleotide sequences are differentially expressed in prostate tumour tissue or in prostate cancer and are derived from the tissues of various organisms such as humans or other mammals (e.g. mice, sheep and dogs). The methods of the invention are useful for diagnosing and treating prostate cancer in mammals. The prostate cancer, as well as for identifying modulators of prostate cancer or agents that inhibit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABK92115-ABK92263 represent prostate cancer-associated polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prostate cancer. The nucleic acid sequences are particularly useful in gene therapy, as a vaccine or in antisense applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176 CGCGTGTTCTTCTGGTGGCTCAATCCCTTGTTTAAAATTGGCCATAAACGGAGATTAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAAGATGATATGTATTCAGTGCTGCCAGAAGACCGCTCACAGCACCTTGGAGAGGAGTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                          present invention relates to methods of detecting a prostate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3978 BP; 1113 A; 817 C; 956 G; 1092 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 93.9%; Score 3973.2;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3975; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sednences.
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cytostatic;

mammal;

prostate tumour tissue; human;

gene therapy; gene; cancer;

Mammalia

Prostate

Prostate cancer-associated DNA sequence #21

(first entry)

15-AUG-2002 ABK92135;

ABK92135 standard; DNA; 3978 BP

RESULT 13 ABK92135

CAAGAGCAAT
ATTGAGGAAAGTGCCAAAGTAATCCAGCCCATATTTTTGGGAAAAATTATTAATTA
SAAAATTATGATCCCATGGATTCTGTGGCTTTGAACACAGGGTACGCCTATGCCAGGT(
CTGACTTITTGCACGCTCATTTGGCTATACTGCATCACTTATATTTTATA
GTGCTGGGATGAGGTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGT
CTTAGTAACATGGCCATGGGGAAGACAACCACAGGCCAGATAGTCAATCTGCTGTCCAAT
GATGTGAACAAGTTTGATCAGGTGACAGTGTTCTTACACTTCCTGTGGGCAGGACGACG
CAGGCGATCGCAGTGACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCTTGCTGGG
ATGGCAGTICTAATCATTCTCCTGCCCTTGCAAACTGTTTTGGGAAGTT(
CTGAGGAGTAAAACTGCAACTTTC
ACTGGTATAAGGATAATAAAATGTACGCCTGGGAAAAGTCATTTTCAAATCTTATTACC
aatttgagaaagaaggatttccaagattctgagaagttcctgcctcagggggatgat
TTGCCTTCGTTTTCAGTCCAAGCAAAATCATCGTGTTTGTGACCTT
CTCCTCGGCAGTGTGATCACAGCCAGCGGGTGTTCGTGGCAGTGACG
GTGCGGCTGACGGTTACCCTTTCTTCCCCT(
GTCAGCATCCGAAGAATCCAGACCTTTTTGCTACTTGATGAGATATCACAGCG
CAGCTGCCGTCAGATGGTAAAAGATGGTGCATGTGCAGGATTTTACTGCT"
AAGGCATCACAGACCCCCAACTCTACAAGGCCTTTCCTTTACTGTCAGACCTGGCGGAATTG
TTAGCTGTGGTCGGCCCCGTGGGACAGGGAAGTCATCACTGTTAAGTGCCGTGGTCGG

Qy Db	1496	GAATTGGCCCCAAGTCACGGCTGGTCAGCGTGCATGGAAGAATTGCCTATGTGTCTCAG 1555	
Q _Y Db	1556	CAGCCCTGGGTGTTCTCGGGAACTCTGAGGAGTAATATTTTATTTGGGAAGAAATATGA 1615 	
QV	. 1616	AAAGTCATAAAGGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTG 167 	
QY	1676	SGATGGTGATCTGACTGTGATAGGAGATCGGGGAACCACGCTGAGTGGAGGGCAGAAA 173	
qq	1561		
0y	1736	~	
G Å	79	CTOTCAGTGCAGTAGACCATTAGAGAGAGATGCTGACATCTATCT	
· 6	9	CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTGTTTTTTGTCAA 1740	
δy	1856	TTTTGCATGAGAAGATCACAATTTTAGTGACTCATCAGTTGCAGTACCTCAAAGCTGCA 191	
qq		TTTGCATGAGAAGATCACAATTTTAGTGACTCAGTTGCAGTACCTCAAAGCTGCA 180	
Š Š		97	
3 (0 0	icavaitutgatattgaaagatggtaaaatggtgcagaaggggacttacactgagttc 186	
Oy Db	1976		
Qy	2036	CTCCAGTTCCAGGAACTCCCACACATAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG 209	
qq	1921	98	
Οy	0	ß	
qq	1981	CTCAACAATCTTCTAGACCCTCCTTGAAAGATGGTGCTCTGGAGAGCCAAGATACAGAG 204	
ΟÝ	2156	TTCTGAAGGAAAGTTGGTTTTCAGGCC 221	
qa	2041	ATGTCCCAGTTACACTATCAGAGGAGAACCGTTCTGAAGGAAAAGTTGGTTTTCAGGCC 210	
Qy	21	TATAAGAATTACTTCAGAGCTGGTGCTCACTGGATTGTCTTCATTTTCCTTATTCTCCTA 2275	
අු	10	aagaattacttcagagctggtgctcactggattgtcttcattttccttattctcta 216	
Qy	27	GGTGGCTTTCATACTGGGCAAAC 233	
අ	2161	ACTGCAGCTCAGGTTGCCTATGTGCTTCAAGATTGGTGGCTTTCATACTGGGCAAAC 222	
Óγ	2336	CACTGTAAATGGAGGAGAAATGTAACCGAGAAGCTAGAT 239	
οp	2221	CAAAGTATGCTAAATGTCACTGTAAATGGAGGAAATGTAACCGAGAAGCTAGAT 228	
ΟŸ	2396	TAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTGGCATA 245	
qq	2281	PACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTGGCATA 234	
ΟŊ	2456	TCACAAACTTTGCACAACAAA 251	
Q	2341	CAAGATCTCTATTGGTATTCTACGTCCTTGTTAACTCTTCACAAAACTTTGCACAACAAA 240	
ο _γ	51	ATGTTTGAGTCAATTCTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGA 2575	
<u>අ</u>	2401	TGTTTGAGTCAATTCTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAG	

3541 3716 3601 3776 3661	21 21 31 56		RESULT 14 AAS63922 ID AAS63922 standard; cDNA; 6140 BP. XX AC AC AC AC AS63922; XX XX XX XX AC XX	DE Human prostate cDNA sequence #439 XX XX XX OS Homo sapiens. XX YX	04-OCT-2001. 27-MAR-2001; 27-MAR-2000; 09-MAY-2000; 13-MAY-2000; 13-JMAY-2000;	PR 27-JUN-2000; 2000US-0605783. PR 10-AUG-2000; 2000US-06316215. PR 29-AUG-2000; 2000US-0651236. PR 06-SEP-2000; 2000US-0657279. PR 02-OCT-2000; 2000US-0669426. XX PA (CORI-) CORIXA CORP. XX	PI Xu J, Dillon DC, Mitcham JL, He Fanger GR, Retter WW, Stolk JA, PI Li SX, Wang A, Skeiky YAW, Hepi XX WPI; 2001-639232/73. DR WPI; 2001-639232/73. DR P-PSDB; AAU69824. XX P-PSDB; PAU69824.
2576 2461 2636 2521 2696 2581	2756 TATTTTTGGAAACGTCAAGAGATGTGAAGCGCCTGGAATCTACAACTCGGAGTCCAGTG 281 [11] [1] [1] [1] [1] [1] [1] [1] [1] [1]		3056 TTGGCACTGTCCTAT [11111111111] 2941 TTGGCACTGTCCTAT 3116 GCTGAAGTTGAGAAT [111111111]	3176 AAAGAAGCACCTTGGGAATATCAGAAACGCCCACCAGCCTGGCCCCATGAAGGAGTG 3235	3296 CTGACAGCACTCATTAAATCACAAGAAAAGGTTGGCATGTGGGAAGAACCGGAGCTGGA 335 11111111111111111111111111111111111	3416 GATAAGANCTTGACAA 	1421 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
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peptides and polynucleotides useful for
                     AACCATTGCACACAGATTGAACACCATTATTGAC 3835
                                                                                 ACTTCCAATGGACAGCCCTCGACCTTAACTATT 4075
Kalos MD;
Carter D;
                                                                                                                                                                                                                                                                                                                        static; immunostimulant; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Harlocker SL, Jiang Y,
A, Day CH, Vedvick TS,
Ppler WT, Henderson RA;
                                                                                                                                                                                                                                                                                                        6
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The invention relates to isolated prostate-specific polypeptides, pulpoptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides (or antigenic epitopes antibodies raised against the polypeptides (or antigenic epitopes derived from them) and antigen-presenting cells expressing the polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polynucleotides and the antigen-presenting cells are useful for stimulating and/or expanding of cancer especially prostate cancer. Compositions comprising the polynucleotide and/or polypeptide are useful for stimulating an immune response, and for treating cancer. The oligonucleotide is useful for polynucleotide of the invention. cancer prostate especially cancer, English. οţ Page 412-414; 579pp; and Claim

Sequence 6140 BP; 1737 A; 1260 C; 1353 G; 1780 T; 10 other;

ä 248 292 308 352 368 412 428 472 488 532 548 899 592 608 652 712 728 772 788 832 848 908 896 Gaps TGACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCTTGCTGGGATGGCAGTTCTAA 892 TTGATCAGGTGACAGTGTTCTTACACTTCCTGTGGGCAGGACCACTGCAGGCGATCGCAG ATAAAGAAGTTTTAAGAGCTGAGAATGACGCACAGAAGCCTTCTTTAACAAGAGCAATCA TAAAGTGTTACTGGAAATCTTATTTAGTTTTTGGGAATTTTTACGTTAATTGAGGAAAGTG CCATGGATTCTGTGGCTTTGAACACAGGGTACGCCTATGCCACGGTGCTGTTTTGCA CGCTCATITIGGCTATACTGCATCACTTATATTTTATCACGTTCAGTGTGCTGGGATGA CCATGGGGAAGACAACCACAGGCCAGATAGTCAATCTGCTGTCCAATGATGTGAACAAGT TGACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCTTGCTGGGATGGCAGTTCTAA Length 6140; Indels 22; <u>ب</u> DB Score 3910.2; Pred. No. 0; 0; Mismatches 92.4%; ilarity 97.1%; Conservative 0 ery Match st Local Similarity tches 4040; Conserv 309 353 369 413 429 473 489 533 549 593 713 773 789 606 609 653 699 729 833 893 Query Best Match ò qq ŏ qq ö qq ò g ò DP ద δ g g . q ò ò ٥y 셤 οy οy g g Q ò

1088 1208 1388 1432 1448 1508 1552 1612 1628 1672 1808 1852 1928 1972 TAATAAAAATGTACGCCTGGGAAAAGTCATTTCAAATCTTATTACCAATTTGAGAAAGA AGGAGATTTCCAAGATTCTGAGAAGTTCCTGCCTCAGGGGGATGAATTTGGCTTCGTTTT TCAGIGCAAGCAAAAICAICGIGITIGIGACCIICACCACCIACGIGCICCICGGCAGIG **ATGGTAAAAAAATGGTGCATGTGCAGGATTTTACTGCTTTTTGGGATAAGGCATCAGAGA** 1373 ATGGTAAAAAGATGGTGCATGTGCAGGATTTAACTGCTTTTTGGGATAAGGCATCAGAGA TTGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCCTGGACGATCCTCTAGTGCAG GCCCCGTGGGAGCAGGGAAGTCATCACTGTTAAGTGCCGTGCTCGGGGAATTGGCCCCAA TCTCGGGAACTCTGAGGAGTAATATTTATTTGGGAAGAAATATGAAAAGGAACGATATG AGATCACAATTTTAGTGACTCATCAGTTGCAGTACCTCAAAGCTGCAAGTCAGATTCTGA GTCACGGGCTGGTCAGCGTGCATGGAAGAATTGCCTATGTGTCTCAGCAGCCCTGGGTGT TATTGAAAGATGGTAAAATGGTGCAGAAGGGGACTTACACTGAGTTCCTAAAATCTGGTA TAGATTTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAAGTGAACAACCTCCAGTTCCAG 1029 1089 1133 696 1389 1433 1449 1493 1553 1569 1733 1793 1509 1613 1629 1673 1689 1749 1809 1853 1869 1913 1929 1973 1989 g Ω QQ ΩD ٥ÿ ŏλ g Óγ QQ à qq Ω q οχ g à Ob Ω qq 9 g δ g qq g δ οy qq ŏ ò g g qq ŏ δ ά

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	209	CTT 2108 CTT 2152	7A 2168 	T 2228 	C 2288 C 2332	234	T 2408 - T 2452	Т 2468 Т 2512	A 2528 - A 2572	т 2588 Т 2632	C 2648 	G 2708 2752	A 2768 	T 2828 T 2872	G 2888 - 2932	T 2948 T 2992	T 3008 3052	306	312	A 3172
	5 ANGALITIGGCICCCTITTAAAGAAGGAATAATGAGGAAAGTGAGGAAAGTGACTCCAGTTCCGGTTCCGGTTCCGGTTCCGGAAAGAAA	9 GARLICCCACACARIGARICGIACCTICITAGAGICTICGGITTGGGICTGACATT 3 GAACTCCCACACATAAGGAAICGTACCTICTCAGAGTCTTCGGTTTGGICTCAACAAT	9 CTAGACCCTCCTTGAAAGATGGTGCTCTGGAGAGCCAAGATACAGAGAATGTCCCAGTTA	9 CACTATCAGAGGAGAACCGTTCTGAAGGAAAGTTGGTTTTCAGGCCTATAAGAATTACT 	TCAGAGCTGGTGCTCACTGGATTGTCTTCATTTTCCTTATTCTCCTAAACACTGCAGCTC	9 AGGTTGCCTATGTGCTTCAAGATTGGTGGCTTTCATACTGGGCAAACAAA	9 TAAATGTCACTGTAAATGGAGGAAATGTAACCGAGAAGGTAGATCTTAACTGGTACT 	9 TAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTTGGCATAGCAAGATCTCTAT	9 IGGIATICTACGICCITGITAACICITCACAAACITIGCACAACAAAAIGITIGAGICAA 	9 TTCTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGAATTTTAAATCGTT	9 TCTCCAAAGACATTGGACTTGGATGATTTGCTGCCGCTGACGTTTTTAGATTTCATCC	9 AGACATTGCTACAAGTGGTTGGTGTGGTCTCTGTGGCTGTGGCCGTGATTCCTTGGATCG	9 CAATACCCTTGGTTCCCCTTGGAATCATTTTCATTTTTCTTCGGCGATATTTTTTGGAA	9 CGTCAAGAGATGTGAAGCGCCTGGAATCTACAACTCGGAGTCCAGTGTTTTCCCACTTGT	9 CATCTTCTCCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAAGAGAGTGTCAGG	9 AACTGTTTGATGCACACCAGGATTTACATTCAGAGGCTTGGTTCTTGTTTTGACAACGT	9 CCCGCTGGTTCGCCGTCCGTCTGGATGCCATCTGTGCCATGTTTGTCATCGTTGCCTTGCTTG	TTGGGTCCCTGATTCTGGCAAAAACTCTGGATGCCGGGCAGGTTGGTT	ATGCCCTCACGCTCATGGGGATGTTTCAGTGGTGTGTTCGACAAAGTGCTGAAGT	3 ATGCCCTCACGCTCATGGGGATGTTTCAGTGGTGTGTTCGACAAAGTGCTGAAGTTGAG
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5	3 8	g S	Qy Db	Qy Dp	Qy Db	Oy Db	OY Db	Qy Db	Oy Dp	Qy Db	O.Y Db	O P D	Oy Db	Oy Db	Qy Db	O Dp	OY Db	. Q	λo	g

QY	3129	ATATGATGATCTCAGTAGAAAGGGTCATTGAATACACAGACCTTGAAAAAGGAACCACCTT
Qy	18	GGGAATATCAGAAACGCCCACCACCAGCCTGGCCCCATGAAGGAGTGATAATCTTTGACA 324
qq	3233	
οy	3249	TCATGTACAGTCCAGGTGGCCTCTGGTACTGAAG
qq	3293	GTGAACTICATGTACAGTCCAGGTGGGCCTCTGGTACTGAAGCATCTGACAGCACTCT
Qy	3309	AAATCACAAGAAAAGGTTGGCATTGTGGGAAGAACCGGAGCTGGAAAAAGTTCCCTCA 3
QQ		TAAATCACAAGAAAAGGTTGGCATTGTGGGAAGAACCGGAGCTGGAAAAAGGTTCCCTCA 341
QY	3369	TCAGCCCTTTTTAGATTGTCAGAACCCGAAGGTAAAATTTGGATTGATAAGATCTTGA 342
Dp	3413	CTCAGCCCTTTTTAGATTGTCAGAACCCGAGGTAAAATTTGGATTGATAAGATCTTGA 3
QY		ACTGAAATTGGACTTCACGATTTAAGGAAAAATGTCAATCATACCTCAGGAACCTG 348
qa		AACTGAAATTGGACTTCACGATTTAAGGAAGAAATGTCAATCATACCTCAGGAACCTG 3
QY		TTGTTCACTGGAACAATGAGGAAAAACCTGGATCCCTTTAAGGAGCACACGGATGAGG 354
qa	3533	TTGTTCACTGGAACAATGAGG
QY	3549	CTGTGGAATGCCTTACAAGAGGTACAACTTAAAGAAACCATTGAAGATCTTCCTGGTA 360
qa		
Οy		IGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGGACAAAGACAACTGG 366
qq	3653	IGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGGACAAAGACAACTGG
ογ	3669	CAGGGCAATTCTCAGGAAAATCAGATATTGATTATTGATGAAGCGACGG 372
qa	3713	GTGCCTTGCCAGGGCAATTCTCAGGAAAAATCAGATATTGATTATTGATGAAGCGACGG 37
Qy		SATGAGTTAATACAAAAAAAATCCGGGAGAAATTTGCCC 378
QQ	3773	TGGATCCAAGAACTGATGAGTTAATACAAAAAAAATCCGGGAGAAATTTGCCC 383
ογ	3789	CCGTGCTAACCATTGCACACAGATTGAACACCATTATTGACAGCGACAAGATAA 384
qq	3833	CTGCACCGTGCTAACCATTGCACACAGATTGAACACCATTATTGACAGCGACAAGATAA 389
QY	3849	TGGTTTTAGATTCAGGAAGACTGAAAGAATATGATGAGCCGTATGTTTGCTGCAAATA 3908
QC C	3893	TGGTTTTAGATTCAGGAAGACTGAAAGAATATGATGAGCCGTATGTTTTGCTGCAAAATA 3952
ÓΥ	3909	AAGAGAGCCTATTTTACAAGATGGTGCAACAACTGGGCAAGGCAGAAGCCGCTGCCCTCA 3968
QQ	3953	AAGAGAGCCTATTTTACAAGATGGTGCAACAACTGGGCAAGGCAGAGAGCCGCTGCCTCA 4012
Qy	3969	CTGAAACAGCAAAACAG 3985
qq	4013	CTGAAACAGCAAAACAGGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTCAAACTCCT 4072
Qy	3986	3982
qa	4073	GACCTCAAGTGATCCACCTGCCTTGGCCTCCCAAACTGCTGAGATTACAGGTGTGAGCCA 4132
QY	3986	GIATACTTCABAAGAAATTATCCACATATTGGTCACACAGACAC 4030
qa	4133	133 CCACGCCCAGCCTGAGTATACTTCAAAAGAAATTATCCACATATTGGTCACACTGACCAC 4192
Qy	4031	ATGGTTACAAACACTTCCAATGGACAGCCCTCGACCTTAACTATTTTCGAGACAGCACTG 4090
qa	4193	GGTTACAAACACTTCCAATGGACAGCCCTCGACCTTAACTATTTTCGAGACAGCACG 42

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292

GGTGGCTCAATCCCTTGTTTAAAATTGGCCATAAACGGAGATTAGAGGAAGATGATATGT

233 249 293 309

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ATTCAGTGCTGCCAGAAGACCGCTCACAGCACCTTGGAGAGGAGTTGCAAGGGTTCTGGG

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The present invention describes polynucleotide sequences (I) which encode prostate-specific proteins (II). (I) and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. (I), (II), antibodies to (II), fusion proteins comprising (II), and isolated T cells prepared using (I) or (II) are used treat cancer in a patient. In a matchodies are also used in the detection of cancer in a patient. The cancer that is diagnosed or treated is particularly prostate cancer. (I) and (II) can be used in vaccines. The antibodies or (I) can be used for monitoring the progression of cancer in a patient. (I) and (II) can also be used to improve diagnostic and therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    methods for prostate cancer. They can indicate the level of metastasis as well as the prostate volume. AAH93357 to AAH93944 and AAM01115 to AAM01318 represent polynucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and
               TGAATCCAACCAAAATGTCAAGTCCGTTCCGAAGGCATTTTCCACTAGTTTTTGGACTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ייסי pulynucleotide encoding a prostate-specific protein, diagnosing, monitoring and treating prostate cancer in a for use in vaccines -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SL, Jiang Y,
                                                                                                                                                                                                                                                                                                                                                cancer; prostate-specific; diagnosis;
therapy; metastasis; ss.
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Retter MW,
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Kalos MD, Fanger GR, Day
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cytostatic; gene
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llarity 97.1%; Conservative

Similarity

Best Local Sim Matches 4040;

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Query Match

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Searched:	2054640 segs, 14551402878 residues
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Listing first 45 summaries

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Lee, K., Belinsky, M.G., Bell, D.W., Testa, J.R. and Kruh, G.D. Isolation of MoAr-B, a widely expressed multidrug resistance-associated protein/canalicular multispecific organic cancer Res. 58 (13), 2741-2747 (1998)
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Direct Submission
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                   /organism="Homo sapiens"
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1 GAGAAAGAAGGAGATTTCCAAGATTCTGAGAAGTTCCTGCCTCAG	1 TTCGTTTTTCAGTGCAAGAAATCATCGTGTTTGTGACCTTCAC	GGGCAGTGTGATCACAGCCAGCCGCGTGTTCGT 	GCIGACGGTTACCCTCTTCCTCCCCTCAGCCATTGAGAGGGTGT 	CATCCGAAGAATCCAGACCTTTTGCTACTTGATGAGATATCACAGGGCAACGGTCAGCT	GCCGTCAGATGGTAAAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTTGGGATAAGGC 	ATCAGAGACCCCAACTCTACAAGGCCTTTCCTTTACTGTCAGACCTGGCGAATTGTTAGC 	TGTGGTCGCCCCGTGGGAGCAGGGAAGTCATCACTGTTAAGTGCCGTGCTCGGGGAATT 	GGCCCCAAGTCACGGGCTGGTCAGCGTGCATGGAAGAATTGCCTATGTGTGT	CIGGGIGITCICGGGAACICTGAGGAGIAATATITIATITGGGAAGAATATGAAAGGA 	acgatatgaaaagtcataaggcttgtgctctgaaaaaggattacagct 	TGGTGATCTGACTGTGATAGGAGATCGGGGAACCACGCTGAGTGGAGGGCAGAAAGCACG 	GGTAAACCTTGCAAGAGCAGTGTATCAAGATGCTGACATCTATCT	CAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTT	GCATGAGAAGATCACAATTTTAGTGACTCATCAGTTGCAGTACCTC	GATTCTGATATTGAAAGATGGTAAAATGGTGCAGAAGGGGACTTACACTGAGTTCCTAAA 	ATCTGGTATAGATTTTGGCTCCCTTTAAAGAAGGATAATGAGGAAAGTGAACAACCTCC	AGTICCAGGAACTCCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGT"	ACAATCTTCTAGACCCTCCTTGAAAGATGGTGCTCTGGAGAGCCAAGATACAGAGAATGT
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Reed,S.G., Kalos,M.D., Retter,M.W., Stolk
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Compositions and methods for the therapy
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Qy	2581 2651	AAATCGTTTCTCCAAAGACATTGGACACTTGGATGATTTGCTGCCGCTGACGTTTTTAGA 2640 	
Qy	2641	TITCATCCAGACATIGCTACAAGIGGTIGGIGIGICTCTGIGGCTGIGGCCGIGATICC 2700 	
Qy Db	2701 2771	TTGSATCGCAATACCCTTGGTTCCCCTTGGAATCATTTTTCATTTTCTTCGGCGATATTT 2760 	
Qy Dp	2761	TTTGGAAACGTCAAGAGATGTGAAGCGCCTGGAATCTACAACTCGGAGTCCAGTGTTTTC 2820 	
Qy Db	2821	CCACTTGTCATCTTCTCTCCAGGGGTTCTGGACCATCCGGGGTACAAAGCAGAAGAGAG 2880 	
δλ	2881	GTGTCAGGAACTGTTTGATGCACACCAGGATTTACATTCAGAGGCTTGGTTCTTGTTTT 2940	

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	 951 G	941	001 C 071 C	061 A 131 A	121 A 	181 # 251 #	241 311	301 P	361 TT 431 TT	421	481 G 1 551 G	541 GG 611 GG	601 T 671 T	661	721 #	781 850	841 910	901 GC 1 970 GC

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                                                                                                                                                                                                                                                                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 6082)
4030 TGCCCTCACTGAAACAGCAAAACAGGTATACTTCAAAAGAAATTATCCACATATTGGTCA 4089
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Pred. No. 0;
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qa	da aa	da Bb	QY	Sy da	Qy Dp	da Db	Qy Dp	QY	QY Db	QY	QY	Qy Bb	Qy Db	Qy Dp	Qy Dp	Qy Db	QY Dp	Oy
TGGGAATTTTACGTTAATTGA 420 	AAATTATTAATTTTGAAAA 480 	ACGCTATGCCACGGTGCTGAC 540	ATTTTATCACGTTCAGTGTCC 600	99			NATCGTGCCTTGCTGGGATGGC	3GAAGTTGTTCTCATCACTGAG 900	CCATGAATGAAGTTATAACTGG 960	TTTCAAATCTTATTACCAATTT 1020 	CCTCAGGGGATGAATTTGGC 1080	CCTCACCACCTACGTGCTCCT 1140		GGTGTCAGAGCAATCGTCAG 1260	ATCACAGCGCAACCGTCAGCT 1320 			AAGTGCCGTGCTCGGGGAATT 1500
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.1630 ATTGAAAGATGGTAAAATGGTGCAGAAGGGGACTTACACTGAGTTCCTAAA 1980 GATCACAATTTTAGTGACTCATCAGTTGCAGTACCTCAAAGCTGCAAGTCA TGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCCTGGACGATCCTCT AGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAAATTTT PAGAGCTGGTGCTCACTGGATTGTCTTCATTTTCCTTATTCTCCTAAACAC **AATGTCACTGTAAATGGAGGAGGAAATGTAACCGAGAAGCTAGATCTTAA** GGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTGGCATAGCAAG CTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGAATTT

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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T.
and Henderson,R.A.
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Catarrhini; Hominidae; Homo.
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3490 3430 3420 3480 3550 3610 3600 3670 3660 3720 3790 3780 3849 3840 3909 3900 3960 4029 4020 4089 4080 4140 3969 GATCTTGACAACTGAAATTGGACTTCACGATTTAAGGAAGAAAATGTCAATCATACCTCA TCCTGGTAAAATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGGACAAAG GACAGCACTGTGAATCCAAAAATGTCAAGTCCGTTCCGAAGGCATTTTCCACTAGTT TTCCCTCATCTCAGCCCTTTTTAGATTGTCAGAACCCGAAGGTAAAATTTGGATTGATAA **ACAACTGGTGTGCCTTGCCAGGGCAATTCTCAGGAAAAATCAGATATTGATTATTGATGA** ATTTGCCCACTGCACCGTGCTAACCATTGCACACAGATTGAACACCATTATTGACAGCGA CAAGATAATGGTTTTAGATTCAGGAAGACTGAAAGAATATGATGAGCCGTATGTTTTGCT CACTGACCACATGGTTACAAACACTTCCAATGGACAGCCCTCGACCTTAAACTATTTTCGA 3371 3301 3361 3431 3421 3491 3481 3551 3541 3611 3601 3671 3661 3731 3721 3781 3850 3841 3910 3901 3970 3961 4030 4021 4090 4081 4150 4210 3791 4141 4201 4270 δ QQ δŻ QΩ ò g Qγ qq δ QQ οy g qq δy δy g ò qq q Q g ο̈́ ρy ò Óγ q g οy οy g Ω QQ

RESULT 6
AY081219
LOCUS
DEFINITION

AY081219 5759 bp mRNA linear PRI 01-JUL-2002 HOmo sapiens multidrug resistance-associated protein (ABCC4) mRNA, complete cds.

AY081219 AY081219 GI:21655122

ACCESSION VERSION

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ESAKVIOPIFLGKIINYFENYDDMDSVALNTAYATATVLTFCTLILAIIHHLYFYHVO
CAGMENTRAVAMCHHYTRALRLSNAAMGKTTTGOIVNLLSNDVNKFOTVLGTFTLIE
ESAKVIOPIFLGKIINYFENYDDMDSVALNTAYATATVLTFCTLILAIIHHLYFYHVO
CAGMENTRAVAMCHYTRAIRLSNAAMGKTTTGOIVNLLSNDVNKFOTTFDTTHYNG
PLOAIAVTALLWMEIGISCLAGMAVLIILLELQSCFGKIESSLRSKTATFTDARIRTM
NEVITGIRIIKMYAWEKSFSNLITINEKREISKILRSSCLRGNNLASFFSASKIIVFV
TFTTYVLLGWYTTASKYFVAYUTKGRYTRYTLFFPSAIERYSEAT YSIRRIOFFLLL
DEISORNROLPSDGKKWYHVODFTAFWDKSETPTRGGLSFTVRPGELLAVGFYGGG
KSSLLSAVLGELAPSHGLYIGDRGTTLSGGGRARVNLARAVYDDADIYLLDDPLSAVD
AEVSRHIFFELCICQLHEKITILLYHOLQYTKAASOITLKDGRWYGKTTFFERKSG
IDFGSLLKKNDESEQPPYCOTPTLANTFESSSWASQQSSRPSLKOGALESODTENV
PVTLSBENRSEGKVGFQAXKSYFRAGAHHIVFIFLILLNTAAQVAYVLODWMLSYWAN
KQSMLNYTWOGGONTTGKLDLANTGATTANDER TRUTTENTAAOVAYVLODWMLSYWAN
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RAZKAERROQELFDAHODLEFRAFFLETTSRWFAVRLDGTOMFVITARFGSLILAK

TALDAGQVGLALSYALTLMGWFQWCVRQSEVENMMISVERVIEYTDLEKEAPWEYGK

PPPAMPHEGVITFDNVNFWYSPGGPLVLKHLTALIKSQEKVGIVGRTGAGKSSLISAL

PRLSBPEGKIWIDKILTTEIGHDLKKKMSITPQEPVLETGTWRKNLDPFNEHTDEEL

NNALGBVGLKTIEDLIQKKMDTELAESGSNESVGGQCLVCLARAILKRNQILIIDEAT

ANVDPRTDELLQKK TREKFAHOTTVLTAHRLNTIIDSDKINVLDSGRLKEVDEPYVLL

ONNESLEYKWVQQLGKAEAAALTETAKQVXFRKNYPHIGHTDHMVTNTSNGQPSTLTI
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Adachi,M., Sampath,J., Sun,D. and Schuetz,J.D.
Direct Submission
Submitted (22-FEB-2002) Pharmaceutical Sciences, St. Jude
Children's Research Hospital, 332 North Lauderdale St., N
38105-2794, USA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 5759)
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/protein_id="AaL88745.1"
/db_xref="GI:21655123"
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Matches 4130; Conservative 0
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QQ		AAATGTCACTGTAAATGGAGGAGGAGGAAATGTAACCGAGAAGCTAGATCTTAACTGGTACT 245
QY	2409	AGGAATITATICAGGITTAACIGTAGCIACCGTICITTIGGCAFAGCAAGAICTTTT 246
qq	2453	TAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTTGGCATAGCAAGATCTCTAT 2512
Q <u>y</u>	4 6	GTTAACTCTTCACAAACTTTGCACAACAAAATGTTTGAGTCAA 252
đ	27	GGTATTCTACGTCCTTGTTAACTCTTCACAAACTTTGCACAACAAAATGTTTGAGTCAA
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Οy	2709	CCCCTTGGAATCATTTTCATTTTTCTTCGGCGATATTTTTGGAAA 276
qq	2753	ACCCTTGGTTCCCCTTGGAATCATTTTCTTTCTTCGCGATATTTTTTGGAAA 2
QY	2769	SCCTGGAATCTACAACTCGGAGTCCAGTGTTTTCCCACTTGT 282
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aniata; Vertebrata; Euteleostomi; tarrhini; Hominidae; Homo. , Harlocker,S.L., Jiang,Y., R., Day,C.H., Retter,M.W., and Meagher,M.J. therapy and diagnosis of prostat 2001;	/Organism="Homo sapiens" /db_xref="taxon:9606" BASE COUNT 1737 a 1260 c 1353 g 1780 t 10 others ORIGIN Query Match Best Local Similarity 97.1%; Pred. No. 0; Matches 4040; Conservative 0; Mismatches 3; Indels 118; Gaps	189 233 249 293	Oy 309 ATAAAGAAGTTTTAAGACTGAGAATGACGCACAGAAGCCTTCTTTAACAAGAGCAATCA 368 [Qy 609 GGTTACGAGTAGCCATGTGCCATATGATTATCGGAAGGCACTTCGTCTTAGTAACATGG 668	QY 729 TTGATCAGGTGACAGTGTTCTTACACTTCCTGTGGGCAGGCCACTGCAGGCGATCGCAG 788
QY 3429 CAACTGAAATTGGACTTCACGATTTAAGGAAGAAATGTCAATCATACCTCAGGAACCTG 3488 HIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	3653 3669 3713 3729	3773 CAANGGGATCCAAGAACTGATGAGTTAATACAAAAAAAATCCGGGAGAAATTTGCCC 3789 ACTGCACCGTGCTAACCATTGCACACAGATTGAACACCATTATTGACAGGACAAGATAA 11111111111111111111111111111111	909 909 953 969 013	QY 3986	Db 4193 ATGGTTACAACACTCCAATGGACAGCCTTGACTATTTTTTTT	Db 4313 GTAAACCACATTGTTTTTTTTTTTGGCAACAATATTTATATATA

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                                                                                                                                                                                          CCTTGTTTAAAATTGGCCATAAACGGAGATTAGAGGAAGATGATGT 292
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                                                                                                                                                                                                                 CCATGTGCCATATGATTTATCGGAAGGCACTTCGTCTTAGTAACATGG
                                                                                                                                        3; Indels 118;
                                                                                                                  DB 6; Length 6140;
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O 0151633-A 536 19-JUL-2001;
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                                                                                                               Score 3910.2;
Pred. No. 0;
0; Mismatches
                      Location/Qualifiers
1. 6140
Corganism="Homo sapiens"
Ab_xref="texon:9606"
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DNA

6140 bp Sequence 536 from Patent W00151633. AX200906 AX200906.1 GI:15390773

DEFINITION ACCESSION VERSION KEYWORDS

RESULT 8 AX200906 rocus

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1012	1028 1072	1088 1132	1148 1192	1208 1252	1268 1312	1328 1372	1388 1432	1448 1492	1508 1552	1568 1612	1628 1672	1688 1732	1748 1792	1808 1852	1868 1912	1928 1972	1988 2032	2048 2092
953 CTGCAACTTTCACGGATGCCAGGATCAGGACCATGAATGA	969 TAATAAAAATGTAGGCCTGGGAAAAGTCATTTTCAAATCTTATTACCAATTTGAGAAAGA 	029 AGGAGATTCCAAGATTCTGAGAAGTTCCTGCCTCAGGGGGATGAATTTGGCTTCGTTTT	089 TCAGTGCAAGCAAAATCATCGTGTTTTGTGACCTTCACCACCTACGTGCTCCTCGGCAGTG	149 TGATCACAGCCAGCCGCGTGTTCGTGGCAGTGACGCTGTATGGGGCTGTGCGGCTGACGG	1209 TTACCCTCTTCTCCCCCCTCAGCCATTGAGAGGGTGTCAGAGGCAATCGTCAGCATCCGAA 	1269 GAATCCAGACCTTTTTGCTACTTGATGATATCACAGGGCAACCGTCAGCTGCGTCAG	1329 ATGGTAAAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTTGGGATAAGGCATCAGAGA 	1389 CCCCAACTCTACAAGGCCTTTCCTTTACTGTCAGACCTGGCGAATTGTTAGCTGTGGTCG 	1449 GCCCCGTGGGAGCAGGAAGTCATCACTGTTAAGTGCCCTGCTGGGGAATTGGCCCCAA 	509 GTCACGGGTGGTCAGCGTGCATGGAAGAATTGCCTATGTGTCTCAGCAGCCCTGGGTGT	569 TCTCGGGAACTCTGAGGAGTAATATTTATTTGGGAAGAAATATGAAAAGGAACGATATG 	629 AAAAAGTCATAAAGGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTGGAGGATGGTGATC 	689 TGACTGTGATAGGAGATCGGGGAACCACGCTGAGTGGAGGCCAGAAAGCACGGGTAAACC 	1749 TTGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCCTGGACGATCCTCTGATGCAG 	809 TACATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTGTCAAATTTTGCATGAGA 	869 AGATCACAATTTTAGTGACTCATCAGTTGCAGTACCTCAAAGCTGCAAGTCAGATTCTGA 	929 TATTGAAAGATGGTAAAATGGTGCAGAAGGGACTTACACTGAGTTCCTAAAATCTGGTA 	989 TAGATTTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAAGTGAACACCTCCAGTTCCAG
qa	Qy Dp	Qy Dp	. QQ	Oy Dp	Qy Dp	Oy Db	O.y D.b	Oy Db	oy Dp	Oy 1 Db 1	oy Dp	Qy	Oy Db	O.y	Oy 1 Db 1	Qy 1 Db 1	Qy 1 Db 1	Qy 1 Db 2

Qγ	04	AACTCCCACACTAAGGAATCGTACCTTCTAGAGTCTTCGGTTTGGTCTCAACAATCTT
QQ	2093	GAACTCCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGGTCTCAACAATCTT 2152
Qγ	2109	GCTCTGGAGAGCCAAGATACAGAGAATGTCCCAGTT
QO	2153	TAGACCCTCCTTGAAAGATGGTGCTCTGGAGAGCCAAGATACAGAGAATGTCCCAGTTA 2
οy	16	CGTTCTGAAGGAAAAGTTGGTTTTCAGGCCTATAAGAATTACT
q	2213	actatcagaggagaaccgttctgaaggaaagttggttttcaggcctataagaattact
Qy	2229	TGGATTGTCTTCATTTTCCTTATTCTCCTAAACACTGCAGCTC
QΩ	2273	SAGCTGGTCCTCACTGGATTGTCTTTTTCCTTATTCTCCTAAACACTGCAGCTC
Óγ	2289	TGGTGGCTTTCATACTGGGCAAACAAACAAAGTATGC
QQ	2333	GTTGCCTATGTGCTTCAAGATTGGTGGCCTTTCATACTGGGCAAACAAA
QY	2349	GGAAATGTAACCGAGAGCTAGATCTTAACTGGTACT
qq	2393	STCACTGTAAATGGAGGAGGAATGTAACCGAGAAGCTAGATCTTAACTGGTACT
Qγ	2409	TTATTCAGGTTTAACTGTAGCTACCGTTCTTTTGGCATAGCAAGATCTCTAT
qq	2453	- 10
Óγ	2469	CTACGTCCTTGTTAACTCTTCACAAACTTTGCACAACAAAAATGTTTGAGTCAA
q _a	2513	GGTATTCTACGTCCTTGATTAACTCTTCACAAACTTTGCACAACAAAATGTTTGAGTCAA
Qy	2529	TTCGGTATTATTCTTTGATAGAAATCCAATAGGAAGAATTTTAAATCGT
qq	2573	CTGAAAGCTCCGGTATTTTTTTTTTGATAGAAATCCAATAGGAAGAATTTTAAATCGTT
òγ	2589	3ACATTGGACACTTGGATGATTTGCTGCCGCTGACGTTTTTAGATTTCATCC
qq	2633	CTCCAAAGACATTGGACACTTGGATGATTTGCTGCCGCTGACGTTTTTAGATTTCATCC
Qγ	2649	SCTACAAGTGGTTGGTGTGTCTCTGTGGCTGTGGCCGTGATTCCTTGGATCG
qq	2693	CATTECTACAAGTGGTTGGTGGTCTCTGTGGCTGTGGCCGTGATTCCTTGGATCG
Qy	2709	CTTGGTTCCCCTTGGAATCATTTTCATTTTTCTTCGGCGATATTTTTGGAAA
QQ	2753	CONTROLL CONTROLL
Qγ	2769	GAGATGTGAAGCGCCTGGAATCTACAACTCGGAGTCCAGTGTTTTCCCACTTGT
qa	2813	STCAAGAGATGTGAAGCGCCTGGAATCTACAACTCGGAGTCCAGTGTTTTCCCACTTGT
Óγ	2829	CTCTCCAGGÉGCTCTGGACCATCCGGGCATACAAAGCAGAAGAGGGGGTGTCAGG
qq	œ	ATCTTCTCTCCAGGGGCTCTGGGACCATCCGGGCATACAAAGCAGAAGAGAGGTGTCAGG
ΟŊ	2889	TTGATGCACACCAGGATTTACATTCAGAGGCTTGGTTCTTGTTTTTGACAACGT
В	, 2933	TGTTTGATGCACACCAGGATTACATTCAGAGGCTTGGTTCTTGTTTTGACAACGT
δŏ	2949	CGTCCGTCTGGATGCCATGTGTGTGTTGTCATCATCGTTGCCT
qa	2993	CGGCTGGTTCGCCGTCCGGTCTGGATGCCATCTGTGCCATGTTTGTCATCGTTGCCT 30
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යු	'n	GGGTCCCTGATTCTGGCAAAAACTCTGGATGCCGGGCAGGTTGGTT
δλ	9	ATGCCCTCACGCTCATGGGGATGTTCAGTGGTGTGTTCCACAAAGTGCTGAAGTTGAGA 3128
qq	3113	SCCCTCACGCTCATGGGGATGTTTCAGTGGTGTTCGACAAAGTGCTGAAGTTGAGA 31

Db 4253 TGAAT Qy 4151 GTAAA Qy 4313 GTAAA Qy 4211 GTTCA Db 4373 GTTCA	RESULT 9 AX267562 LOCUS LOCUS DEFINITION SEG ACCESSION AX2	KEYWORDS SOURCE hum ORGANISM HOM ORGANISM HOM RAM MAM REFERENCE 1 AUTHORS XU,	and TITLE Com JOURNAL Pat. PEATURES	BASE COUNT ORIGIN Ouery Match Best Local Sin Matches 4040;	Oy 189 GGTGGC Db 233 GGTGGC Qy 249 ATTCAC Db 293 ATTCAC	Qy 309 ATAAAA Db 353 ATAAAA Qy 369 TAAAAG Db 413 TAAAAG	429	Oy 489 CCATGG	Qy 609 GGTTAC
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Oy 3129 Db 3173 Oy 3189 Db 3233 Oy 3249 Db 3293	Oy 3309 Db 3353 Oy 3369 Db 3413		Qy 3549 Db 3593 Qy 3609 Db 3653	Oy 3669 Db 3713 Oy 3729 Db 3773	Oy 3789 Db 3833 Qy 3849 Db 3893		DB 4013 QY 3986 DB 4073	Qy 3986 Db 4133 Qy 4031 Db 4193	

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1, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
1los, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H.,
2dvick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A., Hepler, W.T.
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.karyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
.mmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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659 GGTPAGGAGTAGCARTGGCCARTGATTTTAATCGGAGGCCTTCGTCTTAGTAACAAGT 728 713 CHTGGGGGAAGACCACCAGGCCCARTGATTCTCTCTCTCTCTCTCTCTATAGTAACAAGT 772 713 CHTGGGGGAAGACCACCAGGCCCAGATTAATCCTCTCTCTCT	_								·											
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qq	1793	TGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCCTGGACGATCCTCTCAGTGCAG 185	Δ.
Qy	1809	PAGATGCGGAAGTTAGCAACTTGTTCGAACTGTGTATTTGTCAAATTTTGCATGAGA 1868	m
qq	1853	AGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAAATTTTGCATGAGA 191	~
Qy	1869	CACAATTITAGTGACTCATCAGTTGCAGTACCTCCAAAGCTGCAAGTCAGATTCTGA 192	~
QG	1913	ACAATTTTAGTGACTCATTGCAGTTGCAAAGCTGCAAGTTCTGA 197	~
QY	1929	SAAAGATGGTAAAATGGTGCAGAAGGGGACTTACACTGAGTTCCTAAAATCTGGTA 198	~
qq	1973	ATTGAAAGATGGTAAAAATGGTGCAGAAGGGGACTTACACTGAGTTCCTAAAATCTGGTA 2	01
Qy	1989	GCTCCCTTTTAAAGAAGGATAATGAGGAAAGTGAACAACCTCCAGTTCCAG 204	~
QΩ		AGATITIGGCTCCCTTTTAAAGAAGGATAATGAGGAAAGGTACAACCTCCAGTTCCAG 209	0)
δλ	2049	TAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGGTCTCAACAATCTT 210	~
QQ	2093	AACTCCCACACAAAGGAATCGTACCTTCTAGAGTCTTCGGTTTGGTCTCAACAATCTT 2	~
QY.	2109	TAGACCCTCCTTGAAAGATGGTGCTCTGGAGAGCCAAGATACAGAGAATGTCCCAGTTA 216	
QQ	2153	AGACCCTCCTTGAAAGAFGGTGCTCTGGAGAGCCAAGATACAGAGATGTCCCAGTTA 221	~
QY	2169	GGAGAACCGTFCTGAAGGAAAAGTTGGTTTTCAGGCCTATAAGAATTACT 222	_
qu	2213	TATION TO THE CONTROLL OF THE CONTROLL OF THE CONTROL OF THE CONTR	٥,
οy	2229	TGGTGCTCACTGGATTGTCTTCATTTTCCTTATTCTCCTAAACACTGCAGCTC 228	_
QQ	2273	CAGAGCTGCTCACTGGATTGTCTTCATTTTCCTTATTCTCCTAAACACTGCAGCTC 233	•
QY	2289	GGTTGCCTATGTGCTTCAAGATTGGTGGCTTTCATACTGGGCAAACAAA	
qq	2333		
QY	2349	3GAGGAGAAATGTAACCGAGAAGCTAGATCTTAACTGGTACT 240	
qq		AAATGTCACTGTAAATGGAGGAGGAAATGTAACCGAGAAGCTAGATCTTAACTGGTACT 24	•
Qy	2409	TTAACTGTAGCGTTCTTTTTGGCATAGCAAGATCTCT	_
qq	2453	AGGAATITATICAGGITTAACIGIAGGTACCGTICTITITGGCATAGCAAGATCICTAI 25	~
QY	2469	TAACTCTTCACAAACTTTGCACAACAAAATGTTTGA	~
QQ	2513	GGTATTCTACGTCCTTGTTAACTCTTCACAACTTTGCACAAAAATGTTTGAGTCAA 257	~
QY	2529	ATTATTCTTTGATAGAAATCCAATAGGAAGAATTTTAAATCGTT 25	_
Dp	2573	ICTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGAATTTTAAATCGTT 263	۵.
Qy	2589	GATGATTTGCTGCCGCTGACGTTTTTAGATTTCATCC 26	_
QQ	2633	CTCCAAAGACATTGGACACTTGGATGATTTGCTGCCGCTGACGTTTTTAGATTTCATCC 269	•
Qy	2649	ATTGCTACAAGTGGTTGGTGTGGTCTCTGTGGCTGTGGCCGTGATTCCTTGGATCG 270	
QΩ	9	ACAITECTACAAGTGGTTGGTGTGTGTGTGGCTGTGGCCGTGATTCCTTGGATCG 2	
Οy	2709	AATACCCTTGGTTCCCCTTGGAATCATTTTCATTTTTTTT	
qq	2753	IACCCTTGGTTCCCCTTGGAATCATTTTCATTTTTCTTCGGCGAAATTTTTTGGAAA 281	
Qy	2769	CTCGGAGTCCAGTGTTTTCCCACTTGT 282	
qq	2813	GTCAAGAGATGTGAAGCGCCTGGAATCTACAACTCGGAGTCCAGTGTTTTCCCACTTGT 287	

	AAGA	CTGA	-	GACC	CCAC	ATGG	ATGG	TGAAT TGAAT	GTAA	GTAAA	GTTCP GTTCP		AFC	cds AF0 AF0	HOH HOM	Mam 1 Lee Iso	res ani Can	966	Iso	unp 3 Lee Dir	Sub 770			
	3953	3969	3986	4073	3986	31	4193	4091	4151	4313.	4211 (4373 (RESULT 10 AF071203	LOCUS	ACCESSION VERSION	KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE	TOURNAL	PUBMED PUBMED REFERENCE	TITLE	COURNAL REFERENCE AUTHORS TITLE	JOURNAL EATURES SOURCE		gene	
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ACAAA	ACAAA	CTTGG	CCATG	CCATG	GGCAG	GGCAG	TTCGA TTCGA	CAGAC	CAGAC	ATGAA(TACTGA TACTGA	CCGGAC	CCGGA	AAATTI AAATTI	TGTCAA 	CCTTT	AAACCA	FTAGTG	TAGT	FATTGA FATTGA	AAAAA AAAAA	CATTA	AGCCGT 	CAAGG
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CATCC	CATCC	ACATTO ACATTO	TGCCA	I GCCA5	rcrggz	rcreg2	TCAGTO CAGTO	CATTGA	ATTG	AGCCTG	1966CC	167666	GTGGG	ACCCGA 11111	AAGGAA AGGAA	AACCT	CAACT	GGATC	GGATC	AAAAA 	TTAAT TTAAT	AGATT AGATT	GAATA	CAACA
TGGAC	TGGAC	GATTT.	CTGGA	CTGGA	AAAAC	AAAAC	ATGTT	AGGGTC	AGGGTC	CCACC	CCAGG	3GCAT7	3GCAT1	CAGAP CAGAP	SATTI	AGGAAA 	SAGGTA	AATCA	AATCA	TCAGG 	ATGAG	CACAC	TGAAA 	тсстс
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Οy	QQ	Qy Dp	οy	QQ	ço ç	ĝ ,	oy D	δ δ	3 8	2 d	Qy Dp	δ	g G	g G	Oy Dp	Oy.	oy Db	Qy	Ор	oy do	Qy Db	Qy Db	QY	οy

Db 3953 A Oy 3969 C Oy 3969 C Oy 3966		TGAAACAGCAAAACAG 3985	AC.	3882	GACCTCAAGTGATCCACCTGCCTTGGCCTCCCAAACTGCTGAGATTACAGGTGTGAGGCA 4132		409	425	TGAATCCAACCAAAATGTCAAGTCCGTTCCGAAGGCATTTTCCACTAGTTTTTGGACTAT 4150		GTAAACCACATTGTACTTTTTTTACTTTGGCAACAAATATTTATACATAC	GTAAACCACATTGTACTTTTTTTTTTTGGCAACAAATATTTATACATAC	GTTCATTTGAATATTTCTCCC 4231 	AF071203 Homo sapiens ABC transporter MOAT-B isoform (MOAT-B) mRNA, partial			Homo sapiens. Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.	I (bases 1 to 2940) Lee,K., Bellinsky,M., Bell,D.W., Testa,J.R. and Kruh,G.D. Teolation of MOMT-B a widely composed multidans	a widely expressed protein/canaliculated transporter	Cancer Res. 58 (13), 2741-2747 (1998) 98324262		id Kruh, G.D.	d di	3 (bases 1 to 2940) Lee, K., Bellnsky, M.G., Bell, D.W., Testa, J.R. and Kruh, G.D.	P	ladelphia, PA 19111, US fiers	(o	13	<pre>//</pre>	<pre><12682 /gene="MOAT-B" /note="truncated; MRP/cMOAT-related ABC transporter" /codon start=1</pre>	1 11552 : : : : : : : : : : : : : : : : : :
Db 3953 Qy 3969 Db 4013 Qy 3986 Db 4133 Qy 4031 Db 4193 Qy 4031 Db 4253 Qy 4211 Db 4313 Qy 4211 Db 4373 Qy 4211 Db 4373 Qy 4151 Db 4373 Qy 4115 DcCus SOURCE JUTILE JUTILE JOURNAL FEATURES FEATURES SOURCE SOURCE SOURCE	AAG?	CTG2	CTG2	;	GACC	CCAC	ATGG	ATGG	TGAA	TGAA	GTAA	GTAA	GTTC GTTC		b i	AF •					0 8 8	96	L L	lun	ω ä i	Sul)				
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AEERCQELFDAHQDLHSEAMFLETTSRWFAVRLBAITARAYSSLOGIMTIRAYR
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PAT 29-AUG-2001
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Sequence 681 from Patent W00151633.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T.
and Henderson,R.A.
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                                                            AATCGTACCTTCTCAGAGTCTTCGGTTTGGTCTCAACAATCTTCTAGACCCTCCTTGAAA
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CGGGGAACCACGCTGAGTGGAGGGCAGAAAGCACGGGTAAAACCTTGCAAGAGCAGTAT
                 CAAGATGCTGACATCTTCTCCTGGACGATCCTCTCAGTGCAGTAGATGCGGAAGTTAGC
                          ACTCATCAGTTGCAGTACCTCAAAGCTGCAAGTCAGATTCTGATATTGAAAGATGGTAAA
                                                                                                                        ATGGTGCAGAAGGGGACTTACACTGAGTTCCTAAAATCTGGTATAGATTTTGGCTCCCTT
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Pred. No. 5.1e-257;
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Sequence 824 from Patent WO0173032.
AX267850
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                     CGGGGAACCACGCTGAGTGGAGGGCAGAAAGCACGGGTAAACCTTGCAAGAGCAGTGTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATGGTGCAGAAGGGGACTTACACTGAGTTCCTAAAATCTGGTATAGATTTTGGCTCCCTT
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                                                                                                                                                                                                                                                                                          AGTAATATTTTTTTTGGGAAGAAATATGAAAAGGAACGATATGAAAAAGTCATAAAGGCT
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CTTTCCTTTACTGTCAGACCTGGCGAATTGTTAGCTGTGGTCGGCCCCGTGGGAGCAGGG
                                                                                                                     CTTCCTTTACTGCCAGACCTGGCGAATTGTTAGCTGTGGCCGCCCCGTGGGAGCAGGG
                                            CATGTGCAGGATTTTACTGCTTTTTGGGATAAGGCATCAGAGACCCCAACTCTACAAGGC
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                                                                                                                    uses thereof
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae;
1 (bases 1 to 2275)
Schuetz,J. and Fridland,A.
Multidrug resistance associated proteins and uses th
Patent: WO 0058471.A 10 05-0CT-2000;
ST. JUDE CHIEDREN'S RESEARCH HOSPITAL (US)
                                                                                                                                                                                                            2 others
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                                                                                                                                                                                                                                         Score 651.8; DB 6;
Pred. No. 7.6e-156;
0; Mismatches 2;
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Sequence 10 from Patent WO0058471.
AX046474
                                                                                                                                                                         /organism="Homo sapiens"/db_xref="taxon:9606"
                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                             /note="Unknown"
                        AX046474.1 GI:11344431
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INV 21-APR-2001

linear

DNA

176082 bp

AC007144

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Losophila melanogaster

Ekkaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Bopterar; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

Ephydroidea; Drosophilidae; Drosophila.

Scalniker,S.E., Adams,M.D., Kronmiller,B., Tyler,D., Wan,K.H.,

Holt,R.A., Frans,C.A. Gocayne,J.D., Amanatides,P.G., Brandon,R.C.,

Rogers,Y., An,H., Baldwin,D., Banzon,J., Beeson,K.Y., Busam,D.A.,

Carlson,J.W., Center,A., Champe,M., Davenport,L.B., Dietz,S.M.,

Dodson,K., Dorsett,V., Doup,L.E., Doyle.C., Dresnek,D., Farfan,D.,

Ferriera,S., Frise,E. Galle,R.F., Garg,N.S., George,R.A.,

Gonzalez,M., Houck,J., Hoskins,R.A., Hostin,D., Howland,T.J.,

Ibeywam,C., Jalall,M., Kruse,D., Li,P., Mattel,B., Moshrefi,A.,

MIntosh,T.C., Moy,M., Murphy,B., Nelson,C., Nelson,K.A., Nunoo,J.,

Phouanenavong,S., Pitrans,G.S., Patel,S., Pfeiffer,B.,

Stapleton,M., Strong,R., Svirskas,R., Tector,C., Williams,S.M.,

Zaveri,J.S., Smith,H.O., Rubin,G.M. and Venter,J.C.

Sequencing of Drosophila chromosome 2L, region 38F-39A
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Submitted (24-MaR-1999) Drosophila Genome Center, Lawrence Berkeley
Laboratory, MS 64-121, Berkeley, CA 94720, USA
On Apr 21, 2001 this sequence version replaced gi:7264767.
Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley Mational Laboratory, MS 64-121
Berkeley, CA 94720
This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones.
For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
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           region 38F-39A, BAC clone
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/clone=ib="RPCI-98 (Roswell Park Cancer Institute
/clone_lib="RPCI-98 (Roswell Park Cancer Institute
pbacsophila melanogaster BAC library, partial EcoRI
pBACe3.61"
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/strafia="y; cn bw sp"
/db xref="taxon 7227"
/chromosome="2L"
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       21,
       melanogaster, chromosome
Drosophila melanogaster, chrc
BACR06G10, complete sequence.
AC007144
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op	Oy Db	Oy Dp	Q Dp	oy Db	O D	Q D	Q Dp	Qy Dp	oy Dp	Oy Dp	g ç	oy ob	Qy Db	Q D	oy Op	QY Db	QY Db	δ΄

92172 GTCCACCCAGTTACACATACCATGTTCCAAGGAGTCTCCCGCACCGCTCTGTACTTCTT 92113 92772 CATGCCGATCTCATAGTGATTATGGACAAGGGAAAAATATCGGCTGTTGGCACCTATGAG 92713 92592 TACTCCCGGCAAAGTAGTCGTGTAAGCAGAGTCAGTGTAACTTCGGTGGATTCCTCACG 92533 92292 GGTTAAAAACAACGACTCCTTTCATCTACGGACATTTACATCTTCAGTGGAATCAATGC 92233 92112 CCATGCGAATCCATCGGGCAGAATCCTCAATCGATTTGCCATGGACTTGGGGCAAGTGGA 92053 2433 2030 GAACAACCTCCAGTTCCAGGAACTCCCACACATAAGGAATCGTACCTTCTCAGAGTCTTCG 2089 2794 ATCTACAACTCGGAGTCCAGTGTTTTCCCACTTGTCATCTTCTCTCCAGGGGCTCTGGAC 2853 GACGATCCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATT 1849 1910 GCTGCAAGTCAGATTCTGATATTGAAAGATGGTAAAATGGTGCAGAAGGGGACTTACACT 1969 GGTTTTCAGGCCTATAAGAATTACTTCAGAGCTGGTGCTCACTGGATTGTCTTCATTTTC 2263 2264 CTTATTCTCCTAAACACTGCAGCTCAGGTTGCCTATGTGCTTCAAGATTGGTGGCTTTCA 2323 GACGATCCTTTGAGTGCTGTGGACACCCATGTGGGACGCCATTTATTCGAGGAGTGCATG 1850 IGTCAAATTTTGCATGAGAAGATCACAATTTTAGTGACTCATCAGTTGCAGTACCTCAAA GAGTTCCTAAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAAGT GGCGATTCTAATCAGGAACAAGTTAATGCAGAAGGCGATTCCAGAAATGATAAGTCGACC 2090 GTTTGGTCTCAACAATCTTCTAGACCCTCCTTGAAAGATGGTGCTCTGGAGAGCC-----2145 - AAGATACAGAGAATGTCCCAGTTACAGAGGAGAACCGTTCTGAAGGAAAAGTT 2324 TACTGGGCAAACAAACAAAGTATGCTA------AATGTCACTGTAAATGGAGGAGG 2374 AAATGTAACCGAGAAGCTAGATCTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGT AGCTACCGTTCTTTTGGCATAGCAAGATCTCTATTGGTATTCTACGTCCTTGTTAACTC 2494 TTCACAAACTTTGCACAACAAATGTTTGAGTCAATTCTGAAAGCTCCGGTATTATTCTT 2554 IGATAGAAATCCAATAGGAAGAATTTTAAAATCGTTTCTCCAAAGACATTGGACACTTGGA GGTCTCTGTGGCTGTGGGTGGTTCCTTGGATCGCAATACCCTTGGTTCCCTTGGAAT 2734 CATTITCATTITCTTCGGCGATATTTTTGGAAACGTCAAGAGATGTGAAGCGCCTGGA 2434 2674 1790 1970 2204 2614 92892 92652 QQ δy Q ά qq Qy q δ P ò qq οy Dp οy qq ŏ g Q g QΥ q $^{\circ}$ qq οy QQ οχ g Ω g Dp Ω g ŏ

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2854 91812	2914 91752	2974	3034 91632	3094	3154	3208 91452	3268 91392	3322 91332	3382	3442	3502	~	91092	3570	3624	3684 (3744 c	3804 (
Qy Dp	Qy Db	Qy Db	Qy Db	Qy	Oy Dp	OY Db	Qy Db	Oy Dp	Qy Dp	Qy Db	Qy Dp	Qy	ρρ	Oy Op	Qy Db	Qy Dp	Qy Db	Qy Db

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Disabilita metabogaster

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Roppera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroides; Drosophilae; Drosophila.

Bephydroides; Drosophilae; Drosophilae;

Ephydroides; Drosophilae; Drosophilae;

Benos, M.D., Celniker, S.E., Holt, R.A., Evans, C.A., Gocayne, J.D.,

Amanatides, P.G., Scherer, S.E., Holt, R.A., Evans, C.A., Gocayne, J.D.,

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Miklos, G.L., Abrill, J. Baxter, E.G., Helt, G., Nelson, C.R., Gabor

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Challer, M., Galsser, K., Glodek, M., Gong, F., Gorrell, J. H., Gulz, C.R., Ferrac, C., Ferrac,
                                                                                                                                                                                                                                                                                      267284 bp DNA linear INV 11-OCT-2000 Drosophila melanogaster genomic scaffold 142000013386055 section 61 AE003668 AE002690 AE003668.3 GI:10799497 HTG.
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Adams,M.D., Celniker,S.E., Gibbs,R.A., Rubin,G.M. and Venter,C.J.
Direct Submission
Submitted (21-MR-2000) Celera Genomics, 45 West Gude Drive,
Rockville, MD, USA
                                      90732 GTACTCTAGTGGAGTTCGGATCACCATTCGAACTACTGACCCAATCGTGGAGCAAAGTCT 90673
3864 GAAGACTGAAAGAATATGATGAGCCGTATGTTTTGCTGCAAAATAAAGAGAGC---CTAT 3920
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                                                                                                                                                    Db 90672 TTTACGGGATGGTGCTCCAGACGG 90648
                                                                                                                    3921 TTTACAAGATGGTGCAACAGTGGG 3945
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Drosophila melanogaster
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VERSION
KEYWORDS
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AUTHORS
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MEDLINE
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mRNA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GVAGIGTIEKLLARSKNNASYEKIEFBAIRCLKAIMNNTWGLNVVLNDOGHSVULLA
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                                                                                                                                                                                                      LMGLLKVILPHRPDLKVILMSATVREQDFCDYFNNCPMFRIEGVMFPVKMLYLEDVLS
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HLKGKNSLERSANSRFEKPIDYVEYLQNGEHSTHKVYQCVESLRVALTSNPISWIKEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VNIPMPPPPPGGGGAPPPPPPPPMPGRAGGGPPPPPPPPPPMPGRAGGPPPPPPPGMGGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPPPMPGMMRPGGGPPPPPMMGPMVPVLPHGLKPKKKWDVKNPMKRANWKAIVPAKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SDKAFWVKCQEDKLAQDDFLAELAVKFSSKPVKKEQKDAVDKPTTLTKKNVDLRVLDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KTAONLAIMLGGSLKHLSYEQIKICLLRCDTDILSSNILQOLIOYLPPPEHLKRLQEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NSKKFSKILELILLLGNYMNSGSKNEAAFGFEISYLTKLSNTKDADNKQTLLHYLADL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KFSEVMGKFAEECRQQVDVLGKMQLQMEKLYKDLSEYYAFDPSKYTMEEFFADIKTFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DAFQAAHNDNVRVREELEKKRRLQEAREQSAREQQERQQRKKAVVDMDAPQTQEGVMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLLEALOTGSAFGQRNRQARRQRPAGAERRAQLSRSRSRTRVTNGQLMTREMILNEVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       605 ATGAGGTTACGAGTAGCCATGTGCCATATGATTTATCGCAAGGCACTTCGTCTTAGTAAC 664
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Pred. No. 4.7e-145;
0; Mismatches 1587;
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50.8%;
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Best Local Similarity
Matches 1751; Conserv
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 QY
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188707 CATGCCGATCTCATAGTGATTATGGACAAGGAAAAATATCGGCTGTTGGCACCTATGAG 188648 188587 GCGATTCTAATCAGGAACAAGTTAATGCAGAAGGCGATTCCAGAAATGATAAGTCGACC 188528 188527 TACTCCCGGCAAAGTAGTCGTGTAAGCAGAGTCAGTGTAACTTCGGTGGATTCCTCTACG 188468 188407 GGATTGGGCATATATGGGAAATACTTTTCCGCCGCCTCTGGATGGCTAATGGTCATCCTG 188348 188228 Db 187987 TGAAATCCTGCCCCCAGTGCTCGATTGCATACAGATATTCTTACAATCAGTGGAAT 187928 Db 187867 GGCTTTTCATTTTCTTGGCACTTGAGGACTTGAGGACTTGAAAAGATTGGA 187808 GCTGCAAGTCAGATTCTGATATTGAAAGATGGTAAAATGGTGCAGAAGGGGACTTACACT 188647 GARATGCTTARARAGTGGCCAGGACTTTTGGCACTCAGGAAATG TGTCAAATTTTGCATGAGAAGATCACAATTTTAGTGACTCATCAGTTGCAGTACCTCAAA GAGTTCCTAAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAAGT 2030 GAACAACCTCCAGTTCCAGGAACTCCCACACAAACGAATCGTACCTTCTCAGAGTCTTCG GACGATCCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATT 188467 GAGTCTATACTGGACAATGAAAGACAACCTGCTCAGGAGTCGCGATCCCAAGGGAAAATT CTTATTCTCCTAAACACTGCAGCTCAGGTTGCCTATGTGCTTCAAGATTGGTGGCTTTCA 188287 TACTGGTAAGTATGCTTAATTGAACTATGTTGTTCACAATTAATAAATCTTCGTTCACAG AGCCCTAGTAATCTTTGCTCTGCTTCGAACCCTGCTCTTCTTCAGCATGGCATGCACTC 2090 GITIGGICTCAACAATCTICTAGACCCTCCTIGAAAGAIGGIGCICIGGAGAGCC-----AAGATACAGAGAATGTCCCAGTTACACTATCAGAGGAGAACCGTTCTGAAGGAAAAGTT GGTTTTCAGGCCTATAAGAATTACTTCAGAGCTGGTGCTCACTGGATTGTCTTCATTTC 188347 GIIGCCIICTICTGTCTGGGCACTCAAATITTGGCITCTGGAGGTGACTACTTCCTTICC TACTGGGCAAACAAACTATGCTA------AATGTCACTGTAAATGGAGGAGG AGCTACCGTTCTTTTGGCATAGCAAGATCTCTATTGGTATTCTACGTCCTTGTTAACTC AAATGTAACCGAGAAGCTAGATCTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGT 2494 TICACAAACTITGCACAAAAATGTTTGAGTCAATTCTGAAAGGTCCGGTATTATTCTT GGTCTCTGTGGCTGTGGCCGTGATTCCTTGGATCGCAATACCCTTGGTTCCCCTTGGAAT 187927 TATAGGAGTTCTGTGCATCACAAATCCGTGGTATTTGATAAATACCATCACGATGTTCTT CATTITCATITITCTTCGGCGATATITITTGGAACGTCAAGAGATGTGAAGCGCCTGGA 1730 1850 188881 2145 188827 1910 1970 2324 1790 2264 2374 2434 2204 188167 188107 2614 188227 2674 2734 g οy ŏ g δy 셤 ŏ g ò qq δy g ŏ qq ŏ qq ò qq a qq g ö ò qq ŏ g qq Qγ δλ ŏ qq ò ŏ δλ

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          187267 AAAGATIGGCAICGIGGGCAGAACIGGTGCCGGAAAGICCCTTATAAAIGCCCTCTT 187208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCACCAGCCTGGCCCCATGAAGGAGTGATAATCTTTGACAATGTGAACTTCATGTACAG 3267
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                                                                                                   187747 CATCAGAGCTATGGAAGCTCAGGACTTACTCACCAAGGAATACGATAACTACCAGGATAT
                                                                                                                                                                                                                              2974 IGCCAICTGTGCCATGTTTGTCATCGTTGCCTTTGGGTCCCTGATTCTGGCAAAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                          187507 TCAGTGGGGAATGGCAATCCGCTGAGCTGGAAACTCCATGACTTCTGTGGAAAGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         187027 CITAGAAGAGGIGAGTAATTACCAAACCIGACAATCATAACTATAATTAAACCATTITCC
                                                                                                                                              3034 TCTGGATGCCGGGCAGGTTGGTTTGGCACTGTCCTATGCCCTCACGCTCATGGGGGATGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              187087 CACCCTGCGCTGCAATTTGGATCCCTTTGAACAGTATGCTGATGAAAAATTGTGGGAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D 186907 TTGCCGAGGCGGATCCAACTACAGTCTAGGTCAGGGGAGTTGGTCTGCTTGGCCAGGG
                                                              2854 CATCCGGCCATACAAAGCAGAAGAGGTGTCAGGAACTGTTTGATGCACACCAGGATTT
                                                                                                                                                                                                                                                                       TCTGTTTTGCGTGGCCTACGTCATATCGGTAACCCTAATGAGCTATTTTAACCCCCCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAATTCTCAGGAAAAATCAGATATTGATTATTGATGAAGCGACGGCAAATGTGGATCCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3804 CCATTGCACACAGATTGAACACCATTATTGACAGCGACAAGATAATGGTTTTAGATTCAG
                                                                                                                                                                                                                                                                                                                                                                                                  TCAGTGGTGTTCGACAAAGTGCTGAAGTTGAGAATATGATGATCTCAGTAGAAAGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAAGGTTGGCATTGTGGGAAGAACCGGAGCTGGAAAAAGTTCCCTCATCTCAGCCCTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AACAATGAGGAAAAACCTGGATCCCTTTAAAGGAGCACACGGATGAGGAACTGTGGAATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----AGGTACAACTTAAAGAAACCATTGAAGATCTTCCTGGTAAAATGGATACTGAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3744 GAACTGATGAGTTAATACAAAAAAAAATCCGGGAGAAATTTGCCCACTGCACCGTGCTAA
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Db 186727 CCATAGCTCACAGGTTGAACACGATCATCGACAGGGTCATGGTTCTGGACGCTG 186668

Qy 3864 GAAGACTGAAAGAATATGATGAGGGCGTATGTTTTGCTGCAAAATAAAGAGAGC---CTAT 3920

Qy 186667 GTACTCTAGTGGAGTTCGGATCACCATTCGAACTACTGACCCAATCGTGGAGCAAAGTT 186608
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QY 3921 TTTACAAGATGGTGCAACAACTGGG 3945

Db 186607 TTTACGGGATGGTGCTCCAGACGGG 186583

Search completed: December 18, 2002, 16:57:54 Job time: 7681.22 secs

Appli Appli Appli Appl Appl

Sequence 1, Appendix No. 1, Ap

US-09-425-453A-5 US-09-425-453A-7 US-09-425-453A-1 US-09-425-453A-11 US-09-425-453A-13 US-09-425-453A-15 US-09-425-453A-17 US-09-425-453A-17 US-09-265-703-1 US-09-265-703-1 US-09-248-026-3

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PCT-US93-11667-3 US-08-951-912-3

US-08-136-742A-1 US-07-637-621-1

ALIGNMENTS

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APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C16
CURRENT APPLICATION NUMBER: US/09/605,785
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 835
SOFTWARE: FESTERQ for Mindows Version 3.0
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; Patent No. 6321716
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Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Amas S.
Carter, Samuel
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
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 US-09-605-785-535
   ID NO 535
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          GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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                    TCCTGGTAAAATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGGACAAAG
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Farder, Staven G.
APPLICANT: Ranger, Garven G.
APPLICANT: Ranger, Gary
APPLICANT: Forter, Mark
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
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Patent No. 6329505
GENERAL INFORMATION:
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Pred. No. 0;
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FILE REFERENCE: 210121.427C9
CURRENT APPLICATION WUMBER: US/09/439,
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FASLSEQ FOR WINDOWS VERSION
SEQ ID NO 533
LENGTH: 6082
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APPLICANT: Hepler, William
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C16
CURRENT APPLICATION NUMBER: US/09/605,785
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 835
SOFTWARE: FastSEQ for Windows Version 3.0
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Pred. No. 0;
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Patent No. 6321716
GENERAL INFORMATION:
APPLICANT: W. Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Renger, Gary R.
APPLICANT: Renger, Marc W.
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Matches 4040; Conservative
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Day, Craig H.
Vedvick, Thomas S
Carter, Darrick
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APPLICANT: Solk, John
APPLICANT: Day, Craig
TILLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLEE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C9
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CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 536
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Patent No. 6329505
GENERAL INFORMATION:
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Lou
APPLICANT: Jiang Yuqui
APPLICANT: Reed, Steven G.
APPLICANT: Ralos, Michael
APPLICANT: Fanger, Gary
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; OTHER INFORMATION: n=A,T,C
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1	9 GAATCCAGACCTTTTGCTACTTGATGAGATATCACAGGGGCAACGGTCAGG	9 ATGGTAAAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTTGGGATAAGGC	CCCCAACTCTACAAGGCCTTTCC 	9 GCCCCGTGGGAGCAAGTCATCACTGTTAAGTGCCGTGCTCGGGGAATTGGCCCCCA	GTCACGGGCTGGTCAGCGTGCATGGAAGAATTGCC	9 TCTCGGGAACTCTGAGGAGTAATATTTTATTTGGAAGAATATGAAAAGGAACGATTIIII 	9 AAAAAGTCATAAAGGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTGGAGGAT 	9 TGACTGTGATAGGAGATCGGGAACCACGCTGAGTGGAGGGCAGAAAGCACGG 	TCCTGGACGATCCT 	9 TAGATGCGGAAGTTAGCAGACACTTGTTGGAACTGTGTATTTGTCAAATTTTGCATGAGA 	9 AGATCACAATTTTAGTGACTCATCAGTTGCAGTACCTCAAAGCTGCAAGTCAGATTCTGA 	TATTGAAAGATGGTAA TATTGAAGATGGTAA		GAACTCCCACACTAAG	CTAGACCCTCCTTGAAAGATGGTGCTCTGGAGAGCCAAGATACAGAGAATGT 	CACTATCAG	TCAGAGCTGGTGCTCACTGGATT 	AGGTTGCCTATGTGCTTCAAGATTGGTGGCTTTCATACTGGGCAAACAAA
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APPLICANT: RAILS, MALOS, MALOS
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ORGANISM: Homo sapiens
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FOR THE THERAPY AND

Jiang, Yuqui Henderson, Robert A Kalos, Michael D. Fanger, Gary R. Retter, Marc W. Stolk, John A. Day, Craig H. Vedvick, Thomas S. Carter, Darrick

rlocker, Susan L.

Mitcham, Jennifer

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  Score 1045.4; DB Pred. No. 7e-292; 0; Mismatches 1
24.7%;
99.9%;
           Best Local Similarity 99.9
Matches 1046; Conservative
  Query Match
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Sequence 824, Application US/09605785 Patent No. 6221716 GENERAL INFORMATION: APPLICANT: Xu, Jiangchun APPLICANT: Dillon, Davin C.

RESULT 5 US-09-605-785-824

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US-09-001-273-1
                         Query Match
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                               ACTCATCAGTTGCAGTACCTCAAAGCTGCAAGTCAGATTCTGATATTGAAAGATGGTAAA
                                                                                                                       TTAAAGAAGGATAATGAGGAAAGTGAACAACCTCCAGTTCCAGGAACTCCCACACTAAGG
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MULTIDRUG RESISTANCE-ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS .
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: SHYJAN, ANDREW
TITLE OF INVENTION: NOVEL MULTIDRUG RESI
TITLE OF INVENTION: POLYPEPTIDE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibeault
STREET: 125 High St.
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NAME: FENTON, Gillian M
REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: MIL-0
TELECHONE: (617) 248-7000
TELEPAX: (617) 248-7000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4781 base pairs
TYPE: nucleic acid
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2174 TCAGAGGAGAACCGTTCTGAAGGAAAAGTTGGTTTTCAGGCCTATAAGAATTACTTCAGA 2233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTGCTGAACAGCTGCTGCTGAGGCCTGACCTGGCCATTCTTCCCAGCAGCGACCTGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                          GGAACTCTGAGGAGTAATATTTTATTTGGGAAGAAATATGAAAAGGAACGATATGAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1874 ACAATTTTAGTGACTCATCAGTTGCAGTACCTCAAAGCTGCAAGTCAGATTCTGATATTG
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                                                         6
  Length 4781;
                                                         Indels
Score 437.4; DB 2;
Pred. No. 9.4e-116;
                                                   0; Mismatches 1296;
10.3%;
                                                Matches 1244; Conservative
                         Similarity
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2713
 ATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTGGCATAGCAAGATCTCTATTGGTA 2473
                         2798 Archaegecererecargecaereargergarecraaagecarreaaggagrierir 2857
                                                                                                                                  CGAAGCCCTATGAAGTTTTTTGACACGACCCCCACAGGGAGGATTCTCAACAGGTTTTCC 2977
                                                                                                                                                                         AAAGACATTGGACACTTGGATGATTTGCTGCCGCTGACGTTTTTAGATTTCATCCAGACA 2653
                                                                                                                                                                                        AGAGAIGTGAAGCGCCTGGAATCTACAACTCGGAGTCCAGTGTTTTCCCACTTGTCATCT 2833
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3844
 CCTGTTTTGTTCACTGGAACAATGAGGAAAAACCTGGATCCCTTTAAGGAGCACACGGAT 3544
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                                                                                                                                                                                                                                                                                                                                             3878 CCGGTGCTGTTCAGTGGCACTGTCAGATCTAGACCCCTTCAACCAGTACACTGAA
                                                                                                                                    3605 GGTAAAATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGGACAAAGACAA
                                                                                                                                                            3845 ATAATGGTTTTAGATTCAGGAAGACTGAAAGAATATGATGAGGCCGTATGTTTGCTGCAA
                                                                 3545 GAGGAACTGTGGAATGCCTTACAAGAGGTACAACTTAAAGAAACCATTGAAGATCTTCCT
                                                                                                   GACCAGATTTGGGATGCCCTGGAGAGGACACATGAAAGAATGTATTGCTCAGCTACCT
                                                                                                                                                                                                         CTGGTGTGCCTTGCCAGGGCAATTCTCAGGAAAAATCAGATATTGATTATTGATGAAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Andrew NOVEL MULTIDRUG RESISTANCE-ASSOCIATED POLYPEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Hanley, Elizabeth A.
REGISTRATION NUMBER: 33,505
RESIGNER/DECET NUMBER: MII-056 (formerly MIL-001)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AATAAAGAGCCTATTTTACAAGATGGT 3933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AACGACAGTTCCCGATTCTATGCCATGTT 4326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/843,459A FILING DATE: 16-APR-1997 CLASSIFICATION: 536 ATTORNATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAHIVE & COCKFIELD, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08843459A
Patent No. 6162616
GENERAL INFORMATION:
APPLICANT: SHYJAN, Andrew
TITLE OF INVENTION: POLYPEPTIDE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 4781 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (617)742-4214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (617)742-4214 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Massachusetts
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EDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC
OPERATING SYSTEM:
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2533 2713 2917 2593 2977 2653 2833 2893 2797 GTATCCTGGTGTTCTTCTGTGGGAATGGCGGGGGGTCTTCCCGTGGTTCTTCTGTG 3097 CCCTTGGTTCCCCTTGGAATCATTTTCATTTTTTGGCGGATATTTTTGGAAACGTCA 2773 2953 3277 3337 3013 3397 3073 3457 3133 3187 3577 3247 3307 3367 3637 3697 3757 3424 3484 1818 AGAATCAGTGATATTGGCCTTGCCGACCTCCGAAGCAAACTCTCTATCATTCTTCAAGAG 3877 CGAAGCCCTATGAAGTTTTTTGACACGACCCCCACAGGGAGGATTCTCAACAGGTTTTCC TTGCTACAAGTGGTTGGTCTGTCTCTGTGGCTGTGGCCGTGATTCCTTGGATCGCAATA ATCTACGCCCTCTCCATGCAGCTCATGCTGAAAGCCATTCGAGGAGTTGTCTTT TTCTACGTCCTTGTTAACTCTTCACAAACTTTGCACAAAAAATGTTTGAGTCAATTCTG GTCAAGGGCACGCTGCGAGCTTCCTCCGGGCTGCATGACGAGGATTTTCCGAAGGATCCTT AAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGAATTTTAAATCGTTTCTCC **AAAGACATTGGACACTTGGATGATTTGCTGCCGCTGACGTTTTTAGATTTCATCCAGACA** AACGAGACCTCGGTGAGTGACAGCATGAAGGACAATCCTCATATGCAGTACTATGCCAGC 3098 GCAGTGGGGCCCCTTGTCATCTTTTCAGTCCTGCACATTGTCTCCAGGGTCCTGATT TCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAAGAGAGGGGTGTCAGGAACTG ATTITATICAGGITTAACTGTAGCTACCGTTCTTTTGGCATAGCAAGATCTCTATTGGTA 2774 AGAGATGTGAAGCGCCTGGAATCTACAACTCGGAGTCCAGTGTTTTCCCACTTGTCATCT CTCACGCTCATGGGGGATGTTTCAGTGGTGTTCGACAAAGTGCTGAAGTTGAGAATATG TGGGAATATCAGAAACGCCCACCACCAGCCTGGCCCCATGAAGGAGTGATAATCTTTGAC 2894 ITTGATGCACCAGGATTTACATTCAGAGGCTTGGTTCTTGTTTTGACAACGTCCCGC TGGTTCGCCGTCCGGTCTGGATGCCATCTGTGTTTTGTCATCATCGTTGCCTTTGGG 3398 ATCGTTCTTATGCACGGCAGATTCCCCAGCCTATGCGGGTCTCGCCATCTTATGCT ATTAAATCACAAGAAAAGGTTGGCATTGTGGGAAGAACCGGAGCTGGAAAAAGTTCCCTC ATCTCAGCCCTTTTTAGATTGTCAGA---ACCCGAAGGTAAAATTTGGATTGATAAGATC AATGTGAACTTCATGTACAGTCCAGGTGGGCCTCTGGTACTGAAGCATCTGACACTC TTGACAACTGAAATTGGACTTCACGATTTAAGGAAGAAAATGTCAATCATACCTCAGGAA 2738 2414 2798 2474 2858 2534 2918 2594 2978 2654 3038 2714 2834 3218 2954 3338 3014 3458 3134 3188 3074 3248 3638 3308 3368 3698 3758 3425

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CTCTTGTGCATAGCTAGAGCCCTGCTCCGCCACTGTAAGATTCTGATTTTAGATGAAGCC 4117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATAATGGTTTTAGATTCAGGAAGACTGAAAGAATATGATGAGCCGTATGTTTTGCTGCAA 3904
3485 CCTGTTTGTTCACTGGAACAATGAGGAAAAACCTGGATCCCTTTAAGGAGCACCACGGAT
                                                                                                                                                     GGTAAAATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGGACAAAGACAA
                                                                                                                                                                                                                             CTGGTGTGCCTTGCCAGGGCAATTCTCAGGAAAAATCAGATATTGATTATTGATGAAGCG
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                                                                                               3938 GACCAGATTTGGGATGCCCTGGAGAGGACACACATGAAAGAATGTATTGCTCAGCTACCT
                                                                         GAGGAACTGTGGAATGCCTTACAAGAGGTACAACTTAAAGAAACCATTGAAGATCTTCCT
                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09061400
Patent No. 6077936
GENERAL INFORMATION:
APPLICANT: SHVAN, Andrew
TITLE OF INVENTION: NOVEL MULTIDRUG RESISTANCE-ASSOCIATED
TITLE OF ENVENTION: POLYPEPTIDE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
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CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/061,400
FILING DATE: 16-APRIL-1998
CLASSIFICATION: 536
ATORNEY/AGENT INFORMATION:
NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REGISTRATION NUMBER: 33,505
REGISTRATION NUMBER: 33,505
RECISTRATION NUMBER: MNI-056CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-7401
TELEPHONE: (617) 227-7410
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AACGACAGTTCCCGATTCTATGCCATGTT 4326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AATAAAGAGGCCTATTTTACAAGATGGT 3933
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TYPE: nucleic acid
STRANDEDNESS: single
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STATE: Massachusetts
COUNTRY: USA
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STRANDEDNESS:
TOPOLOGY: line
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                                                                                Length 4847;
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                                                                                   DB 3;
                                                                              Score 437.4; DB 3;
Pred. No. 9.4e-116;
0; Mismatches 1296;
                                                                          Query Match 10.3%;
Best Local Similarity 48.8%;
Matches 1244; Conservative
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                                                       2864 ATCTACGCCCTCTCCATGGCAGTCATGCTGATCCTGAAAGCCATTCGAGGAGTTGTCTTT
                                  ATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTTGGCATAGCAAGATCTCTATTGGTA
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AGAATCAGTGATATTGGCCTTGCCGACCTCCGAAGCAAACTCTCTATCATTCCTCAAGAG 3943
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                                       CCTGTTTTGTTCACTGGAACAATGAGGAAAAACCTGGATCCCTTTAAGGAGCACACGGAT
                                                                                                                       GAGGAACTGTGGAATGCCTTACAAGAGGTACAACTTAAAGAAACCATTGAAGATCTTCCT
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APPLICANT: Cole, Susan P.C.
APPLICANT: Deeley, Roger G.
APPLICANT: MULTIDRUG RESISTANCE PROTEIN
NUMBER OF SEQUENCES: 2
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PRIOR APPLICATION DATA:
APPLICATION UNDBER: 07/966,923; 08/029,340
FLING DATE: 27-0CT-1992; 8-MAR-1993
ATTORNEY/AGENT INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/141,893
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Patent No. 5489519
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION
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TELEFAX: (617) 227-5149
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
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LENGTH: 5011 base pairs
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TIME: MASSACHUSETTS
TARE: MASSACHUSETTS
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                                                                                                                                                         77;
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                                                                                                                          Score 390.4; DB 1;
Pred. No. 3.7e-102;
0; Mismatches 1786;
                                                                                                                           Query Match 9.2%;
Best Local Similarity 47.1%;
Matches 1659; Conservative
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                     CDS
196..4788
                                                                   ; NAME/KEY:
; LOCATION:
US-08-141-893-1
                                                    FEATURE
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FILING DATE: 20 CLASSIFICATION:
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                                  CTCTTCACAAACTTTGCACAACAAAATGTTTGAGTCAATTCTGAAAGCTCCGGTATTATT
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CCTCCGAATGAACCTGGACCCATTCAGCCAGTACTCGGATGAAGAAGTCTGGACGTCCCT 4403
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                                           ACAAGAGGTACAACTTAAAGAAACCATTGAAGATCTTCCTGGTAAAATGGATACTGAATT
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APPLICANT: Cole, Susan P.C.
APPLICANT: Deeley, Roger G.
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING
TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSE: PARTEO RESEARCH & DEVELOPMENT INNOVATIONS STREET: Queen's University at Kingston CITY: Kingston STATE: Onlario COUNTRY: CANADA ZIP: K7L 3NG COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,092B
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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FILING DATE: 8-MAR-1993
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APPLICATION NUMBER: 07/966,923
FILING DATE: 27-0CT-1992
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                                                                                                                                                                                                                                                                Length 5011;
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ATTORNEY/AGENT INFORMATION:
NAME: Steeg, Carcal Miernicki
REGISTRATION NUMBER: 39,539
REFERENCE/DOCKET NUMBER: Q1546
TELECOMUNICATION INFORMATION:
TELEPHONE: (613) 545-2342
TELEPHONE: (613) 545-6853
                                                               TELEPHONE: (613) 545-2342
TELEPHONE: (613) 545-6853
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5011 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                    ; NAME/KEY: CDS
; LOCATION: 196..4788
US-08-463-092B-1
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3685 AATTCTCAGGAAAATCAGATATTGATTATTGATGAAGCGACGGCAAATGTGGATCCAAG 3744
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Patent No. 5882875
GENERAL INFORMATION:
APPLICANT: Cole, Susan P.C.
APPLICANT: Deeley, Roger G.
TITLE OF INVENTION: METHODS FOR IDENTIFYING
TITLE OF INVENTION: MUTIDRUG RESISTANT TUMOR CELLS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: LAHIVE & COCKFIELD
STREET: LAHIVE & COCKFIELD
STREET: LAHIVE & COCKFIELD
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: 08/0
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CURRENT APPLICATION DATA:
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STATE: Massachusetts
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                 Score 390.4; DB 2;
Pred. No. 3.7e-102;
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FILING DATE: 26-0CT-1993
APPLICATION NUMBER: 08/407,207
FILING DATE: 20-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                       NAME: DeConti, Giulio A. Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PQI-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                           LENGTH: 5011 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Matches 1659; Conservative
                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: CDS
; LOCATION: 196..4788
US-08-462-109A-1
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                          2005 AGCAGCATCGTGCAGGCGAGTGTCTCCCTCAAACGCCTGAGGATCTTTCTCTCCCATGAG
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- -	* 0	Db 4224 CAACAGTC		4284	3505	4344	Db 4404 GGAGCTGGC	QY 3625 AGCAGAATCA	Db 4464 TGCAGAAGG	Oy 3685 AATTCTCAGG	3745		Qy 3805 CATTGCACAC	4044	OY 3865 AAGACTGAAA Db 4704 AGAAATCCAG		Db 4761 CAGCATGGCC	RESULT 12 US-08-460-907B-1 ; Sequence 1, Applic	; Patent No. 5891724 ; GENERAL INFORMATI ; APPLICANT: DEE	APPLICANT: COL	TITLE OF INVENT NUMBER OF SEQUE	CORRESPONDENCE ADDRESSEE: P STREET: Ouee		COUNTRY: CAN ZIP: K7L 3N6 COMPUTER READAB	; MEDIUM TYPE; ; COMPUTER: IB	SOPTWARE: AS CURRENT APPLICA	FILING DATE: CLASSIFICATION N. CLASSIFICATION	HILLICATION APPLICATION IN FILING DATE:
2270 CTCCTAAACACTGCAGCTCACTTGTGCTTCAAGATTGGTGGCTTTCAT 2324	3084 CTGGGACTACATGAAGGCCATCGGACTCTTCATCTCCTCAGCATCTTCCTTTCAT 3143	2325 ACTGGGCAAACAAACAAAGTATGCTAAATGTCACTGTAAATGGAGGAGGAAATGTAACG 2384 3144 GTGTAACATGTCACTGCTATATTGTAAATTTTTTTTTTT		3204 CATCGTCACGGGACTCAGGAGCACACGAAAGTCCGGCTGAGCGTCTATGGAGCCCTGGG 3263	2445 TITITGGCATAGCAAGAICICIATIGGTATICIACGICCTIGITAA 2490		2491 CTCTTCACAAACTTTGCACAAAAAGTTTGAGTCAATTCTGAAAGCTCCGGTATTATT 2550 1111 1 1 1 1 1 1 1 1					20/1 islociticistoristicated (Structification of the Control of th		3564 ccrcarcracricricciccadagerrcracgregerrccreegeagececr 3623	2791 GGAATCTACAACTCGGAGTCCCAGGTTTTCCCACTTGTCATCTTCTCTCCAGGGGCTCTG 2850	2851 GACCATCCGGGCATACCAAAGCAGAAGGTGTCAGGAACTGTTTGATGCACACCAGGA 2910	3684 CGTCATTCGAGGCGGAGGGGGGGGTTCATCCACCAGAGTGACCTGAAGGTGGA 3743	2911 TTTACATTCAGAGGCTTGGTTCTTGTTTTGACAACGTCCCGCTGGTTCGCCGTCCTT 2970 3744 CGAGAACCAGAAAGCCTATTACCCCAGCATCGTGGCCAACAGGTGGCTGGC			3031 AACTCTGGATGCCGGCAGGTTGGTTTGGCACTGTCCTATGCCCTCACGCGTT 3090 1			3151 GGTCATTGAATACACAGACCTTGAAAAAGAAGCACCCTTGGGATATCAGAAACGCCC 3207 	ACCACCAGCCTGGCCCCATGAAGGAGTGATAATCTTTGACACATGTGAACTTCATACAG		3268 TCCAGGTGGCCTCTGGTACTGACATCTGACAGCACTCATTAAATCACAAGAAAAGGT 3327 	TGGCATTGTGGGAAGAACCGGAGCTGGAAAAGTTCCCTCATCTCAGCCCTTTTTAGATT
δλ	QQ	Qy Dp	δλ	qq	οy	Op	S G	δλ	QQ	λo i	a :	g g	٥ý	g	Oy Dp	Qy	QQ	O _Y	δŏ	QQ .	oy D	Qy	qq	oy da	δλ	CC	Qy Dp	δy

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-ACCCGAAGGTAAAATTTGGATTGATAAGATCTTGACAACTGAAATTGGACT 3444
                                                          TAAGGAAGAAAATGTCAATCATACCTCAGGAACCTGTTTTGTTCACTGGAAC 3504
                                                                                                                                                                                                                      AAAACCTGGATCCCTTTAAGGAGCACACGGATGAGGAACTGTGGAATGCCTT 3564
                                                                                                                                                                TACAACTTAAAGAAACCATTGAAGATCTTCCTGGTAAAATGGATACTGAATT 3624
                                                                                                                                                                                                                                                          CAGGATCCAATTTTAGTGTTGGACAAAGACAACTGGTGTGCCTTGCCAGGGC 3684
                                                                                                                                                                                                                                                                          ACAGATTGAACACCATTATTGACAGCGACAAGATAATGGTTTTAGATTCAGG 3864
                                                                                                                                                                                                                                                                                                                                                                      GTTAATACAAAAAAAATCCGGGAGAAATTTGCCCCACTGCACCGTGCTAAC 3804
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAGAATATGATGAGCCGTATGTTTTGCTGCAAAATAAAGAGAGCCTATTTA 3924
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       beley, Roger G.
YILON: Susan P.C.
YILON: METHODS FOR CONFERRING MULTIDRUG
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E: Floppy disk

IBM PC compatible

SYSTEM: PC-DOS/MS-DOS

ASCII text

ACTI text

ICATION DATA:

N WUMBER: US/08/460,907B
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27-0CT-1992
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llarity 47.1%; Pred. No. 3.7e-102;
Conservative 0; Mismatches 1786;
                                                                                                                                                                                                                                                                   PILLING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Steeq, Carol Miernicki
REGISTRATION NUMBER: 39,539
REFERENCE/DOCKET NUMBER: 01551
TELEPHONE: (613) 545-2342
TELEPRAX: (613) 545-2342
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
CLAMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                   FILING DATE: 26-UCA APPLICATION: 424
CLASSIFICATION: 424
PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/407,207
APPLICATION TO APPLICATION OF APPLICATION NUMBER: 08/407,207
APPLICATION NUMBER: 08/407,207
APPLICATION NUMBER: 08/407,207
APPLICATION: 424
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/029,340
                                                                                               FILING DATE:
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/141,893
FILING DATE: 26-0CT-1993
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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Best Local Similarity
Matches 1659; Conserv
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US-08-460-907B-1
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                                                                                                                                                                                                                                      GAGAGGGTGTCAGAGCAATCGTCAGCATCCGAAGAATCCAGACCTTTTTGCTACTTGAT
                                                               1885 ACATTIGCCGTCTACGTGACCATTGACGAGAACAACATCCTGGATGCCCAGACAGCCTTC
                                                                                                                                                                                           1945 GIGICITIGGCCTIGITCAACAICCTCCGGTTTCCCCTGAACAITCTCCCCAIGGTCAIC
                                                                                                                                                                                                                                                                                 2005 AGCAGCATCGTGCAGGCGAGTGTCTCCCTCAAACGCCTGAGGATCTTTCTCTCCCATGAG
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APPLICANT: Cole, Roger G.
TITLE OF INVENTION: METHODS FOR IDE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 51.
CITY: Boston
CITY: Massachusetts
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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Pred. No. 3.7e-102;
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                            APPLICATION DIABLES:

(LASSIFICATION) 536
FILING DATE:
CLASSIFICATION DATE:
CLASSIFICATION DATE:
APPLICATION NUMBER: 07/966,923
FILING DATE: 27-0CT-1992
APPLICATION NUMBER: 08/1029,340
FILING DATE: 8-MAR-1993
APPLICATION NUMBER: 08/141,893
FILING DATE: 26-0CT-1993
APPLICATION NUMBER: 08/407,207
FILING DATE: 26-0CT-1993
APPLICATION NUMBER: 08/407,207
FILING DATE: 20-MAR-1995
ATTORNEY AGENT INFORMATION:
NAME: DECORT, GIULIO A. JF.
REGISTRATION NUMBER: 90I-002CP8
TELECOMMUNICATION INFORMATION:
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Best Local Similarity 47.1%;
Matches 1659; Conservative
            CURRENT APPLICATION DATA
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US-08-463-179A-1
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                                                                                         1178 GIGACGCIGIAIGGGGCTGTGCGGCTGACGGTTACCCT---CTTCTTCCCCTCAGCCATT
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TGGCATTGTGGGAAGAACCGGAGCTGGAAAAAGTTCCCTCATCTCAGCCTTTTTAGATT
                                      ACCACCAGCCTGGCCCCATGAAGGAGTGATAATCTTTGACAATGTGAACTTCATGTACAG
                                                        GTCAGA---ACCCGAAGGTAAAATTTGGATTGATAAGATCTTGACAACTGAAATTGGACT
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APPLICANT: Cole, Susan P.C.

APPLICANT: Cole, Susan P.C.

APPLICANT: Deeley, Roger G.

TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS

STREET: Queen'S University at Kingston

CITY: Kingston

STATE: Ontario

COUNTRY: CANADA

ZIP: K7L 3N6

COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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Pred. No. 3.7e-102;
0; Mismatches 1786;
                                                                                    CURRENT AFFLLCATION DAIRS.

PRING DATE: 05-UON-95
FILING DATE: 05-UON-95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/966,923
FILING DATE: 27-0CT-1993
APPLICATION NUMBER: 08/029,340
FILING DATE: 8-MAR-1993
APPLICATION NUMBER: 08/141,893
FILING DATE: 26-0CT-1993
APPLICATION NUMBER: 08/407,207
FILING DATE: 20-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Steeg, Carol Miernicki
REGISTRATION NUMBER: 99,539,
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: Q1547 TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (613) 545-2342
TELEFAX: (613) 545-6853
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
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                                                                            CURRENT APPLICATION DATA:
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STRANDEDNESS: double
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US-08-461-384B-1
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                                                                                                                                            4104 AGAGGACCTGGACTTCGTTCTCAGGCACATCAATGTCACGATCAATGGGGGAGAAAAGGT
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                                                              ACCACCAGCCTGGCCCCATGAAGGAGTGATAATCTTTGACAATGTGAACTTCATGTACAG
                                                                                           4044 GCCCAGCAGCIGGCCCCAGGIGGGCCGAGIGGAATICCGGAACTACTGCCTGCGTACCG
                                                                                                                              TCCAGGTGGGCCTCTGGTACTGAAGCATCTGACAGCACTCATTAAATCACAAAAAGGT
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CORRESPONDENCE ADDRESS:
ADDRESSE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS STREET: Queen's University at Kingston CITY: Kingston STATE: Ontario COUNTRY: CANADA ZIP: K7L 3N6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Deeley, Roger G. APPLICANT: Cole, Susan P.C.
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US-08-407-207A-1
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Pred. No. 3.7e-102;
0; Mismatches 1786;
                                                                 SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/407,207A
FILING DATE: 20-MAR-1995
                                                                                                                                       CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/966,923
FILING DATE: 27-0CT-1992
APPLICATION NUMBER: 08/029,340
FILING DATE: 8-MAR-1993
APPLICATION NUMBER: 06/11,1893
FILING DATE: 26-0CT-1993
ATTORNEY, AGENT INFORMATION:
                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: Q1512 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                            NAME: Steeg, Carol Miernicki
REGISTRATION NUMBER: 39,539
                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (613) 545-2342
TELEFAX: (613) 545-6853
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 9.2%;
Best Local Similarity 47.1%;
                 Floppy disk
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COMPUTER READABLE FORM:
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US-08-407-207A-1
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  TTCAAGGACAAGGTGCTGGCCATCAGGCAGGAGGAGCTGAAGGTGCTGAAGAGTCTGCC 1824
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Sequence 55, Appl Sequence 1392, App Sequence 105, App Sequence 24, Appl Sequence 823, App Sequence 823, App Sequence 822, App Sequence 822, App Sequence 822, App Sequence 804, App Sequence 157, App Sequence 157, App Sequence 157, App Sequence 271, App Sequence 27

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Sequence 823, R Sequence 822, A Sequence 822, A Sequence 822, R Sequence 822, R Sequence 822, R

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ALIGNMENTS

Sequence 804, Sequence 3407 Sequence 150, Sequence 177, Sequence 277, Sequence 1080 Sequence 603, Sequence 613, Sequence 462, Sequence 462, Sequence 1011, Sequence 611, S

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APPLICANT: Fanger, Gary R.

APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Wantanabe, Madeleline Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TILE REPERBENGE: 210121.427C27
CURRENT APPLICATION WHERE: US/10/012,896
CURRENT FILING DATE: 2001-12-10
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Houghton, Raymond L.
Vinals de Bassols, Carlota
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Kalos, Michael D.
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Hepler, William T.
Henderson, Robert A.
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Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
Li, Samuel X.
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          APPLICANT: Xu, Jiangonun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Carter, Darrick, Thomas.S.
APPLICANT: Li, Samuel
APPLICANT: Li, Samuel
APPLICANT: Wady, Aljun
APPLICANT: Wady, Aljun
APPLICANT: Hepler, William
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121-427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2011-01-12
NUMBER OF SEQ ID NOS: 934
SEQ ID NO 535
LENGTH.
                                                                                                                                                                                                                                                                     DB 10;
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llarity 99.9%; Pred. No. 0;
Conservative 0; Mismatches
      Xu, Jiangchun
Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
                                                                                                                                                                                                                                 TYPE: DNA
CORGANISM: Homo sapiens
US-09-759-143-535
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Matches 4225; Conserv
INFORMATION:
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16	081 TGGTGATCTGACTGTGATAGGAGAACCACGCTGAGTGGAGGGCAGAAAGCACG 1740 	qq (
17	1741 GGTAAACCTTGCAAGAGCAGTGTATCAAGATGCTGACATCTATCT	δδ Op
18.	1801 CAGIGCAGTAGAGGGGAAGTIAGCAGACACTIGITCGAACTGTGTATTIGTCAAATTTT 1860 	Oy Dp
18	1861 GCATGAGAAGATCACAATTTTAGTGACTCATCAGTTGCAGTACCTCAAAGCTGCAAGTCA 1920 	δγ Dp
19	921 GATTCTGATATTGAAGATGGTAAAATGGTGCAGAAGGGACTTACACTGAGTTCCTAAA 1980 	Qy
19	1981 ATCIGGTATAGATITIGGCTCCCTITIAAAGAAGGATAATGAGGAAAGTGAACAACCTCC 2040 	Oy Dp
20	2041 AGTICCAGGAACTCCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGGTCTCA 2100 1111111111111111111111111111111111	OY Db
21	2101 ACAATCTTCTAGACCCTCCTTGAAAGATGGTGCTCTGGAGGGCCAAGATACAGAGATGT 2160 11111111111111111111111111111111111	Qy Db
21.	161 CCCAGTTACACTATCAGAGGAGAACGGTTCTGAAGGAAAAGTTGGTTTTCAGGCCTATAA 2220 	oy Db
222	221 GAATTACTTCAGAGCTGGTCACTGGATTGTCTTCATTTTCCTTATTCTCCTAAACAC 2280 . 	y d
22	2281 TGCAGCTCAGGTTGCCTATGTGCTTCAAGATTGGTGGCTTTCATACTGGGCAAACAAA	Oy Ob
23	2341 AAGTATGCTAAATGTCACTGTAAATGGAGGAAATGTAACCGAGAAGCTAGATCTTAA 2400 	g g
24	2401 CTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTTGGCATAGCAAG 2460 	o o
24	161 ATCTCTATTGGTATTCTACGTCCTTGTTAACTCTTCACAAACTTTGCACAAAAAGTT 2520 	oy Ob
25 , 25	521 TGAGTCAATTCTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGAATTT 2580 	da d
25	581 AAATCGTTTCTCCAAAGACATTGGACACTTGGATGATTTGCTGCCGCTGACGTTTTTAGA 2640 	d d
26	641 TTTCATCCAGACATTGCTACAAGTGGTTGGTGGTCTCTGTGGCTGTGGCCGTGATTCC 2700	da da
27	2701 TTGGATGGCAATACCCTTGGTTCCCCTTGGAATCATTTTTCATTTTTCTTGGGGGATATTT 2760 	Qy Dp

QY	2761	TGGAAACGTCAAGAGATGTGAAGCGCCTGGAATÇTACAACTCGGAGTCCAGTGTTTTC 2
qq		
δy	2821	CCACTTGTCATCTTCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAAGAGAG 2880
QQ	2891	ACTIGICATCTICICACGGGCTCTGGACCATCCGGGCATACAAGCAGAAGAGAG 29
QY	2881	AGGAACTGTTTGATGCACACCAGGATTTACATTCAGAGGCTTGGTTCTTGTTTT 294
qq	2951	GTCAGGAACTGTTTGATGCACACCAGGATTTACATTCAGAGGCTTGGTTCTTGTTTT 30
QY	94	11141111111111111111111111111111111111
qa	3011	AACGTCCCGCTGGTTCGCCGTCCGGTGCCATCTGTGCCATGTTTGTCATCAT 307
QY	õ	3GATGCCGGCCAGGTTGGTTTGGC 306
qa	3071	TIGCCTTTGGGTCCCTGATTCTGGCAAAAACTCTGGATGCCGGGCAGGTTGGTT
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QΩ	3131	rerectatecereacectearesearerreagistrerereacaaaareere
QY	3121	IATGATGATCTCAGTAGAAAGGGTCATTGAATACACAGACCTTGAAAAAGA 3
qq	3191	3TTGAGAATATGATGATCTCAGTAGAAAGGGTCATTGAATACACAGACCTTGAAAAA
Qy	3181	CCTTGGGAATATCAGAAACGCCCACCACCACCTGGCCCCATGAAGGAGGATAAT 32
qa	3251	
Qy	3241	CCAGGTGGGCCTCTGGTACTGAAGCATCTGAC 330
qa	3311	TTGACAATGTGAACTTCATGTACAGTCCAGGTGGGCCTCTGGTACTGAAGCATCTGAC
QY	3301	ATTAAATCACAAGAAAAGGTTGGCATTGTGGGAAGAACCGGAGCTGGAAAAG 33
qa	3371	CACTCATTAAATCACAAGAAAGGTTGGCATTGTGGGAAGAACCGGAGCTGGAAAAAG 34
QY	3361	CATCTCAGCCCTTTTTAGATTGTCAGAACCCGAAGGTAAAATTTG
qa	3431	CCCTCATCTCAGCCCTTTTTAGATTGTCAGAACCCGAAGGTAAAATTTGGATTGATAA 34
QY	3421	GATTTAAGGAAGAAATGTCAATCATACCTCA 348
qa	3491	CTTGACAACTGAAATTGGACTTCACGATTTAAGGAAGAAAATGTCATCATACCTCA
QY	3481	TTGTTCACTGGAACAATGAGGAAAAACCTGGATCCCT
qa	3551	GAACCTGTTTTGTTCACTGGAACAATGAGGAAAAACCTGGATCCCTTTAATGAGCA
QY	3541	GATGAGGAACTGTGGAATGCCTTACAAGAGGTACAACTTAAAGAAACCATTGAAGAT
qa	3611	ATGAGGAACTGTGGAATGCCTTACAAGAGGTACAACTTAAAGAAACCATTGAAGATCT
Qy	3601	TIGGTAAAATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGGACAAAG 366
qa	3671	AAAATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTG
QY	3661	TTGCCAGGGCAATTCTCAGGAAAATCAGATATTGATTATTGATGA 372
QΩ	3731	AACTGGTGTGCCTTGCCAGGCAATTCTCAGGAAAATCAGATATTGATTATTGATGA 379
δλ	3721	GCAAATGTGGATCCAAGAACTGATGAGTTAATACAAAAAAAA
qq		CGACGGCAAATGTGGATCCAAGAACTGATGAGTTAATAC-AAAAAAAATCCGGGAGAA 3
Qy		CCATTGCACACAGATTGAACACCATTATTGACAGCGA 384
qa	3850	TTGCCCACTGCACCGTGCTAACCATTGCACAGATTGAACACCATTATTGACAGGA 3

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CAAGATAATGGTTTTAGATTCAGGAAGACTGAAAGAATATGATGAGACCGTATGTTTGCT
                                         GCAAAATAAAGAGGCCTATTTTACAAGATGGTGCAACAACTGGGCAAGGCCGC
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APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Hepler, William
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CAN
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780,669
CURRENT PILLIAG DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  METHODS
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Pred. No. 0;
0; Mismatches
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Patent No. US20020051977A1
GENERAL INFORMATION:
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Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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Dillon, Davin C.
Mitcham, Jennifer L.
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Matches 4225; Conservative
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ORGANISM: Homo sapiens
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                              GCCCGTGTACCAGGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACATCTGCTCACGCGT
                                                                 GTTCTTCTGGTGGCTCAATCCCTTGTTTAAAATTGGCCATAAACGGAGATTAGAGGAAGA
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Pred. No. 0;
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CURRENT APPLICATION NUMBER: US/09/822,827
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 535
LENGTH: 6082
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                                                                                       99.5%;
                                                                                      Query Match 99.5
Best Local Similarity 99.9
Matches 4225; Conservative
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                                                   ; TYPE: DNA
; ORGANISM: HOMO
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Qy Db	2101	ATCTTCTAGACCCTCCTIGAAAGATGGTGCTCTGGAGAGCCAAGATACAGAATGT 2.	16 23
VQ .	2161	TTTTCAGGCCTATAA 2	22
Oy Db	2221	GCTCACTGGATTGTCTTTCCTTATTCTCTAAACAC	35
QY Db	2281	TCAGGTTGCCTATGTGCTTCAAGATTGGTGGCTTTCATACTGGGCAACAACA 2	34
QY Db	2341	CACTGTAAATGGAGGAAGAATGTAACCGAGAAGCTAGATCTTAA 2 	40
QQ .	2401	AGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTTGGCATAGCAAG 2	5.4
QY Db	2461	CFCTATTGGTATTCTACGTCCTTGTTAACTCTTCACAAACTTTGCACAACAAATGTT 2	52
Qy	2521	TCTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGAATTT 2 	ις ι <u>σ</u>
Qy	2581	CCAAAGACATTGGACACTTGGATGATTTGCTGCCGCTGACGTTTTTAGA 2: 	9 1
Qy Db	2641	PATCCAGACATTGCTACAAGTGGTTGGTGGTCTCTGTGGCTGTGGCCGTGATTCC 2	7 7
Qy Db	2701	CTTGGTTCCCCTTGGAATCATTTTCATTTTT 	7
QQ DD	2761	CTACAACTCGGAGTCCAGTGTTTC 	2820
Q qa	2821	TITCICTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAAGAGAGAG	2880
Oy Db		AACTGTTTGATGCACCAGGATTTACAFTCAGAGGCTTGGTTCTTGTTTT	6 0
QY	3011	CIGGTICGCCGTCCGTCTGGATGCCATCTGTGCCATGTTTGTCATCATCATCATCATCATCATCGCCGTCGTCTGGATGCCATCTGTGCCATGTTTGTCATCAT	3000
QV	3001	TTTGGGTCCCTGATTCTGGCAAAACTCTGGATGCCGGGCAGGTTGGTT	3060
Qy	3061	TGTCCTATGCCCTCACGCTCATGGGGATGTTTCAGTGGTGTGTTCGACAAAGTGCTGA	3120

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Day, Craig H.
Vedvick, Thomas
Carter, Darrick
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Stolk, John A.
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Best Local Similarity 97.1
Matches 4040; Conservative
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 6140
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APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Meagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY ITILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
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Pred. No. 0;
0; Mismatches
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CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
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                                                             4270 CAAGATGCTAGTTCATTTGAATATTTCTCCC
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                                                                                                                                                                             Sequence 536, Application US/10012896
Publication No. US20020183251A1
GENERAL INFORMATION:
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COTHER INFORMATION: n = A,T,C or
US-10-012-896-536
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APPLICAMT: Dillon, Davin C.
APPLICAMT: Mitcham, Jennifer L.
APPLICAMT: Harlocker, Susan L.
APPLICAMT: Jiang, Yuqiu
APPLICAMT: Kalos, Michael D.
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Houghton, Raymond L.
Vinals de Bassols, C
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Hepler, William T.
Henderson, Robert A.
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qq		TCTCGGGAACTCTGAGGAGTAATTTTATTTGGGAAGAATACGAAAGGAACGATATG	1672
Qy P	1629	AAAAAGTCATAAAGGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTGGAGGATGGTGATC	1688
ò		GACTGTGATACGAGAACGGGGAACCACGTGAGTGGAGGGAAAAGAAAACAAAAAACAAAAAAC	1748
7 A	m	TGACTGTGATAGGAGATCGGGGAACCACGCTGAGTGGAGGGCAGAAACACGGGTAAACC	1792
Qy	1749	SCAAGAGCAGTGTATCAAGATGCTGAC	1808
qq	1793	TGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCCTGGACGATCCTCTCAGTGC	1852
Qy	0	TAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAAATTTTGCATGAGA 1	1868
QQ	1853	atgcccaaagttaccagacacttottcgaactgtgtatttgtcaaattttgcatgag	1912
. Oy	1869	AGATCACAATTTTAGTGACTGATCAGTTGCAGTACCTCAAAGCTGCAAGTCAGATTCTGA 1 	1928
ò	ič	ATTRADAGATROTAAAATGGTGCAGAAAAGGGGAATTACAACTTCTAAAAATGCTGCAGAAAGATGAAAAATGAAAAAGATGAAAAAAAA	. 0
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δy	1989	AGATTTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAAGTGAACAACCTCCAGTTCCAG	04
Ob	2033		2002
Qy	2049	AACTCCCACACAAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGGTCTCAACAATCTT	10
q a .	2093	CTCCACACTAAGGAATCGTACTTCTCAGAGTCTTCGGTTTGGTCTCAACAATCTT	S
ΟY	2109	CTAGACCCTCCTTGAAAGATGGTGCTCTGGAGAGCCAAGATACAGAGAATGTCCCAGTTA 2	16
qq	2153	TAGACCCTCCTTGAAAGATGGTGCTCTGGAGGCCAAGATACAGAGAATGTCCCAGTTA	-
Οy	16	CACTATCAGAGGAGAACCGTTCTGAAGGAAAGTTGGTTTTCAGGCCTATAAGAATTACT 2	2228
qq	21	ACTATCAGAGGAGAACCGTTCTGAAGGAAAAGTTGGTTTTCAGGCCTATAAGAATTACT	27
QY	22	TIGECTTCATTTCCTTATTCTCCTAAACACTGCAGCTC	28
qq	2273	CAGAGCTGGTGCTCGATTGTCTTCTTTTCCTTATTCTCCTAAACACTGCAGCTC	3
δy	2289	CAAACAAAGTATGC	2348
QQ	2333	STTGCCTATGTGCTTCAAGATTGGTGGCTTTCATACTGGGCAAACAAA	σ
ΟŊ	2349	AAATGTCACTGTAAATGGAGGAGGAAATGTAACCGAGAAGCTAGATCTTAACTGGTACT	
qq	2393	STCACTGTAAATGGAGGAGGAAATGTAACCGAGAAGCTAGATCTTAACTGGTACT	2452
Qy	2409	TTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTGGCATAGCAAGATCTCTAT	46
QQ	2453	AGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTTGGCATAGCAAGAFCTCTAT	2512
Oy		TGGTATTCTACGTCCTTGTTAACTCTTCACAAACTTTGCACAAAAATGTTTGAGTCAA	7
qq	2513	GGTATTCTACGTCCTTGTTAACTCTTCACAACTTTGCACAACAAAATGTTTGAGTCAA	L)
δλ	2529	TTCTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGAATTTTAAATCGTT 2	2588
QQ	2573	CTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGAATTTTAAATCGTT	2632
δδ.	2589	TCTCCAAAGACATTGGACACTTGGATGATTTGCTGCCGCTGACGTTTTAGATTTCATCC 2	2648

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                                         CATCTTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAAGAGAGGTGTCAGG
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FINVENTION: DIAGNOSIS OF PROSTATI
FEBRICE: 210121.477C23
APPLICATION NUMBER: US/09/759,143
FILING DATE: 2001-01-12
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Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
Li, Samuel
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Dillon, Davin C.
Mitcham, Jennifer L.
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Skeiky, Yasir A.W.
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CURRENT APPLICATI
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OTHER INFORMATION: n=A,T,C
                                             NAME/KEY: misc_feature
NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for.
SEQ ID NO 536
LENGTH: 6140
                                  sapiens
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ORGANISM: HOMO
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US-09-759-143-536
                                       FEATURE:
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CTAGACCCTCCTTGAAAGATGGTGCTGGAGAGCCAAGATACAGAGAATGTCCCAGTT	TTGGTTT.		rccttat		CATACTG		CCGAGAA		PTCTTTT		TTTGCA		TCCAATA		GCCGCTC		GGCTGT		TTTTCT		TCGGAG1		ATACAA		GGCTTGG		TGCCATG		CGGGCAG		TGTTCGA		CACAGAC		CCATGAA	CCATGAA
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TAAATCACAAGAAAAGGTTGGCATTGTGGGAAGAACGGGAGCTGGAAAAAGTTCCCTCA CTCAGCCCTTTTTAGATTGTCAGAACCCGAAGGTAAAATTTGGATTGATAAGATCTTGA AACTGAAATTGGACTTCACGATTTAAGGAAGAAAATGTCAATCATACCTCAGGAACCTG ACTGTGGAATGCCTTACAAGAGGTACAACTTAAAGAAACCATTGAAGATCTTCCTGGTA AATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGGACAAAGACAACTGG ITTGTTCACTGGAACAATGAGGAAAAACCTGGATCCCTTTAAGGAGCACACGGATGAGG TGCACCGTGCTAACCATTGCACACAGATTGAACACCATTATTGACAGGGACAAGATAA GETTTTAGATTCAGGAAGACTGAAAGAATATGATGAGCCGTATGTTTTGCTGCAAAATA CCTCAAGTGATCCACCTGCCTTGGCCTCCCAAACTGCTGAGATTACAGGTGTGAGCCA GAAACAGCAAAACAG----

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                                                                                                                                             APPLICANT: Mitchan, Davin C.
APPLICANT: Mitchan, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Fatter, Marc W.
APPLICANT: Day, Craig H.
APPLICANT: Day, Craig H.
APPLICANT: Day, Craig H.
APPLICANT: Day, Craig H.
APPLICANT: Li, Samuel
APPLICANT: Harlocker, Milliam
APPLICANT: Harlocker, Milliam
APPLICANT: Horal, John
APPLICANT: Horal, John
APPLICANT: Horal, John
APPLICANT: HORALOCKER, TILE OF INVENTION: DIAGNOSTIFON SAND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSTS OF PROSTATE CANCER
TITLE OF INVENTION: DIAGNOSTS OF PROSTATE CANCER
CURRENT FILIS DATE INVENTION: DAGOSTATE CANCER
TITLE OF INVENTION: DAGOSTATE CANCER
CURRENT FILIS DATE INVENTION: DAGOSTATE CANCER
TITLE OF INVENTION NUMBER: US/09/780,669
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Pred. No. 0;
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                                                                                            Sequence 536, Application US/09780669 Patent No. US20020051977A1
                                                                                                                                  Xu, Jiangchun
Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
            4373 GTTCATTTGAATATTTCTCCC 4393
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GTTCATTTGAATATTTCTCCC
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NAME/KEY: misc_feature
LOCATION: (1)...(6140)
OTHER INFORMATION: n-A,T,C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 536
                                                                                                                      GENERAL INFORMATION:
APPLICANT: Xu, Jia
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1629 AAAAGTCATAAAGGCTTGTGCTCTGAAAAGGATTTACAGCTGTTGGAGGATGGTGATC 111111111111111111111111111111111111	()-() ()-()	1989 TAGATTTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAAGTGAACAACCTCCAGTTCCAG 11111111111111111111111111111111111	2169 CACTATCAGAGGACACCGTTCTGAAGGAAAGTTGGTTTTCAGGCCTATAAGAATTACT	349 TAAATGTCACTGTAATGGAGGAATGTAACCGGAAGCTAGATCTTAACTGGTAG 379 TAAATGTCACTGTAATGGAGGAGGAATGTAACCGGAAGCTAGATCTTAACTGGTAG 379 TAAATGTCACTGTAAATGGAGGAGAATGTAACCGGAAGCTAGATCTTAGTTAACTGGTAC 409 TAGAATTTAATTCAGGTTAACTGTAGCTACCGTTCTTTTGGCATAGCAAGATCTCTA 4111111111111111111111111111111111111	NGAAATCCAATAGGAAGAATTTTAAATC NGAAATCCAATAGGAAGAATTTTAAATC NGAAATCCAGTGACGAATTTTAAATC TGCTGCCGCTGACGTTTTAGATTTCA IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
oy oy oy	oy oy	64 C C C C C C C C C C C C C C C C C C C		6 6 6 6 6 6	90 AA

Qy Db	2709	CAATACCCTTGGTTCCCCTTGGAATCATTTTCATTTTCTTCGGCGATATTTTTTGGAAA 	2768
Qy Db	2769	CGTCAAGAGATGTGAAGCGCCTGGAATCTACAACTCGGAGTCCAGTGTTTTCCCACTTGT	2828
Qy	2829	CATCTTCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAAGAGGGGTGTCAGG	2888
Oy Db	2889	AACTGTTTGATGCACACCAGGATTTACATTCAGAGGCTTGGTTCTTGTTTTTGACAACGT 	2948
Qy	2949	CCCGCTGGTTCGCCGTCCGTCTGGATGCCATCTGTGCCATGTTTGTCATCATGTTTGCCTTGCTTG	3008
QY	3009	TTGGGTCCCTGAŤTCTGGCAAAAACTCTGGATGCCGGGCGGGTTGGTTTGGCACTGTCCT 	3068
QY Db	3069	ATGCCCTCACGCTCATGGGGATGTTTCAGTGGTGTGTTCGACAAAGTGCTGAAGTTGAGA 	3128
Qy	3129	ATATGATGATCTCAGTAGAAAGGTCATTGAATACACAGACCTTGAAAAGAAGCACCTT 	3188
Qy Db	3189	GGGAATATCAGAAACGCCCACCACCAGCGCCCCATGAAGGAGTGATAATCTTTGACA 	3248
Oy Db	3249	ATGTGAACTTCATGTACAGTCCAGGTGGGCCTCTGGTACTGAAGCATCTGACAGCACTCA	3308
Qy	3353	TTAAATCACAAGAAAAGGTTGGCATTGTGGGAAGAACCGGAGCTGGAAAAAGTTCCCTCA : 	3368
Qy Db	3369	TCTCAGCCCTTTTTAGATTGTCAGAACCCGAAGGTAAAATTTGGATTGATAAGATCTTGA :	3428
δγ	3429	actgaaattggacttcacgatttaaggaagaaatgtcaatcatactcaggaacctg 	3488 3532
O _Y	3489	TITICITCACTGGAACAATGAGGAAAACCTGGATCCCTTTAAGGAGCACACGGATGAGG 	3548
Qy	3549 3593	AACTGTGGAATGCCTTACAAGAGGTACAACTTAAAGAAACCATTGAAGATCTTCCTGGTA 	3608
Oy Db	3653	AAATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGGACAAAGACAACTGG : 	3668 3712
Oy Db	3669 3713	TGTGCCTTGCCAGGGCAATTCTCAGGAAAATCAGATATTGATTATTGATGAAGCGACGG :	
Qy Db	3729	CAAATGTGGATCCAAGAACTGATGAGTTAATACAAAAAAAA	3788 3832
Oy	3789	ACTGCACCGTGCTAACCATTGCACACAGATTGAACACCATTATTGACAGCGACAAGATAA 3	3848

293 ATTCAGTGCTGCCAGAAGACCGCTCACAGCACCTTGGAGAGGTTGCAAGGGTTCTGG 309 ATAAAGAAGTTTAAGAGCTGAGAATGACGCACAGAAGCCTTCTTAACAAGAGCAATC.		549 CGCTCATTTGGCTATACTCATCACTTATATTTTATCACGTTCAGTGCTGGGATGA 608	669 CCATGGGGAAGACCACAGGCCAGATAGTCAATCTGCTGTCCAATGATGTGAACAAGT 728 11111111111111111111111111111111111	789 TGACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCTTGCTGGGATGGCAGTTCTAA 84 	849 893 909		1029 AGGAGATTTCCAAGATTCTGAGAAGTTCCTGCCTCAGGGGGATGAATTTGGCTTCGTTTT 1088	7 1089 TCAGTGCAAGCAAAATCATCGTGTTTGTGACCTTCACCACCTACGTGCTCCTCGGCAGTG 1148 	1149 TGATCAC 	1209	/ 1269 GAATCCAGACCTTTTTGCTACTTGATGAGATATCACAGGGCAACCGTCAGCTGCCGTCAG 1328	1329 ATGGTAAAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTTGGGATAAGGCATCAGAGA 1388
	da oy	OY OY OY	Oy Oy Oy	QY Db	oy Db	D Qy	QY	Qy Dp	QY	QY	QV	OY Db
	Qy 3969 CTGAAACAGCAAAACAG 3985	3986	4091 TGAATCCAACCAAAATGTCAAGTCGTTCCGAAGGCATTTCCACTAGTTTTTGGACTAT 415 4253 TGAATCCAACCAAAATGTCAAGTCGTTCCGAAGGCATTTTCCACTAGTTTTTTGGACTAT 413 4151 GTAAACCAACTAAAATGTCAAGTCGTTCCCGAAGGAATTTGCCACTAGTTTTTGGACTAT 431 4151 GTAAACCACATTTTTTTTACTTTGGCAACAAATATTTAACATACAAAAATGTCAAGTGTTTTTTAGTTTTTAGTTTTTAGTTTTTAGTTTTTAGTTTTTAGTTTTAGTTTTTT	Db 4313 GTAAACCACATTGTACTTTTTTACTTTGGCAACAATATTTATACATAC	RESULT 8 US-09-822-827-536 ; Sequence 536, Application US/09822827	; Patent No. US20020081680A1 ; GENERAL INFORMATION: ; APPLICANT: Xu, Jiangchun ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND ; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER ; FILE REPERENCE: 210121.534C1 ; CHEDERW ADDITORATON MINDED. 115/00/202 827	CURRENT FILING DATE: 2001-03-28 NUMBER OF SEQ ID NOS: 982 SOFTWARE: FastSEQ for Windows Version 3.0	LENGTH: 6140 TYPE: DNA ORGANISM: Homo sapiens FEATURE:	; NAME/KEY: misc_feature ; LOCATION: (1)(6140) ; OTHER INFORMATION: n-A,T,C or G US-09-822-827-536	Query Match 92.4%; Score 3910.2; DB 10; Length 6140; Best Local Similarity 97.1%; Pred. No. 0; Matches 4040; Conservative 0; Mismatches 3; Indels 118; Gaps 1;	TCANTCCTTGTTTAAAATTGGCCATAAACGGAGATTAGAGGAAGATGATGT 248	249 ATTCAGTGCCACAAAGACGCTCACAGCACCTTGGAGAGGTTGCAAGGGTTCTGGG 30

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1448 1492 1508 1552 1568	1612 1628 1672 1688	73:741	1808 1852 1868 1912	1928 1972 1988 2032	2048 2092 2108 2152	2168 2212 2228 2272	2288 2332 2348 2392	2408 2452 2468 2512
CCCCAACTCTACAAGGCCTTTCCTTTACTGTC CCCCAACTCTACAAGGCCTTTCCTTT	GTCACGGGCTGGTCAGCGTGCAAGAATTGCCTATGTGTGTCTCAGCAGCCCTGGGTG TCTCGGGAACTCTGAGGAGTAATTTTATTTGGGAAGAAATAGAAAAGGAAGGAACGATGTTTTGGGAAGAAATAGGAAATAGGAAAATGGAAATGGAAATGGGAACTGTCTGAGGAACTGTTTATTTGGGAAGAAATAGGAAATGGAAAAGGAAGG		TIGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCCTGGACGATCCTCTCAGTGCAG [111111111111111111111111111111111111	AGATCACAATTTTAGTGACTCATCAGTTGCAGTACCTCAA 	TAGATTTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAACTGAACACCCCCAGTTCCAG [CTAGACCCTCCTTGAAAGATGGTGCTCTGGAGAGCCAAGATACAGAGAATGTCCCAGTTA	TCAGAGCTGGTGCTCACTGGATTGTCTTCATTTTCTTTATTTTCCTAAACACTGCAGCTC	TAAATGTCACTGTAAATGGAGGAATGTAACCGAGAAGCTAGATCTTAACTGGTACT [
443.505	1553 1569 1613 1629	68 68 73	1749 1793 1809 1853	1869 1913 1929 1973	1989 2033 2049 2093	2109 2153 2169 2213	2229 2273 2289 2333	2349 2393 2409 2453
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Qy	469	TGGTATTCTACGTCCTTGTTAACTCTTCACAAACTTTGCACAACAAAATGTTTGAGTCAA 2528
Qy	2529	TTCTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGAATTTTAAATCGT 2588
Qy Dp	2589 7	IGGACACTTGGATGATTTGCTGCCGCTGACGTTTTAGATTTCATCC 2641
QY	2649 A	STGGCCGTGATTCCTTGGATCG 270
óy Db	2709 C	9 .1
Qy Db	2769 C	rcccactrct 28
QQ .	2829 C	8 6
Qy	2889 A 1 2933 A	AACTGTTTGATGCACCAGCAGTTTACATTCAGAGCTTGGTTCTTGTTTTTGACAACGT 2948
QY DP	2949 C	CCGCTGGTTCGCCGTCCGTCTGGATGCCATCTGTGCCATGTTTGTCATCATCGTTGCCT 30
oy ob	3009 T 1 3053 T	11
Qy Db	3069 A 1 3113 A	2 2
Qy Db	3129 A	TATGATGATCTCAGTAGAAAGGGTCATTGAATACACAGACCTTGAAAAAGAAGCACCTT 318
QY	3233 G	324)
QY	3249 A 1 3293 A	5
QY	3309 T	CCGGAGCTGGAAAAGTTCCCTCA 336.
Qy	3369 TO 1 3413 TO	CTCAGCCCTTTTAGATTGTCAGAACCCGAAGGTAAAATTTGGATTGATAAGATCTTGA 342;
QY .	3429 C	CAACTGAAATTGGACTTCACGATTTAAGGAAAATGTCAATCATACCTCAGGAACCTG 3488
Qy	3489 TE	TTRGTTCACTGGAACAATGAGGAAAAACCTGGATCCCTTTAAGGAGCACACGGATGAG 3548
Qy	3549 A	

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                                 AAATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGGACAAAGACAACTGG
                                                                           TGTGCCTTGCCAGGGCAATTCTCAGGAAAATCAGATATTGATTATTGATGAAGCGACGG
                                                                                                                       4073 GACCTCAAGTGATCCACCTGCCTTGGCCTCCCAAACTGCTGAGATTACAGGTGTGAGCCA
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Publication No. US20020183251A1
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Ralos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
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                                                                                                                                                                                                                                                                                                                                          238 AGATGATATGTATTCAGTGCTGCCAGAAGACCGCTCACAGCACCTTGGAGAGGAGTTGCA
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APPLICANT: Meagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
                                                                                                                                                                                                                                                                                             Score 3739.2;
                                                                                                                                                                                                                                                                                                       Pred. No. 0;
0; Mismatches
                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1007
                                                                                 Carlota
                                            Hural, John
McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, C
                                                                                                                                                                                                                                                                                           Ouery Match 88.4%;
Best Local Similarity 99.8%;
Matches 3744; Conservative
                                   Henderson, Robert
             Skeiky, Yasir A.W.
Hepler, William T
                                                                                                                                                              FILE REFERENCE: 210121.427C27
                                                                                            Foy, Teresa
Fanger, Gary R.
                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens
US-10-012-896-1007
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APPLICANT:
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TIGGTTCGCCGTCCGTCTGGATGCCATCTGTCCATGTTTGTCAT 2997 CTCACGCTCATGGGGATGTTTCAGTGGTGTGTTCGACAAAGTGC 3117 TCCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGGTC rgcctatgtgcttcaagattggtggctttcatactgggcaaacaa TTCTCTCCAGGGGCTCTGGACCATCCGGGGATACAAAGCAGAAGA ATCAGAGAGAACCGTTCTGAAGGAAAAGTTGGTTTTCAGGCCTA **AATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTTGGCATAGC** ATTCTACGTCCTTGTTAACTCTTCACAAACTTTGCACAAAAT TCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAAGA TGTCACTGTAAATGGAGGAGGAAATGTAACCGAGAAGCTAGATCT AAAAGACATTGGACACTTGGATGATTTGCTGCCGCTGACGTTTTT NTTGCTACAAGTGGTTGGTGTGTCTCTGTGGCTGTGGCCGTGAT ACCCTTGGTTCCCCTTGGAATCATTTTCATTTTTTTTCGGCGATA AGAGATGTGAAGCGCCTGGAATCTACAACTCGGAGTCCAGTGTT STTTGATGCACACCAGGATTTACATTCAGAGGCTTGGTTCTTGTT

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                                                           TAAGATCTTGACAACTGAAATTGGACTTCACGATTTAAGGAAGAAATGTCAATCATACC
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Publication No. US20020183251A1
GENERAL INFORMATION:
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APPLICANT: Xu, Jiangchun APPLICANT: Dillon, Davin C. APPLICANT: Mitcham; Jennifer L. APPLICANT: Harlocker, Susan L. APPLICANT: Jiang, Yuqiu

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APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Wantanabe, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR T
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427027
CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
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Houghton, Raymond L.
Vinals de Bassols, Carlota
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Best Local Similarity 99.9%;
Matches 3741; Conservative
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Hepler, William T.
                                              Day, Craig H.
Vedvick, Thomas
Carter, Darrick
Kalos, Michael D
Retter, Marc W.
Stolk, John A.
                                                                                           Li, Samuel X.
Wang, Aijun
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Sequence 613, Application

RESULT 11 US-09-925-300-613

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GENERAL INFORMATION:
APPLICANT: Craig Rosen,
APPLICANT: Craig Rosen,
TITLE OF INVENTION: Nucleic Acids, Proteins and
FILE REFERENCE: PA101
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: PATENTIN Ver: 2.0
SEQ ID NO 613
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28.8%;
Best Local Similarity 98.9%;
Matches 1221; Conservative 4
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; OTHER INFORMATION: n equals
US:09-925-300-613
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THE THERAPY AND
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APPLICANT: Fanger, Gary R.
APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Meagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
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CURRENT APPLICATION NUMBER: US/10/012,896
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McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
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Vedvick, Thomas S.
Carter, Darrick
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Hepler, William T.
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                                                                                                                                               Score 1045.4; DB 9
Pred. No. 1.3e-291;
0; Mismatches 1;
                                  3.0
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FRASESEQ for Windows Version
SEQ ID NO 824
                                                                                                                                               24.7%;
                                                                                                                                                              Best Local Similarity 99.9
Matches 1046; Conservative
                                                                              TYPE: DNA ORGANISM: Homo sapiens
                                                                                                               US-10-012-896-824
                                                                LENGTH: 1074
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Skeiky, Yasir A.W.
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US-09-780-669-824
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Pred. No. 1.3e-291;
0; Mismatches 1;
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APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: U., Samuel
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Walliam
APPLICANT: Skeiky, Walliam
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE C?
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759.143
CURRENT FILING DATE: 2001.01-12
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Patent No. US20020022248A1
GENERAL INFORMATION:
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Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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Dillon, Davin C.
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Matches 1046; Conser
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AGTAATATITTATTTGGGAAGAAATATGAAAAGGAACGATATGAAAAAGTCATAAAGGCT
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APPLICANT: Xu, Jingchun
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Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
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Dillon, Davin C.
Mitcham, Jennifer L.
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Vedvick, Thomas
Carter, Darrick
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Retter, Marc W.
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APPLICANT: Hepler, William
APPLICANT: Hural, John
APPLICANT: Horal, John
APPLICANT: Mowelll, Patricia D.
APPLICANT: Moughton, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121, 427C24
CURRENT APPLICATION NUMBER: US/09/780,669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FastERO for Windows Version 3.0
SEQ ID NO 824
                                                                                                                                                                                        Score 1045.4; DB 10; Length 1074; Pred. No. 1.3e-291;
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                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                       24.78;
                                                                                                                                                                                                            Matches 1046; Conservative
                                                                                                                                            ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-780-669-824
                                                                                                                                                                                                  Similarity
                                                                                                                                                                                        Query Match
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.534C1
CURRENT APPLICATION NUMBER: US/09/822,827
CURRENT FILING DATE: 2001.03-28
NUMBER: OF SQI IN NOS: 982.
SOFTWARE: FastSEQ for Windows Version 3.0
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Patent No. US20020081680A1
GENERAL INFORMATION:
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Search completed: December 18, 2002, 21:40:09 Job time : 144.455 secs

Scoring table:

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Eukaryota; Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 861)

NIH-MCO http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapba-remail.nih.gov

Tissue Procurement: ArCC

CDNA Library Preparation: Life Technologies, Inc.

CONA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.llnl.gov

Plate: LLAM13215 row: e column: 24

High quality sequence stop: 622.

1. 861
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B1770470 603055440
UG687 Homo sapien
BQ045143 UI-CF-ENI
BQ770412 UI-M-FIO-
BM553470 AGBNCOURT
BM695701 UI-E-COI-
BM695701 UI-E-COI-
BM695701 UI-M-EXO-
BQ763313 UI-M-FIO-
BQ763313 UI-M-FIO-
BB436535 BB436535
BQ275598 IXO2905 X
BG167408 602342662
BM512329 ij709903 X
BM705344 UI-E-CII-
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Perfect score:
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805.2 802.2 798.8 787.2 769.2 761.6

Score

Result

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/note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
- 'near+ size 1.1 kb. Library constructed by Life
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                                                                                                                       Score Bull.,
Pred. No. 6e-116;
                                                                                                                       Score 805.2; DB 14;
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                                                                                                                                         0; Mismatches
/organism="Homo sapiens"
      /db_xref="taxon:9606"
/clone="IMAGE:6016895"
                                                                                         198 д
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98.8%;
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                                                                                                                                        832; Conservative
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BG697157
602660381F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4803357 5',
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S NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: capabbs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10699 row: a column: 22
High quality Sequence stop: 820.
                                                                                                                                                                                                                                                                                 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:4803357"
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Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT
Average insert size 1.5bb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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Pred. No. 1.8e-115;
0; Mismatches 13; Indels 4;
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98.0%;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 862)
Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y.,
Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fax: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
Email: genomics@hri.co.jp
Email: genomics@hri.co.jp
Research Institute; CDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.
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                                         478 CCACTGCACAGAGCTCTCCAGGTCCAAGACCTGTTGGTTCCAAGCCCTGGAGCCAACTGC
                                                                                                                         TGCTTTTTGAGGTGGCACTTTTTCATTTGCCTATTCCCACACACCTCCACAGTTCAGTGGCA
                                                                                                                                    GGCGTAGAAGTTTTTGTACTGT-AAAGAGACCTACCTCAGGTTGCTGGTTGCTGTGTGGT
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                                                                                                                                                                 GGGCTCAGGATTTCGTGGGTCTGTTTTCCTTTCTCACCGCAGTCGTCGCACAGTCTCTCT
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                                                                                                                                                                                     GGGCTCAGGATTTCGTGGGTCTGTTTTCCTTTCTCACCGCAGTCGTCGCACAGTCTCTCT
                                                                                           Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
                                                                                                                                                                                                                                                                                                                                 CACTGCTGTCATCAGTTGAATGGTCAGCGTT 5698
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/clone_lib="NT2RP3"
                                                                                                                                                                                                                                                                                                                                                                                                                                        AU132064.1 GI:10992418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HRI human cDNA project
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
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AUTHORS
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                                                                                                 862;
                                                        4 others
                                                                                                 Length
/cell_type="teratocarcinoma"
/cell_line="NT2"
/note="Vector: pMell8SFL3; mRNA fro
cells after 2-weeks retinoic acid
1 230 c 227 g 213.t
                                                                                                 ..
                                                                                              Score 798.8; DB :
Pred. No. 6e-115;
0; Mismatches 41
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95.2%;
                                                                                                                             Conservative
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GAAGTGATGGAGAAATGGGGATAACTTCTCAGTGGGGGAACGGCAGCTCTTGTGCATAGCT
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BI770993
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AGENCOURT_8122242 Lupski_dorsal_root_ganglion Homo sapiens cDNA BQ898022
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pcMv-SPORT6 (Life Technologies); Site_1:
NotI: Site_2: SalI: cDNA made by oligo-dr priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACCCTCCG-3' and
5'-GACTAGTTCTAGATCGCGAGCGCCCCT(15)-3'. Size selected >
1 kb for average insert length 1' kb. This is a primary library non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life
                                                                                                                                                                                                                           Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-refaail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lln.gov
Plate: LLAM1360 row: m column: 13
High quality sequence stop: 701.
                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhin1; Hominidae; Homo.
1 (bases 1 to 935)
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                                                                                                                                                                                             NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xxef="taxon:9606"
/clone="IMAGE:6179508"
/clone_lib="Lupski_dorsal_root_ganglion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="dorsal root ganglia"
/dev_stage="adult, 36 yr"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 787.2; DB 14;
Pred. No. 3.7e-113;
0; Mismatches 28;
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Best Local Similarity 95.9%;
Matches 842; Conservative
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DEFINITION
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B1770993 851 bp mRNA linear EST 25-SEP-2001
603055332F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5204983 5',
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1 (bases 1 to 851)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                      4208
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Clone distribution: MGC clone distribution information can be found through the I.W.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.p column: 08
                                                                                                                                                                301 GAAGTGATGGAGAATGGGGATAACTTCTCAGTGGGGGAACGGCAGCTCTTGTGCATAGCT
                                             4149 AGAGCCCTGCTCCGCCACTGTAAGATTCTGATTTTAGATGAAGCCACAGGCTGCCATGGAC
                                                                     4209 ACAGAGACAGACTTATTGATTCAAGAGCCATCCGAGAAGCATTTGCAGACTGTACCATG
                                                                                                                                                                                                                                                          4389 ITCTAIGCCAIGITIGCIGCIGCAGAGAACAAGGICGCIGICAAGGGCIGACICCICCCI
                                                                                                                                                                                                                                                                                                                                                                                                                                         601 TTCTATGCCATGTTTGCTGCTGCAGAGAACAAGGTCGCTGTCAGGGCTGACTGCTCCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTTGACGAAGTCTCTTTTAGAGCATTGCCATTCCCT-GCCTGGGGCGGGCCCCTCA
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/db_xref="taxon:9606"
/clone="IMAGE:5204983"
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Location/Qualifiers
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3328 ATAAAGGGCAGGAGTTTCTGCACAGATACCAGGAGCTGCTGGATGACAACCAAGCTCCTT 3387
    GGGTGTCCCAAAGGACGACGTGTGGCAACTCGTGGGCCTCCGACAGCCCC
                                                                                                                                                                                                                                                          Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                BM541578.1 GI:18770340
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98.2%;
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                                                                                                                                                             human.
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/clone_lib="NIH_MGC_122"
/lab_host="DH10B"
/lab_host="DH10B"
/lab_host="DH10B"
/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
Site_1: NotI: Site_2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 026. Note:
this is a NHLMCC Library.
97 a 198 c 184 g 272 t
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8
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Pred. No. 2.5e-110;
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al Similarity 98.6%;
818; Conservative
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1083 bp mRNA linear EST 20-FEB-2002
AGENCOURT_6448278 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5531707
5', mRNA sequence.
BM541578
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Tissue Procurement: ATC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12213 row: m column: 20
High quality sequence stop: 643.
Location/Qualifiers
I. .1083
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//clone="ImAGE:5531707"
//clone="ImAGE:5531707"
//lssue_type="lelomyosarcoma"
//db_xref="Delomyosarcoma"
//colone="ImAGE:5531707"
//clone="ImAGE:5531707"
//clo
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 3.4e-109;
0; Mismatches 10;
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7;

Gaps

8; 887;

.7e-108; DB

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4926

238

178

4986

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418

us-09-647-140a-3.rst

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TATAATTCTGTACATAGCCTATATTTACAGTGAAAATGTAAGCTGTTTATTTTATTAA 4806
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                                                                                      AATAAGCACTGTGCTAATAACAGTGCATATTCCTTTCTATCATTTTTGTACAGTTTGCTG
                                                                                                                                                                                     TACTAGAGATCTGGTTTTGCTATTAGACTGTAGGAAGAGTAGCATTTCATTCTTCTTAG
                                                                                                                                                                                                                                  CTGGTGGTTTCACGGTGCCAGGTTTTCTGGGTGTCCAAAGGAAGACGTGTGGCAATAGTG
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                            Score 757.4; E
Pred. No. 1.7e-
0; Mismatches
                            13.0%;
95.6%;
                                     Best Local Similarity 95.6
Matches 854; Conservative
                            Query Match
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 887)

                                     3447
                                                                                    3507
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                                                                                                                                                                                                                                 3687
                                                                                                                                                                                                                                                                                 3743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LiAMl0606 row: k column: 17
High quality sequence start: 3
High quality sequence stop: 786.
                                                             481
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                                                                                                                                                                                                         661
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National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                               TTTTTTTTTTTACGTGCGATGCGTGGCTGGCTGGCTGGACCTCATCAGCATCG
                                                                                   CCCTCATCACCACCACGGGCTGATGATCGTTCTTATGCACGGGCAGATTCCCCCAGCCT
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/clone_ilb="NCL_CGAP_Skn4"
/tissue_type="squamous cell carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .887
/organism="Homo sapiens"
/db_xref="taxon:9606"
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            TCCAAGCCCTGGAGCCAACTGCTGTTTTGAGGTGGCACTTTTTCATTTGCCTATTCCC
                                                                                                                                                                                                                                                                                                                                          GCCTTCTTC-TTTTGCTGTTGTTTCTAAACAAGAATCAGTCTATCCACAGAGAGTCCCAC
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                                                                                                                                                                                                                                                                       ACACCTCCACAGTTCAGTGGCAGGGCTCAGGATTTCGTGGGTCTGTTTTCCTTTCTCACC
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/db_xref="Laxon:6666"
/db_xref="Laxon:6666"
/clone="lmAGE:4748039"
/clone=lib="NKI_CGAP_SKN4"
/tissue_type="squamous cell carcinoma"
/tissue_type="sq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7;
                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 841)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM10598 row: p column: 24
High quality sequence stop: 805.
Location/Qualifiers
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Contact: Robert Strausberg, Ph.D.
Bmall: cgapbs-rémail.nih.gor
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 CTGGCCCAGGGACAGGTGGAGTTTGACACCCCATCGGTCCTTCTGTCCAACGACGTGT
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Pred. No. 1.1e-100;
0; Mismatches 8; Indels 7;
     GI:13907841
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Best Local Similarity 98.1%;
Matches 789; Conservative (
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AGENCOURT_8754240 NIH_MGC_130 Mus musculus cDNA clone IMAGE:6332709
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Mark Maconochie, Ph.D. and Nancy L. Freeman,
                                                                                                                                                                                                                                                                                                                                                          4922 TCTAGCTGGTGGTTTCACGGTGCCAGGT-TTTCTGGGTGTCCAA-AGGAAGACGTCTGGC 4979
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/lab_host="DH10B (phage-resistant)"
/not="Organ: otocysts; Vector: pGWV-SPORT6.1.ccdb;
/note_"CoRWY: Site_2: Not1; Cloned unidirectionally.
Primer: Oligo dT. Average insert size 1.95 kb.
Constructed by ResGen, Invitrogen Corp. Note: this is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.llnl.gov

Plate: LLAM13790 row. 1 column: 22

High quality sequence stop: 646.
                                                                                                4743 TATATATAATTCTGTACATAGCCTATATTTACAGTGAAAATGTAAGCTGTTTATTATA
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/db_xref="taxon:10090"
/clone="IMAGE:6332709"
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Contact: Robert Strausberg, Ph.D.
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100.0%; Pred. No. 5.8e-98;
Live 0; Mismatches 0;
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/clone_lib="UI-CF-EC1"
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      Normalization and subtraction: two
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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BM973154.1 GI:19590745
                                                181 TCAGGGCCTGGCCACCATCCATGCCTACAACAAAGGCAGGAGTTTTTACACAGGTATCA
                                                                                                                                                                                                                                            CCTGGTGTTCTTCTGTTGGAATGATTGCTGGAGTCTTCCCATGGTTCCTCGTGGCGGT
                              GGGCCCCTTGTCATCCTCTTTTCAGTCCTGCACATTGTCTCCAGGGTCCTGATTCGGGA
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Tol: 319 356 4866
Fax: 319 356 4866
Fax: 319 356 4866
Fax: 319 356 487171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com)
The following repetitive elements were found in this cDNA
Sequence: 1-41, >AT_rich#Low_complexity (matched compliment)
Seq primer: M13 FORWARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAG_LIB-UI-CF-EC1
TAG_TISSUE-Normal Lung Epithelial Cells Tissue nos 369-371
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Bonaldo, M.F., Lennon, G. and Soares, M.B.

(bases 1 to 690)

REFERENCE AUTHORS

ORGANISM

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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 761)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end.one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
                                                                                  5549
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Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
                                                          331
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150 CIGCIGICATCAGITGAATGGTCAGCGTTGCATGTCGTGACCAACTAGACATTCTGTCGC
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1532-3 xana, Kisarazu, Chiba 292-0812, Japan
151: 81-438-52-3975
Fax: 81-438-52-3986
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/db_xref="taxon:9606"
/clone="PLACE1005753"
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/tissue_type="placenta"
/note="Vector: pME18SFL
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Location/Qualifiers
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Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
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AU137090
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Query Match

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716 bp mRNA linear EST 27-FEB-2002 UT-E-CQ1-aew-h-01-0-UT.ST UT-E-CQ1 Homo saplens cDNA clone BM665074

BM665074

BM665074.1 GI:18971693
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Normalization and subtraction: two approaches to facilitate gene
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                     Indels
Pred. No. 3.3e-97;
0; Mismatches 25;
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Bonaldo, M.F., Lennon
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218

5722

86

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="csDl002xc13"
/clone="csDl002xc13"
/clone="lb="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-ol19q(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: fliangelifetech.com URL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AL543173 17I_NFL006_PL2 Homo sapiens cDNA clone CSODIO02xC13 5 prime, mRNA sequence.
AL543173.1 GI:12875651
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full.length cDNA libraries and normalization
Unpublished (2001)
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BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
     GTGGCAGGGCTCAGGATTTCGTGGGTCTGTTTTCCTTTCTCACCGCAGTCGTCGCACAGT
                                                      397 GIGGCAGGGCTCAGGATTTCGTGGGTCTTTTCCTTTCTCACCGCAGTCGTCGCACAGT
                                                                                                                                          GTGGTCACTGCTGTCATCAGTTGAATGGTCAGCGTTGCATGTCGTGACCAACTAGACATT
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218 c 254 q 208 t
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//lab_host="DH10B (Life Technologies) (TI phage resistant)"
//lab_host="DH10B (Life Technologies) (TI phage resistant)"
//note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site_1: ECOR I; Site_2: Not I;
UI-E-COI is a normalized CDNA library containing the following tissue(s): optic nerve. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand CDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded CDNA was ligated to an ECOR I adaptor, diseased with Not I, and cloned directionally into PT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)1B tail. The sequence tag for this library is CCATTAAGTG. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye
              Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 9256
Email: msoares@lue.weeg.ulowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library Preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
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TAG_TISSUE=human optic nerve
TAG_SEQ-CCATTAAGTG"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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and
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Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., 'I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. a Quackenbush, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AW964148 11near 701 bp mRNA linear EST376221 MAGE resequences, MAGH Homo sapiens CDNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Assessment of gene expression patterns in a model metastasis using a 19,200 element cDNA microarray Compublished (2000)
Contact. John Quackenbush
The Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 20850, USA 712: 301 838 3528
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGCTGGCTTCAGTGGACCAGCCTTCATGG 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AW964148
AW964148.1 GI:8153984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: johnq@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human.
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SOURCE
ORGANISM
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VERSION
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AW964148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
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680 bp mRNA linear EST 01-MAY-2001
NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4748274 5',
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                                                                                     MAGH"
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                                                                                                                                                                           DB 10;
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                                                                                                                                                                         Score 667.2; DB 10
Pred. No. 2.1e-94;
0; Mismatches 13
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/ 199 c 176 g 201 t
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         Location/Qualifiers 1. .701
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602623377F1 NCI_CGAP_Skn4
mRNA sequence.
BGG76787
BGG76787.1 GI:13908184
                                                                                                                                                                         Query Match 11.4%;
Best Local Similarity 98.0%;
Matches 686; Conservative
Reverse
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1;
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Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Butherla, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 680)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4940
                                                                                                                                        Email: cgapbs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   420
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                                                                                                                                                                                                                                                  found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10599 row: j column: 19
High quality sequence stop: 680.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="NCI_CGAP_Skn4"
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/clone="IMAGE:4748274"
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5.1.3
Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2002
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OM nucleic - nucleic search, using sw model

Run on:

December 18, 2002, 07:49:35; Search time 141.369 Seconds (without alignments) 16388.716 Million cell updates/sec

Perfect score: Title:

Sequence:

Scoring table:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0

356696 segs, 198428768 residues Searched:

Total number of hits satisfying chosen parameters:

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Minimum DB seq length: 0 Maximum DB seq length: 200000000

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Published_Applications_NA:* Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	ult No.	Score	Query Match	Query Match Length DB	DB	ID	Description
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	4	435.8	7.5	6140	6	US-10-012-896-536	Sequence 536, App
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	19	300.8	5.2	4551	σ	US-09-938-842A-1674	Sequence 1674, Ap

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Gaps

. 0

Length 442; Indels

7.6%; Score 442; DB 10; 100.0%; Pred. No. 3.3e-91; Live 0; Mismatches 0;

Query Match 7.69
Best Local Similarity 100.4
Matches 442; Conservative

55, A 4836 3832 804, 3407 190, 36,	Sequence 36, Appl Sequence 36, Appl Sequence 603, Appl Sequence 824, Appl Sequence 824, Appl Sequence 824, Appl Sequence 824, Appl	**************************************	Sednence 800, App
9 US-09-938-842A-55 10 US-09-960-352-4836 10 US-09-980-107-3832 10 US-09-954-456-804 10 US-09-967-768A-190 10 US-09-957-299-157 10 US-09-967-368A-190 10 US-09-967-368A-190 10 US-09-967-368A-190 10 US-09-967-368A-190	10 US-09-339-38-36 10 US-10-007-805-36 10 US-09-560-863-603 . 9 US-10-012-896-824 10 US-09-759-143-824 10 US-09-822-827-824	10 US-09-925-300-613 10 US-09-815-242-9360 10 US-09-878-574-1080 10 US-09-070-927A-255 10 US-09-756-095-105 10 US-09-778-378A-24 10 US-09-770-149-277 10 US-09-815-242-4147 10 US-09-974-300-6492	10 US-09-815-343-800
4545 418 1936 1977 1977 1977 1448	201 201 473 1074 1074 1074	1427 1752 404 380 3601 3069 6129 697 1812	276
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20 22 22 23 24 0 25 0 27	C 28 33 31 32 34 34 34		45

ALIGNMENTS

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squence 1684, Application US/09954456
; Squence 1684, Application US/09954456
; Patent No. US2002011507A1
; GENERAL INFORMATION:
    APPLICANT: Young, Paul
    TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using
    TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents US/09/954,456
; CURRENT ELING DATE: 2001-09-18
; FILE REPERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/06/23,617
; PRIOR APPLICATION NUMBER: US/06/234,052
; PRIOR FILING DATE: 2000-09-26
; PRIOR FILING DATE: 2000-09-25
; PRIOR PELICATION NUMBER: US/06/235,134
; PRIOR APPLICATION NUMBER: US/06/235,637
; PRIOR PELING DATE: 2000-09-25
; PRIOR PELING DATE: 2000-09-26
; PRIOR PELING DATE: 2000-09-26
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; PRIOR PELING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/06/235,710
; PRIOR PELING DATE: 2000-09-27
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; PRIOR PELING DATE: 2000-09-27
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; PRIOR PELING DATE: 2000-09-27
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US-09-954-456-1684
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Homo sapiens

; ORGANISM: HOMO US-10-012-896-1006 ORGANISM:

Query Match

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                                                                                                                                                                                                                                                                             TGGTCACTGCTGTCATCAGTTGAATGGTCAGCGTTGCATGTCGTGACCAACTAGACATTC
                                                                                                                                                                                                                                                                                            APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Meagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hural, John
McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
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Publication No. US20020183251A1
GENERAL INFORMATION:
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Ralos, Michael D.
APPLICANT: Ralos, Michael D.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Cariet, Day, Craig H.
APPLICANT: Carter, Darick
APPLICANT: Li, Samuel X.
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Hepler, William T.
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                                                           1854 ACACTGCACAGCATCGATCTGGAGATCCAAGAGGGTAAACTGGTTGGAATCTGCGGCAGT 1913
                                                                                         ACTCTACAAGGCCTTTCCTTTACTGTCAGACCTGGCGAATTGTTAGCTGTGGTCGGCCCC 1209
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                                   Gaps
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                                  9;
    Length 3786;
                                  Indels
%; Score 435.8; DB 9;
%; Pred. No. 2.6e-89;
0; Mismatches 1297;
 7.5%;
                            Matches 1243; Conservative
                 Similarity
                 Best Local
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                                                                                               GTCAAGGGCACGCTGCGAGCTTCCTCCCGGCTGCATGACGAGCTTTTCCGAAGGATCCTT
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                                ATCTACGCCCTCCCATGGCAGTCATGCTGATCCTGAAAGCCATTCGAGGAGTTGTCTTT
                                                               2170 ATTIATICAGGITTAACIGIAGCIACCGTICITITIGGCATAGCAAGAICTCTATIGGIA
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SEQ ID NO 1007 LENGTH: 4395

TYPE: DNA

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ATTATEGTECTEGCCCAGGGACAGGTGGTGTGTTGACACCCCCATCGGTCCTTCTGTCC 4373
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CCGGTGCTGTTCAGTGGCACTGTCAGATCAAATTTGGACCCCTTCAACCAGTACACTGAA 4013
                CTGAAACTTGAATCTGAAGTGATGGAGAATGGGGGATAACTTCTCAGTGGGGGAACGGCAG
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                                                               GACCAGATTTGGGATGCCCTGGAGAGACACACATGAAAGAATGTATTGCTCAGCTACCT
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APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Wandeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121,427C27
CURRENT APPLICATION UNMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AACGACAGTTCCCGATTCTATGCCATGTT 4402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence 1007, Application US/10012896 Publication No. US/20020183251A1 GENERAL INFORMATION:
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Ralos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
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Hepler, William T.
Henderson, Robert A.
Hural, John
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Houghton, Raymond L.
Vinals de Bassols, C
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Vedvick, Thomas S.
Carter, Darrick
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ORGANISM: Homo sapiens

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                4074 CIGAAACITGAAICIGAAGIGAIGAGAAAIGGGGAIAACITCICAGIGGGGAACGGCAG 4133
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APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Madgheine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE TELE REPERBLOE: 21012.1.427C27
CURRENT APPLICATION UNDERS: US/10/012,896
CURRENT FILING DATE: 2001-12-10
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Vinals de Bassols, Carlota
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APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jannifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Hang, Yuqiu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Rolk, John A.
APPLICANT: Bay, Craig H.
APPLICANT: Vadvick, Thomas S.
APPLICANT: Vadvick, Thomas S.
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Hepler, William T.
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LOCATION: 4535

CTHER INFORMATION: n = A,T,C or

US-10-012-896-536
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Best Local Similarity 48.8%;
Matches 1243; Conservative
FEATURE
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CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
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Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
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Dillon, Davin C.
Mitcham, Jennifer
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Hepler, William
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Vedvick, Thomas (
Carter, Darrick
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ORGANISM: HOMO
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                                                           7.5%; Score 435.8; DB 10;
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CURRENT FILING DATE: 2001-02-09
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Skeiky, Yasir A.W.
Hepler, William
Hural, John
McNeill, Patricia D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
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SOFTWARF.
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Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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Dillon, Davin C.
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NAME/KEY: misc_feature
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US-09-780-669-536
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LOCATION: (1)...(6140)
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GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121:534C1
CURRENT APPLICATION NUMBER: US/09/822,827
CURRENT PILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSEQ for Windows Version 3.0 6 Length 6140; Indels DB 10; Pred. No. 3.4e-89;); Mismatches 1297; Score 435.8; AACGACAGTTCCCGATTCTATGCCATGTT 4402 AATAAAGAGGCCTATTTTACAAGATGGT 3977 RESULT 7 US-09-822-827-536 Sequence 536, Application US/09822827 Patent No. US20020081680A1 ; 0 ; LOCATION: (1)...(6140) ; OTHER INFORMATION: n=A,T,C or US-09-822-827-536 Query Match 7.5%; Best Local Similarity 48.8%; Matches 1243; Conservative NAME/KEY: misc_feature TYPE: DNA ORGANISM: Homo sapiens LENGTH: 6140 SEQ ID NO 536 3469 3769 3954 3529 4014 3589 4074 3649 4134 3709 4194 4254 3829 4374 3949 qq q g ò a g q qq δλ g ò δ a ŏ g Qγ g οy g ò à δ

2213 2273 2393 2453 2573 2633 1977 2037 2157 2277 2813 2397 3053 2637 2454 TATGCTACCATTTTAATAACCTGTTGCTGGGAGAGACACCGCCAGTTGAGATCAATTCA 2513 2634 GGGCAGGGTTCAGTGCCCTGGTCAGTATATGGTGTCTACATCCAGGCTGCTGGGGGGCCCC 2693 AAAGACATGGATGAAGTTGACGTGCGGCTGCCGTTCCAGGCCGAGATGTTCATCCAGAAC 3113 GTCATAAAGGCTTGTGCTCTGAAAAAGGATTACAGCTGTTGGAGGATGGTGACTTGAACT AAAGAGGCTGTATTACGGAAAGAGCACCCATGAGGAACTGATGATTAAATGGTGAC 2574 GTAAAGAAGGAAAAAGCAGTAAAGCCAGAGGGAAGGGCAGCTTGTGCAGCTGGAAGAGAA GAGATTGGAGGGGGGGGCCAACCTGAGCGGTGGGCAGCGCCAGAGGATCAGCCTTGCC CGGGCCTTGTATAGTGACAGGAGCATCTACATCCTGGACGACCCCCCTCAGTGCCTTAGAT GCCCATGTGGGCAACCACATCTTCAATAGTGCTATCCGGAAACATCTCAAGTCCAAGACA 2098 CCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGGTCTCAACAATCTTCTAGA 2218 TCAGAGGAGAACCGTTCTGAAGGAAAGTTGGTTTTCAGGCCCTATAAGAATTACTTCAGA ACCTGGTGGTTGAGTTACTGGATCAAGCAAGGAAGCGGGAACACCACTGTGACTCGAGGG 2458 ATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTGGCATAGCAAGATCTCTATTGGTA GTGCTGAACAGCTGCTGCCTGAGGCCTGACCTGGCCATTCTTCCCCAGCAGCGACCTGACG AAAGATGGTAAAATGGTGCAGAAGGGGACTTACACTGAGTTCCTAAAATCTGGTATAGAT 2514 AAAAAGGAAACCAGTGGTTCACAGAAGAAGTCACAAGACAAGGGTCCTAAAACAGGATCA 2158 CCCTCCTTGAAAGATGGTGCTCTGGAGAGCCAAGATACAGAGAATGTCCCAGTTACACTA 2694 TTGGCATTCCTGGTTATTATGGCCCTTTTCATGCTGAATGTAGGCAGCACCGCCTTCAGC 2814 AACGAGACCTCGGTGAGTGACAGCATGAAGGACAATCCTCATATGCAGTACTATGCCAGC 2398 GICACTGTAAATGGAGGAGGAAATGTAACCGAGAAGCTAGATCTTAACTGGTACTTAGGA 2278 GCTGGTGCTCACTGGATTGTCTTTTTTCCTTATTCTCTAAACACTGCAGCTCAGGTT 2874 ATCTACGCCCTCTCCATGCAGTCATGCTGATCCTGAAAGCCATTCGAGGAGTTGTCTTT 2934 GTCAAGGGCACGCIGCGAGCTICCTCCCGGCIGCAIGACGAGCTTTTCCGAAGGAICCTT CGAAGCCCTATGAAGTTTTTGACACGACCCCCACAGGGAGGATTCTCAACAGGTTTTCC AAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGAATTTTAAAATCGTTTCTCC 1618 1738 2214 1798 1858 2334 1918 1978 2034 2094 1678 2154 2274 2394 2754 3054 2994 2638 2578 ă 원 ò g οy g ò qq ŏ g ö q ŏ Q 9 9 9 9 9 9 q ò ద ò Ω \ \frac{1}{2} \qquad \qqquad \qqqq \qqq \qqqq \qqq \qqqq \qqq \qqqq \qqq \qqqq \qqq \qqqq \qqq \qqqq \qqq \qqqq \qqq \qqqq \qqq \qqqq \qqq \qqqq \qqq \qqqq 8 g ò ò Qγ g οy qq ò

3413 3473 3057 3533 3117 TIGCTACAAGTIGGTIGGTIGGTCTCTGTGGCTGTGGCCGTGATTCCTTGGATCGCAATA 2757 GCAGTGGGGCCCCTTGTCATCTTTTCAGTCCTGCACATTGTCTCCAGGGTCCTGATT 3233 2997 3177 3653 3231 3291 3411 4013 3588 4073 3351 GTTATCCTGGTGTTCTTCTGTGGGAATGATCGCAGGAGTCTTCCCGTGGTTCCTTGTG AGCATACAGGCCTTGCCACCATCCACGCCTACAATAAAGGGCAGGAGTTTCTGCACAGA TGGCTGGCTGGCGGCTGGACCTCATCAGCCTCATCACCACCACGGGGCTGATG CGGGAGCTGAAGCGTCTGGACAATATCACGCAGTCACCTTTCCTCTCCCACATCACGTCC AGAGATGTGAAGCGCCTGGAATCTACAACTCGGAGTCCAGTGTTTCCCACTTGTCATCT ATCGTTCTTATGCACGGCAGATTCCCCCAGCCTATGCGGGTCTCGCCATCTCTTATGCT GTCCAGTTAACGGGGCTGTTCCAGTTTACGGTCAGACTGGCATCTGAGACAGAAGCTCGA ATTAAATCACAAGAAAAGGTTGGCATTGTGGGAAGAACCGGAGCTGGAAAAAGTTCCCTC TICACCTCGGTGGAGGATCAATCACTACATTAAGACTCTGGTCCTTGGAAGCACCTGCC AATGTGAACTTCATGTACAGTCCAGGTGGGCCTCTGGTACTGAAGCATCTGACAGCACTC ATCAAACCTAAAGAAGAATGGCATTGTGGGGGGGGGACAGGATCAGGGAAGTCCTCGCTG GGGATGGCCCTCTTCCGTCTGGTGGAGTTATCTGGAGGCTGCATCAAGATTGATGGAGTG AGAATCAGTGATATTGGCCTTGCCGACCTCCGAAGCAACTCTCTATCATTCCTCAAGAG CCGGTGCTGTTCAGTGGCACTGTCAGATCAAATTTGGACCCCTTCAACCAGTACACTGAA CTGAAAACTTGAATCTGAAGTGATGGAGAATGGGGATAACTTCTCAGTGGGGGAACGCCAG GACCAGATTTGGGATGCCCTGGAGAGGACACACATGAAAGAATGTATTGCTCAGCTACCT 3114 2698 3174 2758 3234 2818 3294 2878 2938 2998 3058 3534 3118 3594 3178 3654 3292 3352 3834 3894 3469 3529 3589 3649 3709 3354 3414 3474 3714 3774 3412 3954 4014 4074 3232 4134 ò qq δλ g qq δy g Óγ Q P Ωp qq QΥ δ δ QY Db οy Op ٥y G G Οy Qy Db oy Dp οy QQ ò Dp 셤 Qγ . q ò 셤 ò

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APPLICANT: Meagher, Gary R.
APPLICANT: Meagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C27
CURRENT APPLICANTION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FASTSEQ for Mindows Version 3.0
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Vinals de Bassols, Carlota
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Hepler, William T.
Henderson, Robert A.
Hural, John
McNeill, Patricia D.
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Kalos, Michael D.
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Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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GCTACTCTGAGAGACAACATCCTGTTTGGGAAGGAATATGATGAAGAAGAAGATACAACTCT 2093
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GTTATCCTGGTGTTCTTCTGTGGGAATGATCGCAGGAGTCTTCCCGTGGTTCCTTGTG
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Pred. No. 7.8e-87;
0; Mismatches 1296;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                  AACGACAGTTCCCGATTCTATGCCATGTT 4402
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Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
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Jiang, Yuqui
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Vedvick, Thomas S
Carter, Darrick
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Dillon, Davin C.
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Best Local Similarity 48.8
Matches 1243; Conservative
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427024
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Pred. No. 7.8e-87;
); Mismatches 1296; Indels
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CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 535
                                                               AATAAAGAGGCCTATTTTACAAGATGGT 4002
                                              AACGACAGTTCCCGATTCTATGCCATGTT 4402
                                                                                                                               Sequence 535, Application US/09780669 Patent No. US20020051977A1 GENERAL INFORMATION:
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Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
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Dillon, Davin C.
Mitcham, Jennifer L.
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McNeill, Patricia D.
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Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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Hepler, William
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US-09-780-669-535
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                                                               CGGGCCTTGTATAGTGACAGGAGCATCTACATCCTGGACGACCCCCTCAGTGCCTTAGAT
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                                                                                                                                                                                                GTCCAGTTAACGGGGCTGTTCCAGTTTACGGTCAGACTGGCATCTGAGACAGAAGCTCGA 3593
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              2904 TCTCTCCAGGGCTCTGGACCATCCGGGCATACAAAGCAGAAGAGAGGGGTGTCAGGAACTG
                                                                                                              AGAATCAGTGATATTGGCCTTGCCGACCTCCGAAGCAAACTCTCTATCATTCTTCAAGAG
                                                                      2964 TTTGATGCACACCAGGATTTACATTCAGAGGCTTGGTTCTTGTTTTGACAACGTCCCGC
                                                                                                                                               ATCGTTCTTATGCACGGCAGATTCCCCCAGCCTATGCGGGTCTCGCCATCTCTTATGCT
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                                                                                                                                                                                                                                                                                                                                                                           APPLICATION XU, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILLS REPERENCE: 210121.534(1)
CURRENT APPLICATION NUMBER: US/09/822,827
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                       3974 AATAAAGAGGCCTATTTTACAAGATGGT
                                                                                                                                                                                                                                                                   Sequence 535, Application US/09822827
Patent No. US20020081680A1
GENERAL INFORMATION:
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US-09-822-827-535
                                                                                                                                                                                               RESULT 11
US-09-822-827-535
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APPLICANT: Johnson, Kory
APPLICANT: Johnson, Kory
APPLICANT: Castle, Arthur
APPLICANT: Elashoff, Michael
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5038-US
CURRENT APPLICATION NUMBER: US/09/917,800A
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR PLING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 60/222,040
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US-09-917-800A-1578
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PRIOR FILING DATE: 2000-11-02
PRIOR APPLICATION NUMBER: US 60/290,029
PRIOR FILING DATE: 2001-05-11
PRIOR FILING DATE: 2001-05-11
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: US 60/292,336
PRIOR APPLICATION NUMBER: US 60/295,798
PRIOR PILING DATE: 2001-06-06
PRIOR FILING DATE: 2001-06-06
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-19
SERIOR FILING DATE: 2001-06-19
SERIOR FILING DATE: 2001-06-19
SERIOR PAPLICATION NUMBER: US 60/303,459
SERIOR PILING DATE: 2001-07-09
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Sequence 3373, Application US/09880107
Patent No. US20020142981A1
GENERAL INFORMATION:
APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.

US-09-880-107-3373

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      in Liver Cancer
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                                                                                                                                                                                                                                                                 6.5%; Score 382.2; DB 10;
ilarity 48.8%; Pred. No. 5e-77;
Conservative 0; Mismatches 1233;
; TITLE OF INVENTION: Gene Expression Profiles in FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; URRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3373
; LENGTH: 5300
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ORGANISM: Homo sapiens
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Best Local &
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CURRENT APPLICATION NUMBER: US/09/917,800A
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 60/222,880
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Elashoff, Michael
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APPLICANT: Mendrick, Donna
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PRIOR APPLICATION NUMBER: US 60/222,880
PRIOR FILING DATE: 2000-11-02
PRIOR PLICATION NUMBER: US 60/290,029

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US-09-917-800A-479
                                                                                                                                                                                                                                                                                                                                                           DB 10; Length 5728
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                                                                                                                                                                                                                                                                                                                                                        6.4%; Score 373.8; DB 10;
47.7%; Pred. No. 4.2e-75;
Live 0; Mismatches 1307;
           PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR FILING DATE: 2001-05-15
PRIOR FILING DATE: 2001-05-15
PRIOR PELICATION NUMBER: US 60/292,336
PRIOR PELING DATE: 2001-06-06
PRIOR FILING DATE: 2001-06-06
PRIOR FILING DATE: 2001-06-19
PRIOR PELICATION NUMBER: US 60/297,457
PRIOR PELICATION NUMBER: US 60/297,884
PRIOR PLILNG DATE: 2001-06-19
PRIOR PLILNG DATE: 2001-06-19
PRIOR PLILNG DATE: 2001-06-19
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PRIOR FILING DATE: 2001-06-19
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ 1D NOS: 1740
2001-05-11
                                                                                                                                                                                                                                                                            ORGANISM: Rattus norvegicus
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1854 ACACTGCACAGCATCGATCTGGAGATCCAAGAGGGTAAACTGGTTGGAATCTGCGGCAGT 1913
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                                                                                                                                      Ouery Match 6.0%; Score 349.2; DB 9; Best Local Similarity 48.5%; Pred. No. 1.5e-69; Matches 1237; Conservative 0; Mismatches 1233;
                                                                                    ORGANISM: Arabidopsis thaliana US-09-938-842A-1392
   DATE: 2001-06-22
PRIOR FILING DATE: 2001-06-
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1392
LENGTH: 4869
                                                                       TYPE: DNA
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Patent No. US20020160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Krups, Joel
APPLICANT: Zhu, Tonn
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
                                   3931 GGGAAGTCCTCCCTGACTTGGGGCCTGCGGGCTTCAGGAGCCACTGAGGGTGGTATT 3990
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                                                                                                                                                                                                                          GGGAAGTCCTCGCTGGGGATGGCCCTCTTCCGTCTGGTGGAGTTATCTGGAGGCTGCATC
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                                                                                     ATTTTAGATGAAGCCACACCACCATGCACACACAGACACACATATTGATTCAAGAGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/938,842A CURRENT FILING DATE: 2001-08-24 PRIOR APPLICATION NUMBER: US 60/227,866 PRIOR FILING DATE: 2000-08-24 PRIOR APPLICATION NUMBER: US 60/264,647 PRIOR FILING DATE: 2001-01-16 PRIOR APPLICATION NUMBER: US 60/300,111
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3817 ACAGGCGCTGGGAAATCAAGCCTCTTAAATGCCTTATTCAGGATTGTGGAGCTGGAAAA 3876 GGCTGCATCAAGATTGATGGAGTGAGAATCAGTGATATTGGCCTTGCCGACCTCCGAAGC 3929 GACCCCTTCAACCAGTACACTGAAGACCAGATTTGGGATGCCCTTGGAGAGGACACATG 4049 1997 GACCCATTAGTGAACACAACGACGCGATCTCTGGGAATCTCTTGAGAGGGCACACTTG 4056 AAAGAATGTATTGCTCAGCTACCTCTGAAACTTGAATCTGAAGTGATGGAGAATGGGGAT 4109 4290 CACACGGTTCTAGGCTCCGATAGGATTATGGTGCTGGCCCAGGGACAGGTGGTGGTGTT 4349 4350 GACACCCCATCGGTCCTTCTGTCCAACG 4377 4357 AGTICACCGGAGAATCTICTICAAATG 4384 3870 3877 3990 4050 4110 4117 4170 δ qq qq ΩŊ qq qq q g q qq Ω δ QΥ δ δ δλ

Search completed: December 18, 2002, 21:41:29 Job time : 221.369 secs

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US-08-404-531B-32 US-08-476-900A-32 US-08-843-459A-3

ALIGNMENTS

US-08-972-927-1

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US-08-488-546A-7 US-08-488-546A-8 US-08-404-531B-4 US-08-404-531B-5 US-08-476-900A-4 US-08-476-900A-4 US-08-488-546A-5 US-08-001-273-3 US-09-001-273-3

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.../cgn2_c6/ptodata/1/ina/5A_COMB.seq:*
.../cgn2_c6/ptodata/1/ina/6B_COMB.seq:*
.../cgn2_c6/ptodata/1/ina/6A_COMB.seq:*
.../cgn2_c6/ptodata/1/ina/6B_COMB.seq:*
.../cgn2_c6/ptodata/1/ina/PCTUS_COMB.seq:*
.../cgn2_c6/ptodata/1/ina/PcTUS_COMB.seq:*
.../cgn2_c6/ptodata/1/ina/PcTUS_COMB.seq:*
                        GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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US-08-407-207A-1
US-09-605-785-536
US-09-439-313-536
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US-08-463-179A-3
US-08-461-384B-3
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Maximum Match 1008
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                                      GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SHYJAN, ANGREW
TITLE OF INVENTION: NOVEL MULTIDRUG RESISTANCE-ASSOCIATED
TITLE OF INVENTION: POLYPEPTIDE
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                                                                                                                                                                                                                                                                                     COMPUTE READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/061,400
FILING DATE: 16-APRIL-1998
CLASSIFICATION: 536
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Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Blizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFRENCE/DOCKET NUMBER: MNI-056CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 277-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                          NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD,
STREET: 28 State Street
Sequence 1, Application US/09061400 Patent No. 6077936
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99.8%;
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TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 99.8
Matches 4809; Conservative
                                                                                                                                                                                                            CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
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US-09-061-400-1
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O _Y Db	1151	TITCAGGAGAAAATGCGTGGCCGCCACGGATGAACGTGTCCAGAAGATGAATGA	1210
Qy	1211	TA TA	1270
Qy	1271	AAAAATCCGCGAGGAGGAGCGTCGGATATTGGAAAAGCCGGGTACTTCCAGGGTATCAC .	· w 0
Qy	1331	TGTGGGTGTGGCTCCCATTGTGGTGGTGATTGCCAGCGTGGTGACCTTCTCTGTTCATAT	9
Qy	1391	GACCCTGGGCTTCGATCTGACAGCAGCAGGGTTTCACAGTGGTGACAGTCTTCAATTC	70 4t
Qy	1451	CATGACTTTTGCTTTGAAAGTAACACCGTTTTCAGTAAAGTCCCTCTCAGAAGCCTCAGT	1510
Qy Db	1511	GGCTGTTGACAGATTTAAGAGTTTGTTTCTAATGGAAGAGGTTCACATGATAAAGAACAA 	15
Q _Y Db	1571	ACCAGCCAGTCCTCACATCAAGATAGAGATGAAAAATGCCACCTTGGCATGGGACTCCTC	S 3
OV OV	1631	CCACTCCAGTATCCAGAACTCGCCCAAGCTGACCCCCAAAATGAAAAAAGACAAGAGGC	1690 1680
Qy Db	1691	TTCCAGGGCAAGAAAGAGAAGGTGAGCTGCAGCGCACTGAGCATCAGGGGGTGCT 	1750
Qy Db	1751	GGCAGAGCAGAAAGGCCACCTCCTCGACAGTGACGAGGGGCCCAGTCCCGAAGAGGA 	1810
S S	1811	AGAAGGCAAGCACATCCACCTGGGCCACTGCGCTTACAGAGGACACTGCACAGGATCGA	1870
· Qy	1871	TCTGGAGATCCAAGAGGGTAAACTGGTTGGAATCTGCGGCAGTGTGGGAAGTGGAAAAAC	1930
oy.	1931 1921	CTCTCTCATTTCAGCCATTTTAGGCCAGATGACGCTTCTAGAGGGCAGCATTGCAATCAG	1990
Qy	1991	TGGAACCTTCGCTTATGTGGCCCAGCAGCCTGGATCCTCAATGCTACTCTGAGAGACAATGCTACTCTGAGAGACAATGCTACTCTGAGAGACAATGCAACTTCGCTTATGTGGCCCAGCAGCAGCCTGGATCTCAATGCTACTCTGAGAGAAA	2050
QY	2051	NTACAACTCTGTGCTGAA 	2110
Qy	2111	GGAG 	2170
Qy	2171	GGCCAGAGGATCAGCCTTGC 	2230
Qy	2231	CCCCTCAGTGCCTTAGATGCCCATGTGGGC	29

2280	2350	2410	2470	2530	2590 2580	2650 2640	2710	2770	2830	2890	2950	3010	3070	3130	3190	3250 3240	3310	3370
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đ	oy Db	Qy	Oy Db	Qy	Qy Db	. qa	oy op	Qy Op	Qy Op	Qy Db	Qy Db	Qy Db	Oy Dp	Qy	Qy Db	Qy Db	Qy	ογ

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 GCGTCCTCCTACCGAAACCTTGCCTTTCTCGATTTTATCTTTGCACAGCAGTTCCGGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Version #1.
                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Testa, Hurwitz & Thibeault
STREET: 125 High St.
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: SHYJAN, ANDREW
TITLE OF INVENTION: NOVEL MULTIDRUG
TITLE OF INVENTION: POLYPEPTIDE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/001,273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: FEBTYON, Gillian M
REGISTRATION NUMBER: 36.08
REFERENCE/DOCKET NUMBER: MIL-001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5994130
GENERAL INFORMATION:
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TELEPHONE: (617) 248-7000
TELEPAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                            AAGCACTGTGCTAATAACA 4828
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MEDIUM TYPE: Floppy
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LOCATION: 2..4
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TOPOLOGY: lir
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STATE: MA
COUNTRY: US
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    Length
                     Indels
  DB 2;
                     9;
Score 4724.2;
Pred. No. 0;
6; Mismatches
 80.9%;
99.7%;
Query Match 80.9
Best Local Similarity 99.7
Matches 4737; Conservative
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Oy 4397 CATGTTTGCTGCTGCAGAGA		RESULT 3 US-08-843-459A-1 Sequence 1, Application US/0 Sequence 1, Application US/0 Sequence 1, Application US/0 Sequence 1, Application US/0 TITLE OF INVENTION: APPLICANT: SHYJAN, Andre TITLE OF INVENTION: NOVE TITLE OF INVENTION: NOVE MUNBER OF SEQUENCES: 8 CORRESPONDENCE ADDRESS: 8 ADDRESSEE: LAHIVE & CO STREET: 28 State Stree CITY: Boston STATE: MASSACHUSELTS COUNTRY: USA ZIP: 02109 COMPUTER: READABLE FORM: MEDIUM TYPE: Floppy discompanion of the companion	CURRENT APPLICATION DATA: APPLICATION NUMBER: US, FILING DATE: 16-APR-19; CLASSIFICATION: 536 ATTORNEY/AGENT INFORMATION NAME: Hanley, Elizabeth REGISTRATION NUMBER: 3 REFERENCE/DOCKET NUMBER: TELECHONUSCATION INFORMATION FOR SEO ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 4781 base pair: TYPE: nucleic acid STRANDEDNESS: single TOPOLOCY: linear TOPOLOCY: linear TOPOLOCY: linear NAME/KEY: CDS
	TTCCA 3480 ATCAA 3616 ATCAA 3540 CCCTC 3676 CCGAGA 3736 CGAGA 3766 ATTGG 3720 ATTGG 3720	CTGGT 3856 CTGCT 3780 CTTGC 3916 CTTGC 3916 CTTGC 3916 CTTGC 3916 ACTGT 3900 ACTGT 3900 ACTGT 4036 GTGAT 4036 GTGAT 4020	
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Qy 3317 Qy 3371 Qy 3371 Qy 3437 Db 3361 Qy 3497		Oy 3797 Db 3721 Oy 3857 Db 3781 Oy 3917 Db 3841 Oy 3977 Db 3961 Oy 4037	

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TGCTGCAGAGAACAAGGTCGCTGTCAAGGCTGACTCCTCCTGTTGACGA 4456
                                             AACCTTGCCTTTCTCGATTTTATCTTTCGCACAGCAGTTCCGGATTGGCTT 4575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOVEL MULTIDRUG RESISTANCE-ASSOCIATED POLYPEPTIDE
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NN NUMBER: 33,505

OOCKET NUMBER: MNI-056 (formerly MIL-001)

(617)227-7400

(617)227-7400

(617)227-7500

(617)742-4214

S SEQ ID NO: 1:

R SEQ ID NO: 1:

R B base pairs
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BM PC compatible
STEM: PC-DOS/MS-DOS
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ON: 536
INFORMATION:
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1156 1276 1440 1576 1500 1740 1876 2176 1080 1200 1336 1260 1396 1320 1456 1380 1516 1636 1816 1800 1936 1860 1996 2056 2040 2100 1696 1620 1756 1680 1920 1980 2116 1560 CATCTTAGGCATGATTATATGTAATTATTCTGGGACCAACAGGCTTCCTGGGATCAGC CATTAAATTTATCAAAATGTATGCCTGGGTCAAAGCATTTTCTCAGAGTGTTCAAAAAT TGTGGCTCCCATTGTGGTGGTGATTGCCAGCGTGGTGACCTTCTCTGTTCATATGACCCT GGGCTTCGATCTGACAGCAGCACAGGCTTTCACAGTGGTGACAGTCTTCAATTCCATGAC TITIGCTITGAAAGTAACACCGTITTTCAGTAAAGTCCCTCTCAGAAGCCTCAGTGGCTGT TTTGCTTTGAAAGTAACACCGTTTTCAGTAAAGTCCCTCTCAGAAGCCTCAGTGGCTGT CAGTCCTCACATCAAGATAGAGATGAAAAATGCCACCTTGGCATGGGACTCCTCCCACTC CAGTATCCAGAACTCGCCCAAGCTGACCCCCAAAATGAAAAAAGACAAGAGGGCTTCCAG GGGCAAGAAAGAAAGTGAGGCAGCTGCAGCGCACTGAGCATCAGGCGGTGCTGGCAGA GCAGAAAGGCCACCTCCTCGTGACAGTGACGAGCGGCCCAGTCCCGAAGAGGAAGAAGG CAAGCACATCCACCTGGGCCACCTGCGCTTACAGAGGACACTGCACAGCATCGGATCTGGA CCGCGAGGAGGAGCGTCGGATATTGGAAAAAGCCGGGTACTTCCAGGGTATCACTGTGGG 1141 1337 1381 1441 1561 2041 1157 1081 1217 1277 1201 1261 1397 1321 1457 1517 1577 1501 1637 1697 1621 1757 1681 1817 1741 1877 1801 1937 1861 1997 2057 1981 2117 961 1921 유 οy qq QΥ qq QΥ Ωp Qy Db Db Qy qq ολ qq oγ q ò g δy q φ В οy q ô QΩ οy qq ò g δ Db QΥ Dp $^{\circ}$ qq

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TCCCCCAGCCTATGCGGGTCTCGCCATCTTATGCTGTCCAGTTAACGGGGCTGTTCCAATTAACGGGGCTGTTCCAATTAACGGGGCTGTTCTATGCTGTCCCAGTTAACGGGGCTGTTCCAATCCCCAGCTCAACGGGGCTGTTCCAA GTTTACGGTCAGACTGGCATCTGAGACAGAAGCTCGATTCACCTCGGTGGAGAGGATCAA AAACCTCCCTCTTGTCCTAAAGAAAGTATCCTTCACGATCAAACCTAAAAGAGAAGATTGG GAGGACACACATGAAAGAATGTATTGCTCAGCTACCTCTGAAACTTGAATCTGAAGTGAT TCACTACATTAAGACTCTGTCCTTGGAAGCACCTGCCAGAATTAAGAACAAGGCTCCCȚC CCCTGACTGGCCCCCAGGAGGGAGAGGTGACCTTTGAGAACGCAGAGATGAGGTACCGAGA CGACCTCCGAAGCAAACTCTCTATCATTCCTCAAGAGCCGGTGCTGTTCAGTGGCACTGT GGAGAATGGGGATAACTTCTCAGTGGGGAACGGCAGCTCTTGTGCATAGCTAGAGCCCT GCTCCGCCACTGTAAGATTCTGATTTTAGATGAAGCCACAGCTGCCATGGACACAGAGAC AGACTTATTGATTCAAGAGACCATCCGAGAAGCATTTGCAGACTGTACCATGCTGACCAT GGTGGTGGAGTTTGACACCCCATCGGTCCTTCTGTCCAACGACAGTTCCCGATTCTATGC δ

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: COLE, Susan P.C.
APPLICANT: Deeley, Roger G.
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING
TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS STREET: Queen's University at Kingston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/463,092E
FILING DATE: 05-JUN-1995
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: 08/029,340
FILING DATE: 8-MAR-1993
CLASSIFICATION: 435
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26-0CT-1993
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APPLICATION NUMBER: 07/966,923
FILING DATE: 27-0CT-1992
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APPLICATION NUMBER: (
FILING DATE: 26-0CT-1
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CITY: Kingston
STATE: Ontarlo
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Pred. No. 3.7e-121;
                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: Q1546
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 545-6853
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5011 base pairs
TYPE: nucleic acid
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 084407,207
FILING DATE: 20-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Steeg, Carol Miernicki
REGISTRATION NUMBER: 39,539
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Best Local Similarity 52.23
Matches 1360; Conservative
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STRANDEDNESS: double
TOPOLOGY: linear
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; LOCATION: 196..4788
US-08-463-092B-3
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APPLICANT: Cole, Susan P.C.
APPLICANT: Deeley, Roger G.
TITLE OF INVENTION: METHODS FOR IDENTIFYING
TITLE OF INVENTION: MULTIDRUG RESISTANT TUMOR CELLS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
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60 State Street, suite
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US-08-462-109A-3
; Sequence 3, Application US/08462109A
; Patent No. 582875
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                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PELLING DATE: 27-07-1992
APPLICATION NUMBER: 08/029,340
FILING DATE: 8-MAR-1993
APPLICATION NUMBER: 08/11,893
FILING DATE: 26-07-1993
APPLICATION NUMBER: 08/407,207
FILING DATE: 20-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Deconti, Giulto A. Jr.
REGISTRATION NUMBER: 901-002CP4
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATICS:
LENGTH: 5011 base pairs
TYPE: nucleic acid
                                                                                             SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,109A
                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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; LOCATION:
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                                                                                                                                                         NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
                                                                            APPLICANT: Deeley, Roger G.
APPLICANT: Cole, Stann P.C.
TITLE OF INVENTION: METHODS FOR CONFERRING MULTIDRUG
TITLE OF INVENTION: RESISTANCE ON A CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 510; DB 2;
Pred. No. 3.7e-121;
                                                                                                                                                                                                                          Queen's University at Kingston
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/460,907B
FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/141,893
FILING DATE: 26-0CT-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/407,207
FILING DATE: 20-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                          PC-DOS/MS-DOS
                   Sequence 3, Application US/08460907B Patent No. 5891724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/966,923
FILING DATE: 27-0CT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 424
RINGN APPLICATION DATA:
APPLICATION NUMBER: 08/029,340
FILING DATE: 8-MAR-1993
                                                                                                                                                                                                                                                                                                                        COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DAGE
SOFTWARE: ACTT
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REGISTRATION NUMBER: 39,539
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 545-2342
TELEFAX: (613) 545-6853
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 52.23
Matches 1360; Conservative
                                                                                                                                                                                                                                                                ZIP: CANADA
ZIP: K7L 3N6
COMPUTER REARABLE FORM:
MEDIUM TYPE: Flow-
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STRANDEDNESS: double
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                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                             CITY: Kingston
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US-08-460-907B-3
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US-08-460-907B-3
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0y		ACGCTTCTAGAGGGCAGCATTGCAATCAGTGGAACCTTC	00	
qq	2260 TCAGCCCTCTTGGCTGAGATG		2319	
QY Db	2001 GCTTATGTGGCCCAGCAGGCC 	GCTPATGTGGCCCAGCAGGCCTGGATCCTCAATGCTACTCTGAGAGACAACATCCTGTTT	2060	
Qy Db	2061 GGGAAGGAATATGATGAAGAA 2380 GGATGTCAGCTGAGGAACCA	GGGAAGGAATATGATGATGAAGATACAACTCTGTGCTGAACAGCTGCTGCGGGGCCT 	2120 2439	
Qy Db	2121 GACCTGGCCATTCTTCCCAGC 	GACCTGGCCATTCTTCCCAGCAGCGACCTGACGAGAGTTGGAGAGAGA	2180 2499	
Qy Dp	2181 AGCGGTGGGCAGCGCCAGAGG	AGGGGGGGGGGCGGGGGATCAGCCTTGCCGGGCCTTGTATAGTGACAGGAGCATC	2240 2559	
yo di	2241 TACATCCTGGACGACCCCCTC.	TACATCCTGGACGACCCCTCAGTGCCTTAGATGCCCATGTGGGCAACCACATCTTCAAT	2300 . 2619 .	
Qy	2301 AGTGCTATCGGGAAN 2620 AATGTGATTGGCCCCAAGGGG	AGTGCTATCCGGAAACATCTCAAGTCCAAGACAGTTCTGTTTGTTACCCACCAG	2354	
Qy Db	2355 TTACAGTACCTGGTTGACTGT 2680 ATGAGCTACTTGCCGCAGGTG	TTACAGTACCTGGTTGACTGTGATGAGATGATCTTCATGAAAGAGGGCTGTATTACGGAA	2414 2739	
Qy Dp	2415 AGAGGCACCCATGAGGAACTG 	AGAGGCACCCATGAGAACTGATGAATTTAAATGGTGACTATGCTACCATTTTTAATAAC	2474 2799	
Qy Db	2475 CTGTTGCTGGGAGAGACACCG	CTGTTGCTGGGAGACACCGCCAGTTGAGATCAATTCAAAAAGGAAACCAGTGGT -	2531 2859	
Oy Dp	2532 TCACAGAAGAAGTCACAAGACA 	TCACAGAAGAAGTCACAAGACAAGGGTCCTAAAA 	2565 2919	
Qy Dp	2566 CAGGATCAGTAAAGAAGAAA. 1 2920 CAACTGCAGAGACAGCTCAGC.	CAGGATCAGTAAAGAAGAAAAAGCAGTAAAGCCAGAGAGGGCAGCTTGTGCAGCTGG	2625 2979	
Qy Dp	2626 AAGAGAAGGGCAGGGTTCAG 1 2980 AACAGCACCGCAGAACTGCAG	AAGAGAAAGGGCAGGGTTCAGTGCCCTGGTCAGTATATGGTGTCTACATCCAGGCTGCTG	2685 3039	
Oy Db	2686 GGGGCCCCTTGGCA 	GGGGCCCCTTGGCATTCCTGGTTATTATGGCCCTTTTCATGCTGAATGTAGGCCCTTTTCATGCTGAATGTAGGCCGGCGGAGGCCAGGTTTCCGTGTACTGGGACTACATGAAG	2738 3099	
6y B	2739 AGCACCGCCTTCAGCACCTGG 3100 GCCATCGGACTCTTCATCTCC	AGCACCGCCTTCAGCACCTGGTGGTTGAGTTACTGGATCAAGCAAG	2798 3159	
οy		ACTGTGACTCGAGGGAACGAGACCTCGGTGAGTGACAGCATGAAGGACAATCCT	2852	
g	3160 GCGCTGGCTTCCAACTATTGG	CTCAGCCTCTGGACTGATGACCCCATCGTCAACGGGACT	3219	
Qy	2853 CATATGCAGTACTATGCCAGC.	CATATGCAGTACTATGCCAGCATCTACGCCCTCTCCATGGCAGTCATGCTGAAAA	2912 3279	
Oy Dp	2913 GCCATTCGAGGAGTT 3280 GCCGTGTTTGGCTACTCCATG	GCCATTCGAGGAGTTGTCTTTGTCAAGGCACGCTGCGAGCTTCCTCCCGGCTG	2966 3339	

3386 3086 3459 3146 3519 3446 3326 3759 3506 4056 4176 CGGACAGGATCAGGGAAGTCCTCGCTGGGGATGGCCCTCTTCCGTCTGGTGGAGTTATCT 3866 4236 3399 3266 3879 3939 3626 3686 CCCCAGGAGGAGAGGTGACCTTTGAGAACGCAGAGATGAGGTACCGAGAAAACCTCCCT 3746 CITGICCIAAAGAAAGIAICCITCACGAICAAACCIAAAGAGAAGAITGGCATTGTGGGG 3806 GGAGGCTGCATCAAGATTGATGGAGTGAGAATCAGTGATATTGGCCTTGCCGACCTCCGA 3926 CATGACGAGCTTTTCCGAAGGATCCTTCGAAGCCCTATGAAGTTTTTGACACGACCCCC 3026 TATGCGGGTCTCGCCATCTTTATGCTGTCCAGTTAACGGGGCTGTTCCAGTTTACGGTC 3566 3940 cGGATGTCATCTGAAATGGAAACCAACATCGTGGCCGTGGAGGGCTCAAGGAGTATTCA 3999 GAAGGAGAGATCATCATCGATGGCATCAACATCGCCAAGATCGGCCTGCACGACCTCCGC 4296 AGCAAACTCTCTATCATTCCTCAAGAGCCGGTGCTGTTCAGTGGCACTGTCAGATCAAAT 3986 3400 AGTGGGAACCTGGTGAACCGCTTCTCCAAGGAGCTGGACACAGTGGACTCCATGATCCCG TTCCAGGCCAGAATGTTCATCCAGAACGTTATCCTGGTGTTCTTCTGTGTGGGAATGATC TICAAGATCACCATCATCCCCCAGGACCCTGTTTTTTTTCGGGTTCCCTCCGGAATGAAC GAGGTCATCAAGATGTTCATGGGCTCCCTGTTCAACGTCATTGGTGCCTGCATCGTTATC GCAGGAGTCTTCCCGTGGTTCCTTGTGGCCAGTGGGGCCCCCTTGTCATCTTTTCAGTC CTGCACATTGTCTCCAGGGTCCTGATTCGGGAGCTGAAGCGTCTGGACAATATCACGCAG TCACCTTTCCTCTCCCACATCACGTCCAGCATACAGGGCCTTGCCCACCATCCACGCCTAC AATAAAGGGCAGGAGTTTCTGCACAGATACCAGGAGCTGCTGGATGACAACCAAGCTCCT TTTTTTTTTTTGTTTACGTGCGATGCGGTGGCTGGCTGTGCGGCTGGACCTCATCAGCATC 3447 GCCCTCATCACCACCACGGGGCTGATGATCGTTCTTATGCACGGGCAGATTCCCCCAGCC 3820 recarcerrengirracrecererringesergarerecassecaesecresecrese ACAGGGAGGATTCTCAACAGGTTTTCCAAAGACATGGATGAAGTTGACGTGCGGCTGCCG 3460 3387 3747 2967 3087 3147 3207 3327 3760 3567 4057 4177 3867 4237 4297 3027 3267 3507 3627 3687 3807 3927 QY Db δ g Qγ qq δ Оp Qy Db Qy Db δ qq ολ Ω Ωÿ qq Oy Db ò g Q g Qγ рp οy g δ Db οχ Db δλ Op Ω g

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NAME/KEY:
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                                                            GATAACTTCTCAGTGGGGGAACGGCAGCTCTTGTGCATAGCTAGAGCCCTGCTCCGCCAC 4166
                                                                                                                      ATTCAAGAGACCATCCGAGAAGCATTTGCAGACTGTACCATGCTGACCATTGCCCATCGC 4286
                                                                                                                                                                                                                                             CTGCACACGGTTCTAGGCTCCGATAGGATTATGGTGCTGGCCCAGGGACAGGTGGTGGAG 4346
                                                                                                                                                                                                                                                                          CTCAACACCATCATGGACTACACAAGGGTGATCGTCTTGGACAAAGGAGAAATCCAGGAG 4716
                                                                                                                                    4417 CTGAAGGACTTCGTGTCAGCCCTTCCTGACAAGCTAGACCATGAATGTGCAGAAGGCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Cole, Susan P.C.
APPLICANT: Deeley, Roger G.
TITLE OF INVENTION: METHODS FOR IDENTIFYING CHEMOSENSITIZERS NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Deconti, Giulio A. Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PQI-002CP8
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREE: OState Street, suite 510
STATE: Massack...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,179A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/966,923
FILING DATE: 27-0CT-1992
APPLICATION NUMBER: 08/029,340
FILING DATE: 8-MAR-1993
APPLICATION NUMBER: 08/141,893
FILING DATE: 26-0CT-1993
APPLICATION NUMBER: 08/407,207
FILING DATE: 20-MAR-1995
ATTORNEY/AGGNT INFORMATION:
                                                                                                                                                                                                                                                                                                                          TTTGACACCCCATCGGTCCTTCTG 4370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/08463179A Patent No. 6001563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 5011 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASCII text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 536
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1821 CACATCCACCTGGGCCACCTGCGCTTACAGAGGACACTGCACAGCATCGATCTGGAGATC 1880
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                                                                                                                                                                                                                                                                        1881 CAAGAGGGTAAAACTGGTTGGAATCTGCGGCAGTGGGAAGTGGAAAAACCTCTCTCATT
                                                                                                                                                                                                                                                                                                       GGGAAGGAATATGATGAAGAAAGATACAACTCTGTGCTGAACAGCTGCTGCCTGAGGCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1941 TCAGCCATTTTAGGCCAGATGACGCTTCTAGAGGGCAGCATTGCAATCAGTGGAACCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GACCTGGCCATTCTTCCCAGCAGCGACCTGACGGAGATTGGAGAGCGAGGAGCCAACCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2301 AGTGCTAT-----CCGGAAACATCTCAAGTCCAAGACAGTTCTGTTTGTTACCCACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCTTATGTGGCCCAGCAGGCCTGGATCCTCAATGCTACTCTGAGAGACAACATCCTGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2415 AGAGGCACCCATGAGGAACTGATGAATTTAAATGGTGACTATGCTACCATTTTAATAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2860 CCAGGGAAGGAAGCAAAGCAAATGGAGAATGGCATGCTGGTGACGGACAGTGCAGGGAAG
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                                                                                Length 5011;
                                                                                                                         0; Mismatches 1185; Indels
                                                                             Score 510; DB 3;
Pred. No. 3.7e-121;
                                                                           Query Match
Best Local Similarity 52.2%;
Matches 1360; Conservative
196..4788
; LOCATION:
US-08-463-179A-3
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1111 4177 CGGP	3867 GGAC 4237 GAAC	3927 AGCA 4297 TTCA	3987 TTGG 4357 CTGG	4047 ATGA 4417 CTGA	4107 GATA 4477 GAGA	4167 TGTA 4537 ACGA	4227 ATTC 4597 ATCC		4347 TTTG 4717 TACG	8 461-38, ence 3	Patent No. 6 GENERAL INF APPLICANT	TITLE OF NUMBER OF CORRESPON ADDRESS	STREET: CITY: STATE: COUNTRY	ZIP: K COMPUTER MEDIUM COMPUTE	OPERATI SOFTWAR CURRENT A APPLICA	FILING PRIOR APP APPLICA FILING	FILING APPLICA FILING APPLICA	FILING
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9 AGCACCGCCTTCAGCACCTGGTGGTTACTGGATCAAGCAAG	9 ACTGTGACTCGAGGGAACGAGACCTCGGTGAGTGACACCATGAAGGACAATCCT	3 CATATGCAGTACTATGCCAGCATCTACGCCCTCTCCATGGCAGTCATGCTGATCCTGAAA			P ACAGGAGGATCTCAACAGGTTTTCCAAAGACATGGATGAAGTTGACGTGCGGCTGCCG	7 TTCCAGGCCGAGATGTTCATCCAGAACGTTATCCTGGTGTTCTTCTGTGTGGGAATGATCT	GCAGGAGTCTTCCCGTGGTTCCTTGTGGCCAGTGGGGCCCCTTGTCATCCTCTTTTCAGTCCTCTTGTCAGTCTTTTCAGTCTCAGCCCCATCGCCCATCGCCCCTTGGCCTCATCTTCTTC	CTGCACATTGTCTCCAGGGTCCTGATTCGGGAGCTGAAGCGTCTGGACAATATCACGCAG	TCACCTITCCTCCCACATCACGiCCAGCATACAGGCCTTGCCACCATCCAGCCTAC	AATAAAGGGCAGGAGTTTCTGCACAGATACCAGGAGCTGCTGGTGGATGACAACCAAGGTCCT	TITITITITITACTGTGCGATGCGGTGGCTGGCTGTGCGGCTGGACCTCATCAGCATC	GCCCTCATCACCACCACGGGGCTGATGGTCCTTATGCACGGGCAGATTCCCCCAGCC	TATGCGGGTCTCGCATCTCTTATGCTGTCCAGTTAACGGGGCTGTTCCAGTTTACGGTC	AGACTGGCATCTGAGACGAGAGCTCGATTCACCTCGGTGGAGAGGATCAATCA	AAGACTCTGTCCTTGGAAGCACCTGCCAGAATTAAGAACAAGGCTCCCTCC	CCCCAGGAGGGGAGAGGTGACCTTTGAGAAGGCAGGATGAGGTACCGAGAAAACCTCCT	CTIGICCTAAAGAAAGTAICCTTCACGAICAAACCTAAAGAGAAGAITGGCAITGIGGG 	CGGACAGGATCAGGGAAGTCCTCGCTGGGGATGGCCCTCTTCCGTCTGGTGGAGTTATCT
2739	3160	2853	2913	3340	3027	3087	3147	3207	3267	3327 3700	3387 3760	3447	3507	3567	3627	3687	3747	3807
Qy Db	Qy Dp	Qy Dp	Qy Dp	ζς qq	O.Y.	oy da	Oy Dp	Qy	Qy Dp	Qy	Qy Dp	Oy Dp	Qy Dp	oy Op	oy Op	Oy Dp	QY	Qγ

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AAAGAATGTATTGCTCAGCTACCTCTGAAACTTGAATCTGAAGTGATGGAGAATGGG 4106
                                                                                                                                                                                                                                                                                                                                                                                  AAGATTCTGATTTTAGATGAAGCCACAGCCTGCCATGGACACAGAGACAGAGTTATTG 4226
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                                                                                                                 AAACTCTCTATCATTCCTCAAGAGCCGGTGCTGTTCAGTGGCACTGTCAGATCAAAT 3986
                                                                                                                                                                                  GACCCCTTCAACCAGTACACTGAAGACCAGATTTGGGATGCCCTGGAGAGGACACAC 4046
                                                                                                                                                                                                                                                                      AACTICICAGIGGGGAACGGCAGCICITGIGCATAGCIAGAGCCCIGCICCGCCAC 4166
                                                                                                                                                                                                                                                                                                                                     5: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS Queen's University at Kingston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WFORMATION:
TO Cole, Susan P.C.
TT. Decley, Roger G.
TINVENTION: MULTIDRUG RESISTANCE PROTEINS
PS SEQUENCES: 10
PS SEQUENCES: 10
SSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UM TYPE: Floppy disk
UTER: IBM PC compatible
AATING SYSTEM: PC-DOS/MS-DOS
WARE: ASCII text
TAPPLICATION DATA:
ICATION NUMBER: US/08/461,384B
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TAPPLICATION DATA:

ICATION NUMBER: 07/966,923

NG DATE: 27.0CT-1992

TCATION NUMBER: 08/029,340

NG DATE: 8-MAR-1993
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DATE: 26-0CT-1993
ATION NUMBER: 08/407,207
DATE: 20-MAR-1995
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RY: CANADA
K7L 3N6
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2860 CCAGGGAAGGAAGCAAAGCAAATGGAGAATGGCATGCTGGTGACGGACAGTGCAGGGAAG 2919
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                                                                       CAACTGCAGAGACAGCTCAGCAGCTCCTCCTATAGTGGGGGACATCAGCAGGCACCAC
                                                                                                                                                                            2686 GGGGC-----CCCTTGGCATTCCTGGTTATTATGGCCCTTTTCATGCTGAATGTAGGC
                                                                                                                                                                                                           3040 GAGGCTGACAAGGCGCAGACAGGCCAGGTCAAGCTTTCCGTGTACTGGGACTACATGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGAAGGAATATGATGAAGAAAGATACAACTCTGTGCTGAACAGCTGCTGCTGAGGCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2181 AGCGGTGGCCAGCGCCAGAGGATCAGCCTTGCCCGGGCCTTGTATAGTGACAGGAGCATC
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                                                                                                                                                                                                                                                                                                                                Length 5011;
                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                  .0; Mismatches 1185;
                                                                                                                                                                                                                                                                                                                                  Score 510; DB 3; Pred. No. 3.7e-121;
       NAME: Steeg, Carol Miernicki
REGISTRATION NUMBER: 39,539
REFRENCE/DOCKET NUMBER: 01547
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 545-2342
TELEPAX: (613) 545-6853
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                Carol Miernicki
                                                                                                                                                                                                                                                                                                                                Query Match 8.7%;
Best Local Similarity 52.2%;
Matches 1360; Conservative
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                   LENGTH: 5011 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                          ; NAME/KEY: CDS; LOCATION: 196..4788
US-08-461-384B-3
                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: CDNA
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                                            CCCCAGGAGGAGGTGACCTTTGAGAACGCAGAGATGAGGTACCGAGAAAACCTCCCT
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APPLICANT: Deeley, Roger G.
TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEIN
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, SUITE 510
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Patent No. 5489519
GENERAL INFORMATION:
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IBM PC compatible
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CITY: BOSTON
STATE: MASSACHUSETTS
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MEDIUM TYPE: Floppy
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SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
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                                                                                                    CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/966,923; 08/029,340
FILING DATE: 27.0CT-1992; 8-MAR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                RAME: DECORT, GIULLO A. Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: 901-002
TELECOMMUNICATION INPORMATION:
TELEPHONE: (617) 227-7400
TELEPAX: (617) 227-5149
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                  SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/141,893 FILING DATE:
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nucleic acid
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                               CCCCAGGAGGGAGAGGTGACCTTTGAGAACGCAGAGATGAGGTACCGAGAAAACCTCCCT
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APPLICANT: Cole, Susan P.C.
APPLICANT: Deeley, Roger G.
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING
TITLE OF INVENTION: MULTIDRUG RESISTANCE PROFEINS
NUMBER OF SEQUENCES: 9
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2380 GGATGTCAGCTGGAGGAACCATATTACAGGTCCGTGATACAGGCCTGTGCCCTCCTCCCCA 2439
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                 E: PARTEO RESEARCH & DEVELOPMENT INNOVATIONS Queen's University at Kingston
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                                                                                                                                                                                               SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,092B
FILING DATE: 05-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION: 453

PRIOR APPLICATION DATA.

APPLICATION NUMBER: 08/407,207
FILING DATE: 20-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Steeg, Carol Miernicki
REGISTRATION NUMBER: 39,539
REFERENCE/CDCKET NUMBER: 01546
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 545-6853
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/029,340
FILING DATE: 8-MAR-1993
CLASSIFICATION: 435
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APPLICATION NUMBER: 08/141,893
FILING DATE: 26-0CT-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 07/966,923
FILING DATE: 27-0CT-1992
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Matches 1357; Conservative
                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
CORRESPONDENCE ADDRESS:
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196..4788
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                                                                                     COUNTRY: CANADA ZIP: K7L 3N6
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                                               CITY: Kingston
STATE: Ontario
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; LOCATION:
US-08-463-092B-1
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                                                                                                                                                                                                                                                                                                                                       APPLICANT: Cole, Susan P.C.
APPLICANT: Deeley, Roger G.
TITLE OF INVENTION: METHODS FOR IDENTIFYING
TITLE OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.7%; Score 505.2; DB 2; 52.1%; Pred. No. 6.3e-120;
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 State Street, suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/462,109A FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/966,923
FILING DATE: 27-0CT-1992
APPLICATION NUMBER: 08/029,340
FILING DATE: 8-MAR-1993
FILING DATE: 26-0CT-1993
FILING DATE: 26-0CT-1993
APPLICATION NUMBER: 08/141,893
FILING DATE: 20-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                    4717 TACGGCCCCCATCGGACCTCCTG 4740
                                                                                                                                                 4347 TTTGACACCCCATCGGTCCTTCTG 4370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08462109A
Patent No. 5882875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: DeConti, Giulio A. Jr. REGISTRATION NUMBER: 31,503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
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US-08-462-109A-1
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Matches 1357;
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CACATTCACCTGGGCCAGGAGGGACCCTCCCACACTGAATGGCATCACCTTCTCCATC	CAAGAGGGTAAACTGGTTGGAATCTGCGGCAGTGGGAAGTGGAAAAACCTCTCTCT	CCCGAAGGTCCTTTGTGGTGGTGGGCCAGGTGGGCTGCGGGAAGTTGTCCCTGCTC	TCAGCCATTTTAGGCCAGATGACGCTTCTAGAGGGCAGCATTGCAATCAGTGGAACCTTC	TCAGCCCTCTTGGCTGAGATGGACAAAGTGGAGGGCCACGTGGCTATCAAGGGCTCCGTG	GCTTATGTGGCCCAGCCTGGATCCTCAATGCTACTCTGAGAGACAACATCCTGTTT		osanosantanonamananantanonamananananananananananananananananan	GGAGAGC		TTGTATA	TCTGGGGGGACAGAAGCAGCGCGTGAGCCTGGGCCCGGGCCGTGTACTCCAACGCTGACATT	TACATCCTGGACGACCCCCTCAGTGCCTTAGATGCCCATGTGGGCAACCACCTCAAT	-CCGGAAACATCTCAAGTCCAAGACAGTTCTGTTTGTTACCAGG		TTACAGTACCTGGTTGACTGTGATGAAGTGATCTTCATGAAAGAGGGCTGTATTACGGAA	AGAGCTACTIGCCGCAGGTGGACGTCATCATCATGAGTGGCGGCAAGATCTCTGAG	AGAGGCACCCATGAGAACTGAATTTAAATGGTGACTATGCTACCATTTTAATAAC 1	TICECIE	CONTROL OF STREET CANTROL OF STREET CANT	1	GTGACGG	CAGGATCAGTAAAAGGAAAAAAGCAGTAAAGCCAGAGGAAAGGGCAGCTTGTGCAGCTGG		AAGAGAAAGGGCAGGGTTCAGTGCCCTGGTCAGTATATGGTGTCTACATCCAGGCTGCTG	AACAGCACCGCAGAACTGCAGAAAGCTGAGGCCAAGAAGGAGGAGACCTGGAAGCTGATG	GGGGCCCCITGGCATTCTGGTATTATGGCCCTTTTCATGCTGAATGTAGGC 	AGCACCGCCTTCAGCACCTGGTGGGTTGAGTTACTGGATCAAGCAAG	GCCATCGGACTCTTCATCTTCCTCAGCATCTTCCTTTTCATGTGTAACCATGTGTCC	GGGAACGAGACCTCGGTGAGTGACAGCATGAAGGACAATCCT		CATATGCAGTACTATGCCAGCATCTACGCCCTCTCCCATGGCAGTCATGCTGATCCTGAAA	
CCACACT	GTGTGGG	AGGTGGG	AGGGCAG	AGGGGCAC	ATGCTACT		CIGIGCIA CCGTGATA	CGGAGATT	CAGAGATI	ວວອອວວວ	000000000000000000000000000000000000000	ATGCCCAT	CAAGACA	111111 ACAAGACG	CTTCATE	CGTCATO	ATGGTGAC		HEATCANT GGAGAAC	1	SCATGCTG	SCCAGAGG	CTATAGE	AGTATATG	CAAGAAG	TATGGCC	CTGGATC	LIII	GGTGAGT	GACTGAT	CTCCATG	TGGAGCC
GACCCTC	TGCGGCA	111 GTGGGCC	CTTCTAG	AAAGTGG	ATCCTCA	E CAR	I ACAGGT	GACCTGA	II	AGCCTTG	AGCCTGG	SCCTTAGE	CTCAAGT	II III CTGAAGA	SAAGTGA	TCATCA:	AATTTAA	TO TO THE	SATGCAG		SAGAATGO	CAGTAAAC	rccrccrc	CTGGTCA	SCTGAGG	TGGTTAT	TGAGTT	TCAGCAT	SAGACCIC	GCCTCTC	PACGCCCT	
GGAGC	TGGAATC	 GGCCGTG	GATGACG	GATGGAC	GGCCTGG		HOMANGA ACCATAT	CAGCAGC	CAGTGGG	SAGGATC	ccccrc	CCTCAGTO	SAAACAT	l SGGGATG	CTGTGAT	SGTGGAC	ACTGATG	בופנופנים	BGAGCAG	AGACA	i i scaaatge	SAAAAAGC	l Jagcaget	CAGTGCC	SCAGAAAC	SGCATTCC	TGGTGG1	TCCTTCC	GGGAACG	II I	AGCATCI	 cgcrc
TGGGCCA	AACTGGT		TAGGCCA	TGGCTGA	CCCAGCA	E	Algalga TGGAGGA	TTCTTCC	1 11 11 TCCTGCC	AGCGCCA	II AGAAGCA	ACGACCC ATGATCC	CCG	GCCCCAA	TGGTTGA	TGCCGCA	ATGAGGA	200000000000000000000000000000000000000	IIII IIII CAGAGCA(AGTCACA	AAGCAAA	AAAGAAG	i Sacagct(SCAGGGT	CAGAACTO	AGGCGCAC	PCAGCAC	II II	;	CAACTA	ACTATGC	CGAAAGTC
ATTCACC	GAGGGTA	II III GAAGGTG	GCCATTT	GCCCTCT	TATGTGG		TGTCAGC	CTGGCCA	CTGGAAA	GGTGGGC	GGGGGAC	ATCCTGG CTCTTCG	AGTGCTAT	 GTGATTG	CAGTACC	AGCTACT	GGCACCC		GCCAGCA	TCACAGAAGAAGTCACAAGACA		GATCAGT	CTGCAGA	AGAAAGG	AGCACCG	GCTGACA	ACCGCCT	 ATCGGAC	ACTGTGACTCGA	11 11	ATGCAGT	GAGCACAC
2142 CAC	1881 CAA	2200 ccc		2260 TCA	2001 GCT 11 2320 GCC			2121 GAC		2181 AGC	2500 TCT	2241 TAC 2560 TAC		1 2620 AAT	2355 TTA	2680 ATG	2415 AGA			2532 TCA		2566 CAG	2920 CAA			2686 GGGGC 111 3040 GAGGC			2799 ACT		2853 CAT	3220 CAG
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3339 3026 3086 3459 3146 3519 3206 3579 3266 3326 3759 3686 4176 ATTCGAGG----AGTTGTCTTTGTCAAGGGCACGCTGCGAGCTTCCTCCCGGCTG 2966 AAAGGGCAGGAGTTTCTGCACAGATACCAGGAGCTGCTGGATGACAACCAAGCTCCT 3386 CTCATCACCACCACGGGGCTGATGATCGTTCTTATGCACGGGCAGATTCCCCCAGCC 3506 ATCGTTCTGTTTGCTGCCCTGTTTGCGGTGATCTCCAGGCACAGCCTCAGTGCTGGC 3879 GCGGGTCTCGCCATCTCTTATGCTGTCCAGTTAACGGGGCTGTTCCAGTTTACGGTC 3566 CTGGCATCTGAGACAGAAGCTCGATTCACÇTCGGTGGAGAGGATCAATCACATT 3626 CAGGAGGAGAGGTGACCTTTGAGAACGCAGAGATGAGGTACCGAGAAAACCTCCCT 3746 GTCCTAAAGAAAGTATCCTTCACGATCAAACCTAAAGAGAAGATGGCATTGTGGGG 3806 ACAGGATCAGGGAAGTCCTCGCTGGGGATGGCCCTCTTCCGTCTGGTGGAGTTATCT 3866 AAACTCTCTATCATTCCTCAACAGCCGGTGCTGTTCAGTGGCACTGTCAGATCAAT 3986 4236 4296 GGCTGCATCAAGATTGATGGAGTGAGAATCAGTGATATTGGCCTTGCCGACCTCCGA 3926 CACATTGTCTCCAGGGTCCTGATTCGGGAGCTGAAGCGTCTGGACAATATCACGCAG GACGAGCTTTTCGAAGGATCCTTCGAAGCCCTATGAAGTTTTTGACACGACCCC IGGGAGGATTCTCAACAGGTTTTCCAAAGACATGGATGAAGTTGACGTGCGGCTGCCG CAGGCCGAGATGTTCATCCAGAACGTTATCCTGGTGTTCTTCTGTGTGGGAATGATC GGAGTCTTCCCGTGGTTCCTTGTGGCAGTGGGGCCCCTTGTCATCCTCTTTTCAGTC CCTTTCCTCTCCCACATCACGTCCAGCATACAGGGCCTTGCCACCATCCACGCCTAC ACGGGAGCTGGGAAGTCGTCCTGACCCTGGGCTTATTTCGGATCAACGAGTCTGCC

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                                                                                                                                                                                                                                 ATTCAAGAGCCATCCGAGAAGCATTTGCAGACTGTACCATGCTGACCATTGCCCATCGC 4286
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3987 TTGGACCCCTTCAACCAGTACACTGAAGACCAGATTTGGGATGCCCTGGAGAGGACACAC
                    GATAACTTCTCAGTGGGGGAACGGCAGCTCTTGTGCATAGCTAGAGCCCTGCTCCGCCAC
                                                                                                                                                             TGTAAGATTCTGATTTTAGATGAAGCCACAGCTGCCATGGACACAGAGACATTATTG
                                                                        4047 ATGAAAGAATGTATTGCTCAGCTACCTCTGAAACTTGAATCTGAAGTGATGGAGAATGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: PARTED RESEARCH & DEVELOPMENT INNOVATIONS STREET: Queen's University at Kingston CITY: Kingston ATATION STATE: Ontario COUNTRY: CANADA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Deeley, Roger G.
APPLICANT: Cole, Susan P.C.
TITLE OF INVENTION: METHODS FOR CONFERRING MULTIDRUG
TITLE OF INVENTION: RESISTANCE ON A CELL
CONFIDENCE: 9
CORRESPONDENCE: ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,907B
FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
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FILING DATE: 8-MAR-1>>-
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/141,893
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08460907B Patent No. 5891724 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER:
07/966,923
FILING DATE: 27-0CT-1992
CLASSIFTCATION: 424
PRIOR APPLICATION DATA:
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FILING DATE: 20-MAR-1995
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PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                Score 505.2; DB 2;
Pred. No. 6.3e-120;
0; Mismatches 1188;
            REFERENCE/DOCKET NUMBER: 01551
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 545-2342
TELEFAX: (613) 545-6853
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5011 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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US-08-460-907B-1
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                                                          CAGGATCAGTAAAGAAGGAAAAAGCAGTAAAGCCAGAGGAAGGGCAGCTTGTGCAGCTGG
                                                                                                      ACTGTGACTCGA------GGGAACGAGACCTCGGTGAGTGACAGCATGAAGGACAATCCT
                                           2626 AAGAGAAAGGGCAGGGTTCAGTGCCCTGGTCAGTATATGGTGTCTACATCCAGGCTGCTG
                                                                                         GGGGC------CCCTTGGCATTCCTGGTTATTATGGCCCTTTTCATGCTGAATGTAGGC
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                              CCCCAGGAGGGAGGGGACCTTTGAGAACGCAGAGATGAGGTACCGAGAAAACCTCCCT
                                                                                                              CGGACAGGATCAGGGAAGTCCTCGCTGGGGATGGCCCTCTTCCGTCTGGTGGAGTTATCT
                                                                                                                        GGAGGCTGCATCAAGATTGATGGAGTGAGTCAGTGATATTGGCCTTGCCGACCTCCGA
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                                                                                                                                                                                                                                                                          ATGAAAGAATGTATTGCTCAGCTACCTCTGAAACTTGAATCTGAAGTGATGGAGAATGGG
                                                                      CTTGTCCTAAAGAAAGTATCCTTCACGATCAAACCTAAAGAGAAGATTGGCATTGTGGGG
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cole, Susan P.C.
APPLICANT: Deeley, Roger G.
TITLE OF INVENTION: METHODS FOR
NUMBER OF SEQUENCE: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
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MEDIUM TYPE: Floppy disk
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STATE: Massac
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAAGAGGGTAAACTGGTTGGAATCTGCGGCAGTGTGGGAAGTGGAAAAACCTCTCTCATT 1940
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTTATGTGGCCCAGCAGGCCTGGATCCTCAATGCTACTCTGAGAGACAACATCCTGTTT
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                                                                                                                                                                                                                                                                                                                                                                                Length 5011;
                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                             NAME: Deconti, Giulio A. Jr.
REGISTRATION NUMBER: 31.503
REFERENCE/DOCKET NUMBER: PQI-002CP8
TELECOMMUNICATION INFORMATION:
         US/08/463,179A
                                                                 FILING DATE: 27-0CT-1992
APPLICATION NUMBER: 08/029,340
FILING DATE: 8-MAR-1993
APPLICATION NUMBER: 08/141,893
FILING DATE: 26-0CT-1993
APPLICATION NUMBER: 08/407,207
FILING DATE: 20-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                         07/966,923
                                                                                                                                                                                                           TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                           LENGTH: 5011 base pairs
CURRENT APPLICATION DATA:
                                            PRIOR APPLICATION DATA: APPLICATION NUMBER: (
                                                                                                                                                                                                                                                                                      double
         APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 536
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                                                                                                                                                                                                                                                                          nucleic acid
                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                 linear
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TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                             ; LOCATION:
US-08-463-179A-1
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2531 2979 2738 2852 3219 3399 3086 3146 3519 3206 ---AGGGTCCTAAAA 2565 2912 3266 3446 2920 CAACTGCAGAGACAGCTCAGCAGCTCCTCCTATAGTGGGGGACATCAGCAGGCACCAC GAGGCTGACAAGGCGCAGACAGGCAGGTCAAGCTTTCCGTGTACTGGGACTACATGAAG 2415 AGAGGCACCCATGAGGAACTGATTTAAATGGTGACTATGCTACCATTTTAATAAC 2800 TATGCCAGCAGAGCAGGAGGAGGAGGAGGAACGGGGTCACGGGCGTCAGCGGT CAGGATCAGTAAAGAAGGAAAAAGCAGTAAAGCCAGAGGAAGGGCAGCTTGTGCAGCTGG GGGGC-----CCCTTGGCATTCCTGGTTATTATGGCCCTTTTCATGCTGAATGTAGGC GCCATGGGACTCTTCATCTTCCTCATGTTTCCTTTTCATGTGTAACCATGTGTCC 2475 CTGTTGCTGGGAGAGACACCGCCAGTT---GAGATCAATTCAAAAAAGGAAACCAGTGGT CATATGCAGTACTATGCCAGCATCTACGCCCTCTCCATGGCAGTCATGCTGATCCTGAAA CTGCACATTGTCTCCAGGGTCCTGATTCGGGAGCTGAAGCGTCTGGACAATATCACGCAG 2860 CCAGGGAAGGAAGCAAAGCAAATGGAGAATGGCATGCTGGTGACGGACAGTGCAGGGAAG AAGAGAAAGGGCAGGGTTCAGTGCCCTGGTCAGTATATGGTGTCTACATCCAGGCTGCTG 2980 AACAGCACCGCAGAACTGCAGAAAGCTGAGGCCAAGAAGGAGGAGACCTGGAAGCTGATG ACTGTGACTCGA-----GGGAACGAGACCTCGGTGAGTGACAGCATGAAGGACAATCCT CAGGAGCACACGAAAGTCCGGCTGAGCGTCTATGGAGCCCTGGGCATTTCACAAGGGATC 3087 TTCCAGGCCGAGATGTTCATCCAGAACGTTATCCTGGTGTTCTTCTGTGTGGGAATGATC GAGGTCATCAAGATGTTCATGGGCTCCCTGTTCAACGTCATTGGTGCCTGCATCGTTATC 3147 GCAGGAGTCTTCCCGTGGTTCCTTGTGGCAGTGGGGCCCCTTGTCATCCTCTTTTCAGTC TCACCTTTCCTCCCACATCACGTCCAGCATACAGGGCCTTGCCACCATCCACGCCTAC AATAAAGGGCAGGAGTTTCTGCACAGATACCAGGAGCTGCTGGATGACAACCAAGCTCCT GCCATTCGAGG - - - - - AGTTGTCTTTGTCAAGGGCACGCTGCGAGCTTCCTCCCGGCTG 3280 GCCGTGTTTGGCTACTCCATGGCCGTGTCCATCGGGGGGGATCTTGGCTTCCCGCTGTCTG CATGACGAGCTTTTCCGAAGGATCCTTCGAAGCCCTATGAAGTTTTTTGACACGACCCCC ACAGGAGGATTCTCAACAGGTTTTCCAAAGACATGGATGAAGTTGACGTGCGGCTGCCG 3520 CIGCIGGCCACGCCCATCGCCGCCATCATCCGCCCCTTGGCCTCATCTACTTCTTC TCACAGAAGAGTCACAAGACA-

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                                                                     3507 TATGCGGGTCTCGCCATCTCTTATGCTGTCCAGTTAACGGGGCTGTTCCAGTTTACGGTC
                                                                                                    GAGACTGAGAA - - - GGAGGCGCCCTGGCAAATCCAGGAGACACGTCCGCCCAGCAGCTGG
                   3447 GCCCTCATCACCACCACGGGGCTGATGATCGTTCTTATGCACGGGCAGATTCCCCCAGCC
                                       3820 IGCATCGTTCTGTTTGCTGCTCTTTTGCGGTGATCTCCAGGCACAGCCTCAGTGCTGGC
                                                                                                                                          CTTGTCCTAAAGAAAGTATCCTTCACGATCAAACCTAAAGAGAAGATTGGCATTGTGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2440 GACCTGGAAATCCTGCCCAGTGGGGATCGGACAGAGTTGGCGAGAAGGGCGTGAACCTG 2499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 5011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                    : PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS Queen's University at Kingston
APPLICANT: Deeley, Roger G.
TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.7%; Score 505.2; DB 3; 52.1%; Pred. No. 6.3e-120;
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                                                                                                                                                                                                                                                                                       SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,384B
FILING DATE: 05-JUN-95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/966,923
FILING DATE: 27-0CT-1992
APPLICATION NUMBER: 08/029,340
FILING DATE: 8-MAR-1993
APPLICATION NUMBER: 08/141,893
FILING DATE: 26-0CT-1993
APPLICATION NUMBER: 08/407,207
FILING DATE: 20-MAR-1995
ATTONNEY/AGENT INFORMATION:
NAME: Steeq, CATOL Miernicki
REGISTRATION NUMBER: 39,539
                                                                                                                                                                                                                                                                            PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01547
                                                                                                                                                         COUNTRY: CANADA
ZIP: K7L 3N6
COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-PY
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (613) 545-2342
TELEFAX: (613) 545-6853
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5011 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 52.1
Matches 1357; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
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196..4788
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                                                                                  ADDRESSEE: PARTE STREET: Queen's CITY: Kingston STATE: Ontario
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION:
US-08-461-384B-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Sequence 1, Application US/08461384B Patent No. 6025473 GENERAL INFORMATION:

US-08-461-384B-1

APPLICANT: Cole, Susan P.C.

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2240	2300	2354	2414	2474	2531 2859	2565	2625 2979	2685 3039	2738 3099	2798 3159	2852 3219	2912 3279	2966 3339	3026 3399	3086	3146	3206	3579
ACCGTGGCACCCCAGAGGATCAGCCTTGCCCGGGCCTTGTATAGTGACAGGAGCATC	TACATCCTGGACGACCCCTCAGTGCCCATGTGGGCAACCACATCTTCAAT	AGTGCTATCCGGAAACATCTCAAGTCCAAGACAGTTCTGTTTGTTACCCACCAG	TTACAGTACCTGGTTGACGGTGATCTTCATGAAAGAGGGCTGTATTACGGAA	AGAGGCACCCATGAGGAACTGAATTTAAATGGTGACTATGCTACCATTTTTAATAAC	CTGTTGCTGGGAGACACCGCCAGTTGAGATCAATTCAAAAAAGGAAACCAGTGGT 	TCACAGAAGAAGTCACAAAAACAAGGGTCCTAAAA 	CAGGATCAGTAAAGAAGAAAAAGCCAGAGAGGAAGGGCAGCTGTGCAGCTGG	AAGAGAAAGGGCAGGGTTCAGTGCCCTGGTCAGTATATGGTGTCTACATCCAGGCTGCTG	GGGGCCCCTTGGCATTCCTGGTTATTATGGCCCTTTTCATGCTGATGTAGGCCCTTTTCATGCTGATGTAGGCCCCTTTTCATGCTGCGATAGAGGCCAGACGCCAGACGCCAGACGCCAGAGGCCAGACGCCAGAGGCCAGAGGCCAGAGGCCAGAGGCCAGAGGCCAGAGGCCAGAGGCAGGCAGAGGCAGAGGCAGAGAGGCAGAGAGGCAGAGAGGCAGAGAGGCAGAGAGGCAGAGAGGCAGAGAGGCAGAGAGGCAGAGAGGCAGAGAGGCAGAGAGGCAGAGAGGCAG		ACTGTGACTCGA GGGAACGAGCTCGGTGAGTGACTGCATGAAGGACAATCCT	CATATGCAGTACTATGCCAGCATCTACGCCCTCTCCATGGCAGTCATGCTGATCCTGAAA	GCCATTCGAGGAGTTGTCTTTGTCAAGGCACGCTGCGAGCTTCCTCCGGGCTG	CATGACGAGCTTTTCCGAAGGATCCTTCGAAGCCCTATGAAGTTTTTTGACACGCCCCCCCC	ACAGGGAGGATTCTCAAAGATTTCCAAAGACATGGATGAAGTTGACGTGCGGCTGCCG :	TTCCAGGCCGAGATGTTCATCCAGAACGTTATCCTGGTGTTCTTCTGTGTGGGAATGATC		crecrescencececarcecescenterecescecerringecercareractre
2181 2500	2241	2301	2355	2415	2475	2532	2566	2626	3040	2739 3100	2799 3160	2853 3220	2913 3280	3340	3027	3087.	3147	3520
Qy Db	0y Dp	Qy	Qy Dp	Oy Dp	Q Dp	φ	oy Op	Oy .	Oy Db	Qy Db	Qy	Qy Db	Qy	Qy	Oy Dp	Qy Db	ΟŻ	qa.

3326 3759 3819 3746 4476 3506 3879 3566 3626 4056 3806 4176 3866 4236 4356 4046 4416 4226 CTGCACATTGTCTCCAGGGTCCTGATTCGGGAGCTGAAGCGTCTGGACAATATCACGCAG 3266 GGAGGCTGCATCAAGATTGATGGAGTGAGAATCAGTGATATTGGCCTTGCCGACCTCCGA 3926 AGCAAACTCTCTATCATTCTCTCAAGAGCCGGTGCTGTTCAGTGGCACTGTCAGATCAAAT 3986 4287 CTGCACACGGTTCTAGGCTCCGATAGGATTATGGTGCTGGCCCAGGGACAGGTGGTGGTGGAG 4346 CCCCAGGAGGGAGAGACACTITGAGAACGCAGAGATGAGGTACCGAGAAAACCTCCCT 3760 TATTACCCCAGCATCGTGGCCAACAGGTGGCTGGCCGTGCGGCTGGAGTGTGTGGGCAAC TGCATCGTTCTGTTTGCTGCCCTGTTTGCGGTGATCTCCAGGCACAGCCTCAGTGCTGGC TCACCTTTCCTCCTCCACATCACGTCCAGCATACAGGGCCTTGCCACCATCCACGCCTAC AATAAAGGGCAGGAGTTTCTGCACAGATACCAGGAGCTGCTGGATGACAAGCTCCT 3447 GCCCTCATCACCACCACGGGGCTGATGATCGTTCTTATGCACGGGCAGATTCCCCCAGCC 3507 TATGCGGGTCTCGCCATCTCTTATGCTGTCCAGTTAACGGGGCTGTTCCAGTTTACGGTC 4357 CTGGACCCATTCAGCCAGTACTCGGATGAAGAAGTCTGGACGTCCCTGGAGCTGGCCCAC 4417 CTGAAGGACTTCGTGTCAGCCCTTCCTGACAAGCTAGACCATGAATGTGCAGAAGGCGGG TTTTTTTTTTTGTTACGTGCGATGCGGTGGCTGGCTGTGCGGCTGGACCTCATCAGCATC CGGACAGGATCAGGGAAGTCCTCGCTGGGGATGGCCCTCTTCCGTTGGTGGAGTTATCT TIGGACCCCTTCAACCAGTACACTGAAGACCAGATTGGGATGCCCTGGAGAGGACACAC ATGAAAGAATGTATTGCTCAGCTACCTCTGAAACTTGAATCTGAAGTGATGGG GATAACTICICAGIGGGGAACGCCAGCICITGIGCATAGCIAGAGCCCTGCICCGCCAC 3747 CITGICCIAAAGAAAGIAICCIICACGAICAAACCIAAAGAGAAGAITGGCAIIGIGGG ATTCAAGAGACCATCCGAGAAGCATTTGCAGACTGTACCATGCTGACCATTGCCCATCGC 3387 3820 3207 3267 3327 3880 3627 4000 4057 4117 3807 4177 3867 3927 3987 4047 4107 4477 3687 4227 QQ Qγ g οy Db δy g Q_{γ} g ò q qq g Ω ŏ ŏ d οy Db ò g Óγ a ò qq δŽ g g g οy ŏ ò g ò

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                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Deeley, Roger G.
APPLICANT: Cole, Susan P.C.
TITLE OF INVENTION: ANTIBODIES TO A MULTIDRUG RESISTANCE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCCGAAGGTGCTTTGGTGGCCGTGGTGGCCCAGGTGGGCTGCGGGAAAGTTGTCCCTGCTC
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CORRESPONDENCE ADDRESS: 7
CORRESPONDENCE ADDRESS: ADDRESSE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS STREET: Queen's University at Kingston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 505.2; DB 3;
Pred. No. 6.3e-120;
0; Mismatches 1188;
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/407,207A FILING DATE: 20-MAR-1995
                                           TTTGACACCCCATCGGTCCTTCTG 4370
                                                          4717 TACGGCGCCCCATCGGACCTCCTG 4740
                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                             Sequence 1, Application US/08407207A Patent No. 6063621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 07/966,923
FILING DATE: 27-0CT-1992
APPLICATION NUMBER: 08/029,340
FILING DATE: 8-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 8-MAR-1993
APPLICATION NUMBER: 08/141,893
FILING DATE: 26-007-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 39,539
REFERENCE/DOCKET NUMBER: Q1512
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Steeg, Carol Miernicki
REGISTRATION NUMBER: 39,539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (613) 545-2342
TELEFAX: (613) 545-6853
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 8.7%;
Best Local Similarity 52.1%;
Matches 1357; Conservative
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LENGTH: 5011 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: ASCII text CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                      COUNTRY: CANADA
ZIP: K7L 3N6
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
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STATE: Ontario
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CLASSIFICATION:
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; LOCATION:
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4656 4346 GATAACTICICAGIGGGGAACGGCAGCICITGIGCAIAGCIAGAGCCCIGCICCGCCAC 4166 ATTCAAGAGACCATCCGAGAAGCATTTGCAGACTGTACCATGCTGACCATTGCCCATCGC CTGCACACGGTTCTAGGCTCCGATAGGATTATGGTGCTGGCCCAGGGACAGGTGGTGGAG TTTGACACCCCATCGGTCCTTCTG 4370 4477 4537 4107 4167 4657 4347 4717 4227 4287 qq δ g Ş. qq δ g δ

Search completed: December 18, 2002, 21:34:07 Job time : 196.421 secs

Human prostate exp Novel human transp Human ATP-binding Prostate cancer-as Human transporter-DNA encoding novel

transporter-adenosine tr Human transporter-Human prostate exp Human MRP variant
Human multidrug re
Human MDR variant
Human ATP binding
Multidrug resistan
Human MRP variant
Prostate cancer-as

AA290193 AA239556 ABK92125

AAT14910

AAV31497 AAX19817

AAV31498

cDNA encoding mult Multidrug resistan cDNA encoding mult

Human multidrug re Human multidrug re Human multidrug re Multidrug resistan

Human multidrug re Human multidrug re Human TRICH-2 cDNA

AAZ39555 AAZ39555

AAZ30078 AAH81778

437.4

ABL66374

Lung cancer relate CDNA encoding a hu Human differential Novel human transp

Prostate cancer-as Human prostate cDN Human prostate-spe

ABK92135 AAS63922

AAF83647

ALIGNMENTS

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757.8
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Copyright (c) 1993 - 2002 Compugen Ltd.
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Listing first 45 summaries
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RESULT 1 AAZ30079

cDNA encoding a human MPR-related ABC transporter designated MOAT-C. Human; MPR-related ABC transporter; MOAT protein; MOAT-C; MOAT mediated transport; anticancer drug sensitivity; transporter mediated cellular efflux; anticancer; ss. AAZ30079 standard; cDNA; 5838 BP. 26-JAN-2000 AAZ30079;

Location/Qualifiers 126..4439 sapiens Ношо

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

/SIDS2/gcgdata/geneseg/genesegn-emb1/NA2002.DAT:*

/*tag= a /product= "MOAT-C" /note= "MPR-related ABC transporter"

99WO-US06644. 26-MAR-1999; 07-0CT-1999

cDNA encoding a hu
Human ATP binding
Human MRP-beta cDN
Human multidrug re
Multidrug resistan
Human multidrug re
Human multidrug re

AAZ94745 AAA40481 AAV65682 AAC85287 AAT94055 AAT94054 AAD14909

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5838 5838 4847 4847 4781 2167 1761 4101

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4792.6 4791 4724.2 1936.4 1676 925.8

AAZ30079

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DB

Length

Query Match

Score 5838 5838

Result ٠ يو

Description

Human transporter Human transporter-

98US-0079759. 27-MAR-1998; 03-AUG-1998;

(FOXC-) FOX CHASE CANCER CENT

409949735-A1

us-09-647-140a-3.rng

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protein, designated MOAT-C. The protein comprises a multi-domain structure including a tandem repeat of nucleotide binding folds appended C-terminal to a hydrophobic domain, having Walker A and B ATP binding sites and several potential membrane spanning domains. The MOAT nucleic acids are useful for screening a test compound for inhibition of MOAT mediated transport, indicated by restoration of anticancer drug sensitivity, which in turn causes a reduction of transporter mediated cellular efflux of anticancer agents. MOAT DNA or RNA may be used as probes to detect the presence or expression of genes encoding MOAT proteins. Anti-MOAT antibodies are useful for detecting and quantitating
                                                                                                                                                                                               present sequence encodes a human MPR-related
                                                                                                                                                         Claim 11; Page 134-135; 153pp; English.
                                                                                                                  New transporter gene useful for
                      ΣÌ
                      Belinsky
                                                          WPI; 1999-610812/52.
                                                                            P-PSDB; AAY43542
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                      ree
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                    Kruh
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ABC transporter

drugs

anti-cancer

for

screening

ï Bain Sequence 5838 BP; 1422 A; 1432 C; 1509 G; 1475 T; 0 other;

proteins

MOAT

Gaps DB 20; Length 5838; ó Indels ; 0 Ouery Match 100.0%; Score 5838; I Best Local Similarity 100.0%; Pred. No. 0; Matches 5838; Conservative 0; Mismatches

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120 AGAAGATGAAGGATATCGACATAGGAAAAGAGTATATCATCCCCAGTCCTGGGTATAGAA 180 9 9 CCGGGCAGGTGGCTCATGCTCGGGAGCGTGGTTGAGCGGCTGGCGGGTTGTCCTGGAGC AGGGGCGCAGGAATTCTGATGTGAAACTAACAGTCTGTGAGCCCTGGAACCTCCGCTCAG AGAAGATGAAGGATATCGACATAGGAAAAGAGTATATCATCCCCAGTCCTGGGTATAGAA CCGGGCAGGTGGCTCATGCTCGGGAGCGTGGTTGAGCGGCTGGCGGGTTGTCCTGGAGC GTGTGAGGGAGAGCAGCACCTTCTGGGACGCACAGAGCCGTGAAGATTCCAAGTTCA 61 61 121 121 181 δ 셤 ò g δ g ö

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AAGTTGGCCCAGACGCTTCCCTGCGAAGGGTTGTGTGGGATCTTCTGCCGCACCAGGC 601 601

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1140 1080 1140 1440 1500 1320 1380 1440 1560 AGGCGGTGCTGGCAGAGGCCACCTCCTCCTGGACAGTGACGAGCGGCCCAGTC 1800 720 780 840 900 900 960 960 CTTGGGCATTGAATTACCGAACCGGTGTCCGCTTGCGGGGGGCCATCCTAACCATGGCAT TTAAGAAGATCCTTAAAGTTAAAGAACATTAAAGAGAAATCCCTGGGTGAGCTCATCAACA GCTTCCTGGGATCAGCTGTTTTATCCTCTTTTACCCAGCAATGATGTTTGCATCACGGC CTGTTCATATGACCCTGGGCTTCGATCTGACAGCACAGGCTTTCACAGTGGTGACAG TCATCCTGTCCATCGTGTGCCTGATGATCACGCAGCTGGCTTGGCTTCAGTGGACCAGCCT TCATGGTGAAACACCTCTTGGAGTATACCCAGGCAACAGAGTCTAACCTGCAGTACAGCT TGTTGTTAGTGCTGGGCCTCCTCCTGACGGAAATCGTGCGGTCTTGGTCGCTTGCACTGA TCACAGCATATTTCAGGAGAAAATGCGTGGCCGCCACGGATGAACGTGTCCAGGAAGATGA ATGAAGTTCTTACTTACATTAAATTTATCAAAATGTATGCCTGGGTCAAAGCATTTTCTC AGAGTGTTCAAAAATCCGCGAGGAGGAGCGTCGGATATTGGAAAAAGCCGGGTACTTCC AGGGTATCACTGTGGGTGTGGCTCCCATTGTGGTGGTGATTGCCAGCGTGGTGACCTTCT AAGCCTCAGTGGCTGTTGACAGATTTAAGAGTTTGTTTCTAATGGAAGAGGTTCACATGA GGGACTCCTCCCACTCCAGTATCCAGAACTCGCCCAAGCTGACCCCCAAAATGAAAAAG TAAAGAACAAACCAGCCAGTCCTCACATCAAGATAGAGATGAAAAATGCCACCTTGGCAT ACAAGAGGCTTCCAGGGCAAGAAGAAGAAGGTGAGGCAGCTGCAGCGCACTGAGCATC 661 841 1021 1081 1081 1141 1141 1201 1201 1261 1321 1321 1381 1381 1441 1501 1501 1741 661 721 721 781 781 841 901 901 961 961 1021 1261 1441 1561 1561 1621 1621 1681 1681 qq Qλ à qq ò Pp à g ò pp ò Db g δý qq g δ δ ŏ g ò g à q ò g g ò õ g γŏ g à 셤 ò

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ζζ G	2881	CCCTCTCCATGGCAGTCATCATGAAAGCCATTCGAGAGAGTTTTCTTTTCTAAGG 2940
Qγ		ACGCTGCGAGCTTCCTCCCGGCTGCATGACGAGCTTTTCCGAAGGATCCTTCGAAGCC 300
QQ		00
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δy		GGATGAAGTTGACGTGCGGCTGCCGTTCCAGGCCGAGATGTTCATCCAGAACGTTATCC 312
q	3061	-
Qy	3121	TGGTGTTCTTCTGTGGGAATGATCGCAGGAGTCTTCCCGTGGTTCCTTGTGCCAGTGG 3180
QC	3121	GGTGTTCTTCTGTGTGGGAATGGTCGCAGGAGTCTTCCCGTGGTTCCTTGTGGCAGTGG 3
Οÿ	8	GGCCCCTTGTCATCCTCTTTTCAGTCCTGCACATTGTCTCCAGGGTCCTGATTCGGGAGC 3240
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ογ γ		3
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g G	3301	AGGGCCTIGCCACCATCCACGCTACAATAAAGGGCAGGAGTTTCTGCAGAGATACCAGG 3360
δy		CTGCTGGATGACCAACCTACTTTTTTTTTTTTACGTGCGATGCGGTGGCTGG 342
qq	3361	C
οy	3421	CACCACCACGGGCTGATGATCGTTC 34
рp	3421	steceectegacctcarcaccatcacctcarcaccaccacegeectatearcar
ΟŊ	3481	TTATGCACGGCAGATTCCCCCAGCCTATGCGGGTCTCGCCATCTCTTATGCTGTCCAGT 3540
qq	3481.	TATGCACGGGCAGATICCCCCAGCCTATGCGGGTCTCGCCATCTCTTATGCTGTCAGT 35
ΟŊ	3541	TAACGGGGCTGTTCCAGTTACGGTCAGACTGGCATCTGAGACAGAAGCTCGATTCACCT 3600
qq	3541	aacgogocioriccaoitiacooicadacioocaicioadacaoadaacicoaitcaco
οy	3601	CGGTGGAGAGGATCAATAACAATTAAGACTCTGTCCTTGGAAGCACCTGCCAGAATTA 3660
Ор	3601	GGTGGAGAGGATCAATAACACTCTGTCTTTGGAAGCACCTGCCAGAAT
ΟŊ	3661	TCCCCTGACTGGCCCCAGGAGGAGGAGGAGACCTT
qq	3661	AACAAGGCTCCCTCCCTGACTGGCCCCCAGGAGGGAGAGGTGACCTTTGAGAACGC
Qy	3721	GAAAACCTCCTTTGTCCTAAAGAAAGTATCCTTCACGATCAAAC 3
QQ	3721	ATGAGGTACCGAGAAAACCTCCCTCTTGTCTTAAGAAAGTATCCTTCACGATCAAAC
ΟŸ	3781	CTAAAGAGAAGATTGGCATTGTGGGGCGGACAGGATCAGGGAAGTCCTCGCTGGGGATGG 3840
qq	3781	TAAAGAGAATTGGCATTGTGGCGGCGGACAGGATCAGGGAAGTCCTCGCTGGGGATGG 3
Qy	3841	CCCTCTTCCGTCTGGAGTTATCTGGAGGCTGCATCAAGATTGATGGAGTGAATCA 3900
QQ	3841	CCTCTTCCGTCTGGTGGTGTTATCTGGGGCTGCTGAAGATTGATGGAGTGAGATCA 3
ΟŊ	3901	GTGATATTGGCCTTGCCGACCTCCGAAGCAACTCTCTATCATTCTCAGAGCCGGTGC 3960
qq	3901	SATATTGGCCTTGCCGACCTCCGAAGCAAACTCTCTATTCATTC

	DB 5161 TTCCTCCTCCATCAA Qy 5221 TTTCTGCCTTCTTTTTTTTTTTTTTTTTTTTTTTTTTT	5341 5341 5401 5401	5461 5461 5521 5521	5581 5581 5641 5641		2021 SULT 2 Z94745 AAZ94 AAZ94	DT 01-AUG-2000 (first ent) XX DE Human ATP binding casset XX XX ABCC5; ATP binding casset KW Atherosclerosis; lipid of KW lupus erythematosus; dis KW multidrug resistance as KW Dubin Johnson syndrome;
4020 4020 4080 4140		4320 4320 4380 4380	4440 4440 4500 4500	4560 4560 4620 4620	4680 4680 4740 4740 4800	4860 4860 4920	4920 4980 4980 5040 5040
3961 TGTTCAGTGGCACTGTCAGATCAAATTTGGACCCCTTCAACCAGTACACTGAAGACCAGA 11111111111111111111111111111	TICHATOTICAL AND		GTTCCCGATTCTATGCCATGTTTGCTGCAGAGAACAAGGTCGCTGTCAAGGGCTGAC	CCCCTCATCGCGTCCTCCTACCGAAACCTTGCTCGATTTTATCTTTGCACAGGA	ATTCCATATTCATGTAACAAATTTAGTTTTTGTTCTTAATTGCACTCTAAAAGGTTCA	TCTATATATATATCTGTACCTATACCTATATTACAGTGAAATGTAAGCTGTTTTTTTT	TTGCTGTACTAGAGATCTGGTTTTGCTATTAGACTGTAGGAAGGA
Oy 35 Db 399 Oy 400 Db 400	0y 4141 0b 4141 0y 4201		Oy 4381 Db 4381 Oy 4441 Db 4441	Oy 4501 Db 4501 Oy 4561 Db 4561	Oy 4621 Oy 4681 Ob 4681 Oy 4741		Db 4861 Qy 4921 Db 4921 Qy 4981 Db 4981
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         AGAATGGGGATCACAGAGACATTCCTCCGAGCCGGGGAGTTTC
                                                                                                                  TTTGCTGTTGTTTCTAAACAAGAATCAGTCTATCCACAGAGAG
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l disorder; dyslipidemia; psoriasis;
liagnosis; gene therapy; MRP5;
ssociated protein; chromosome 3q25-27;
y; hyperbilirubinemia; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ette ABCC5 (MRP5) cDNA.
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CRAPA134-63). These genes, and polypeptides encoded by them.

CRAPA134-63). These genes, and polypeptides encoded by them.

CRAPA134-63. These genes, and polypeptides encoded by them for a bubin and polypeptides chooses and and polyperic applications, and for call-based assays to screen for pharmacologically disorders, atherosclerosis or other inflammatory diseases such as poriasis and lupus erythematosus.
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                                                                                                                                                                                                                                       triphosphate binding proteins useful for identifying ng atherosclerosis and other inflammatory disorders
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100.0%; Pred. No. 0;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                     Claim 9; Page 123-125; 154pp; English
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Matches 5838; Conservative
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                             WO200018912-A2
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   Homo sapiens
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                                 CCCGTGTGGCCCCACAAGAAGGGGGAGCTCTCAATGGAAGACGTGTGTCTCTGTCCAAGC
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	1561 TAAAGAACCAACCAGTCCTCACATCAAGATAGAGATGAAAAATGCCACCTTGGCAT 1620 	1621 GGGACTCCTCCCACTCCAGTATCCAGAACTCGCCCAAGCTGACCCCCAAAATGAAAAAG 1680 	1681 ACAAGAGGCTTCCAGGGCAAGAAGAGAGAGGTGAGCTGCGCTGCAGCGCACTGAGCATC 1740 	1741 AGGCGGTGCTGGCAGAGCAGAAAGGCCACCTCCTCGACAGAGAGGGGCCCAGTC 1800 		1861 ACAGCATCGATCTGGAGATCCAAGAGGTAAACTGGTTGGAATCTGCGGCAGTGTGGGAA 1920 	1921 GTGGAAAACCTCTCTCATTTCAGCCATTTTAGGCCAGATGACGCTTCTAGAGGCAGCA 1980 	1981 TIGCAATCAGTGGAACCTTCGCTTATGTGGCCCAGCAGCCTGGATCCTCAATGCTACTC 2040 	2041 TGAGAGACAACATCCTGTTTGGGAAGGAATATGATGAAGAAAGA			2221 TGTATAGTGACAGGAGCATCTACATCCTGGACGCCCTCAGTGCCTTAGATGCCCATG 2280 	2281 TGGGCAACCACATCTTCAATAGTGCTATCCGGAAACATCTCAAGTCCAAGACATTCTGT 2340 	2341 TTGTTACCCACCAGTTACAGTACCTGGTTGACTGTGAAGTGATCTTCATGAAGAGG 2400 	2401 GCTGTATTACGGAAAGAGGCACCCATGAGGAACTGATGAATTTAAATGGTGACTATGCTA 2460 	2461 CCATTTTAATAACTGTTGGGAGAGACACCGCCAGTTGAGATCAATTCAAAAAGG 2520 	2521 AAACCAGTGGTTCACAGAAGAAGTCACAAGACAAGGGTCCTAAAACAGGATCAGTAAAGA 2580 	AGGAAAAAGCAGTAAAGCCAGAGGAAGGCAGCTTGTGCAGCTGGAAGAGAAAAGGGCAGG
qa	Qy Db	Qy	Qy Dp	Qy Db	qa . Kö	Oy Dp	oy Op	QY Db	Qy	o o	o O	oy Og	Qy	Oy Dp	Oy Dp	oy Op	Qy Db	, Oy

AAAGCAGTAAAGCCAGAGGAAGGGCAGCTTGTGCAGCTGGAAGAGAAAAGGGCAGG 2640 SGTGAGTGACAGCATGAAGGACAATCCTCATATGCAGTACTATGCCAGCATCTACG CTCCATGGCAGTCATGCTCAAACCCATTCGAGGAGTTGTCTTTGTCAAGG AAGGCTCCCTCCCCTGACTGGCCCCAGGAGGAGGAGGTGACCTTTGAGAACGCAG 3AGTTACTGGATCAAGCAAGGAAGCGGGAACACCACTGTGACTCGAGGGAACGAGA AAGTTTTTGACACGCCCCACAGGGAGGATTCTCAACAGGTTTTCCAAAGACA AGTGCCCTGGTCAGTATATGGTGTCTACATCCAGGCTGCTGGGGGCCCCTTGGCAT GITATTATGGCCCTTTTCATGCTGAATGTAGGCAGCACCGCCTTCAGCACCTGGT GAAGTTGACGTGCGGCTGCCGTTCCAGGCCGAGATGTTCATCCAGAACGTTATCC ITCTTCTGTGTGGGAATGATCGCAGGAGTCTTCCCGTGGTTCCTTGTGGCAGTGG CTTGCCACCATCCACGCCTACAATAAAGGGCAGGAGTTTCTGCACAGATACCAGG CTGGATGACAACCAAGCTCCTTTTTTTTTTTACGTGTGCGATGCGGTGGCTGG CGGCTGGACCTCATCAGCATCGCCCTCATCACCACCACGGGGCTGATGATCGTTC

Qy Db	3721	AGATGAGGTACCGAGAAAACCTCCCTCTTGTCCTAAAGAAAG	
Qy Db	3781	CTAAAGAGAAGATTGGCATTGTGGGGGGGGGACAGGATCAGGGAAGTCCTCGCTGGGGATGG 3840 	
Qy Dp	3841	CCCTCTTCCGTCTGGAGTTATCTGGAGGCTGCATCAAGATTGATGGAGTGAATCA 3900 	
Oy Db	3901	GIGATATIGGCCTTGCCGACCTCCGAAGCAAACTCTCTATCATCCTCAAGAGCCGGTGC 3960 	
Oy Dp	3961 3961	TGTTCAGTGGCACTGTCAGATCAAATTTGGACCCCTTCAACCAGTACACTGAAGACCAGA 4020 	
Oy Dp	4021	TTTGGGATGCCTGGAGAGGACACACATGAAAGAATGTATTGCTCAGCTACCTCTGAAAC 4080 	
Oy Dp	4081	TTGAATCTGAAGTGATGGAGAATGGGGATAACTTCTCAGTGGGGGAACGGCAGCTCTTGT 4140 	
Qy Dp	4141	GCATAGCTAGAGCCCTGCTCCGCCACTGTAAGATTCTGATTTTAGATGAAGCCACAGCTG 4200 	
Qy Dp	4201	CCATGGACACAGAGACTATTGATTCAAGAGACCATCCGAGAAGCATTTGCAGACT 4260 	
Qy Dp	4261	GTACCATGCTGACCATTGCCCATCGCTGCACACGGTTCTAGGCTCCGATAGGATTATGG 4320 	
Oy Op	4321	TGCTGGCCCAGGGACGTGGAGTTTGACACCCCATCGGTCCTTCTGTCCAACGACA 4380 	
oy Og	4381	GTTCCCGATTCTATGCCATGTTTGCTGCTGCAGAACAAGGTCGCTGTCAAGGGCTGAC 4440 	
Qy Dp	4441	TCCTCCCTGTTGACGAAGTCTCTTTCTTTAGAGCATTGCCATTCCCTGCCTG	
Qy Dp	4501	CCCTCATCGCGTCCTCCTACCGAAACCTTGCCTTTCTCGATTTATCTTTCGCACAGCA 4560 	
Qy Dp	4561	GTTCCGGATTGGCTTGTGTTTCACTTTTAGGGAGAGTCATATTTTGATTATTGTATT 4620 	
Oy Dp	4621	ATTCCATATTCATGTAAACAAAATTTAGTTTTTGTTCTTAATTGCACTCTAAAAGGTTCA 4680 	
Qy Dp	4681	GGGAACCGTTATTATAATTGTATCAGAGGCCTATAATGAAGCTTTATACGTGTAGCTATA 4740 	
Qy	4741	TCTATATATATTCTGTACATAGCCTATATTTACAGTGAAAATGTAAGCTGTTTATTTA	

QY	4801	TATTAAAATAAGGACTGTGCTAATAACAGTGCATATTCCTTTCTATCATTTTTGTACAGT 4860
Qy		ATCTGGTTTTGCTATTAGACTGTAGGAAGAGTAGCATTTCATTCTT 49:
δy		TAGCTGGTGGTTTCAGGTGCCAGGTTTTCTGGGTGTCCAAAGGAAGAACGTGTGGCA 498
qa	4921	498
Qy	œί	PCGACAGCCCCTCTGCGCCTCCCACAGCGCTCCAGGGGTGCTG 504
<u>අ</u>	86	AGTGGGCCCTCCGACAGCCCCCTCTGCCGCCTCCCACAGCCGCTCCAGGGGTGGCTG 504
Oy Dp	5041	######################################
δλ	5101	TGGTGTCACTTACTGTTTCTGTCAGGAGGAGGGGGGGGGG
qq	5101	STCCTGGTGTCTTACTGTTTCTGTCAGGAGAGCAGCGGGGGGGAGCCCAGGCCCACT 516
QY	16	CCTCCATCAAGAATGGGGATCACAGAGACATTCCTCCGAGCCGGGGAGTTTC 522(
qq	5161	ICACTCCCTCCATCAAGAATGGGGATCACAGAGACATTCCTCCGAGCCGGGGAGTTT
ò i	2 0	TCTTCTTTTGCTGTTGTTTCTAAACAAGAATCAGTCTATCCACAGAGAG 528
g G	5221	TTCCTGCCTTCTTTTTGCTGTTGTTTCTAAACAAGAATCAGTCTATCCACAGAGA
oy .	28	CAGGTTCCTATGGCTGGCGCTGCACAGAGCTCTCCAGCTCCAAGACCT 534
qq	~	CCACTGCCTCAGGTTCCTATGGCTGGCCACTGCACAGAGCTCTCCAGCTCCAAGACCT 534
δλ	34	TTCCAAGCCCTGGAGCCAACTGCTGCTTTTTGAGGTGGCACTTTTTCATTTGCCT 540
qa	5341	IGGTICCAAGCCCIGGAGCCAACIGCIGCTITITGAGGIGGCACTITITCAITIGCCI 5
δy	5401	ACACCTCCACAGTTCAGTGGCAGGGCTCAGGATTTCGTGGGTCT
g G	5401	ITCCCACACCTCCACAGTTCAGTGGCAGGGCTCAGGATTTCGTGGGTCTGTTTTCCTTT 546
ΟŊ	5461	CAGTCGTCGCACAGTCTCTCTCTCTCTCCCCTCAAAGTCTGCAACTTTAAG 5
qq		CACCGCAGTCGTCGCACAGTCTCTCTCTCTCTCCCCTCAAAGTCTGCAACTTTAAG 55
Qy	5521	TCTTGCTAATCAGTGTCTCACACTGGCGTAGAGTTTTTGTACTGTAAAGAGACCT 558
qq	5521	TITITITITITITITITITITITITITITITITITITI
Qγ	5581	CTCAGGTTGCTGGTGTGTGTGTGTGTGTGTGTGTCCCGCAAACCCCCTTTGTGTGTG
qq	5581	ACCTCAGGTTGCTGGTTGCTGTGTGTGTGTGTGTCCCGCAAACCCCCTTTGTGTGT 5640
Qy	5641	GGGCTGGTAGCTCAGGTGGGGGGGGGGCACTGTCATCAGCTGAATGGTC
qq	5641	
Qγ	5701	CAACTAGACATTCTGTCGCCTTAGCATGTTTGCTGAACACCTTGTGGAAG 5
qq	5701	STCGTGACCAACTTCTGTCGCCTTAGCATGTTTGCTGAACACCTTGTGGAAG
QY	5761	TGAAAATGTGAATAAAATTATTTTGGATTTTGTAAA
qq	5761	:CTGAAAATGTGAATAAAATTTTTGGATTTTTGTAAAAAAAA
δλ	5821	AAAAAAAAAAAAAAA 5838
qq	5821	AAAAAAAAAAAA 583

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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Model multidrug-resistance associated polypeptide useful for improving the effectiveness of a chemotherapeutic regimen to eradicate multidrug-resistant transformed cells especially cancer cells -
                                                                                                                      multidrug-resistance associated protein; human; cytostatic; ppy; cancer cell; drug discovery; cytotoxic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GAATTCTGATGTGAAACTAACAGTCTGTGAGCCCTGGAACCTCCACTCAGAAGATGAA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4847 BP; 1226 A; 1178 C; 1263 G; 1180 T; 0 other;
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Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                /product= "MRP-beta"
                                                                                                                                                                                       Location/Qualifiers
                ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 6; Fig 1A-D; 43pp; English
               AAA40481 standard; cDNA; 4847
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99.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                      2000-430613/37.
                                                                    (first
                                                                                             Human MRP-beta cDNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 4809; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAB10225
                                                                                                                                  chemotherapy;
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                                                                                                                       MRP-beta;
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        TGCCTCCATGCATTCTCAGCACTCAGAATCCTGGATGAGGAGCATCCCAAGGGAAAGTACCA
                                           ATCAGCTGTTTTTATCCTCTTTTACCCAGCAATGATGTTTGCATCACGGCTCACAGCATA
                                                                    TCATGGCTTGAGTGCTCTGAAGCCCCATCCGGACTACTTCCAAACACCAGCACCCAGTGGA
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of a multidurg-resistance phenotype in transformed mammalian cells, including carcinoma and adenocarcinoma cells. A unique fragment cee AAV65683) of the MRP-beta gene was identified by computer assisted searching of a nucleic acid database corresponding to a human endothelial cell (HUMVEC) expression library. It was used the search the HUMVEC expression library. This yielded a 4.78 kb clone, designated fohd013a05m (deposited as ATCC 98409). Two independent cDNA clones comprising approximately 60 residues upstream from fohd013a05m were isolated by hybridisation screening of human brain and librar cDNA libraries using a probe from the 5' end of fohd01305m. The presented sequence of MRP-beta cDNA comprises fohd01305m and 6e additional upstream nucleotides. The invention provides compositions and methods for improving the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This nucleotide sequence codes for novel human multidrug resistance associated protein (MRP-beta, see AAW80597), over-expression of which is thought to be associated with the emergence and/or persistence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated multidrug resistance-associated polypeptide - used to develop products for modulating multidrug resistance, particularly for reducing resistance of tumours to chemotherapeutic drugs
                                                                                                           TCATGTAAACAAAATTTAGTTTTTGTTCTTAATTGCACTCTAAAAGGTTCAGGGAACCGT
             cancer;
                                                                                                                                                                                                                                                                                                                                                                                   Multidrug resistance-associated protein; MRP-beta; human;
tumour; chemotherapy; therapy; ss.
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effectiveness of chemotherapeutic regimens to eradicate multidrug-resistant transformed cells from the body of a mammal, especially a human. The disclosed compositions include MRP-beta nucleic acids, including probes and antisense oligonucleotides (see also AaV65684-88), MRP-beta polypeptides and antibodies, MRP-beta expressing host cells, and non-human mammals that are transgenic or nullizygous for MRP-beta. The disclosed methods include methods for attenuating aberrant MRP-beta gene expression, protein production and/or protein function, and for improving the effectiveness of chemotherapy for a mammal afflicted with a multidrug-resistant tumour, wherein the tumour is of mammary, respitatory tract, urogenital tract, endocrine system or immune system orighn. In addition, methods are disclosed for identifying and using a modulator, such as an inhibitor, that is cytotoxic to cells expressing MRP-beta. 8 \$ 9 9 9 9 9 9 9 9 9 9 9 9 8 8

Sequence 4847 BP; 1225 A; 1179 C; 1263 G; 1180 T; 0 other;

Gaps Length 4847; Indels 19; 10; DB Score 4791; Di Pred. No. 0; 0; Mismatches . 0 82.1%; 99.8%; Conservative cal Similarity 4808; Conserv Match Local Best Loc Matches

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                                     AGCCCTGCTCCCCCACTGTAAGATTCTGATTTTAGATGAAGCCACAGCTGCCATGGACAC
                                                                                               GGGACAGGTGGAGGTTGACACCCCATCGGTCCTTCTGTCCAACGACAGTTCCCGATT
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                                                               AGAGACAGACTTATTGATTCAAGAGACCATCCGAGAAGCATTTGCAGACTGTACCATGCT
                                                                                        GACCATTGCCCATCGCCTGCACACGGTTCTAGGCTCCGATAGGATTATGGTGCTGGCCCA
                                                                                                                                                                      TCATGTAAACAAAATTTAGTTTTTGTTCTTAATTGCACTCTAAAAGGTTCAGGGAACCGT
                                                                                                                                                                                                                                                                          CTATGCCATGTTTGCTGCTGCAGAGACAAGGTCGCTGTCAAGGGCTGACTCCTCCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                Multidrug-resistance associated polypeptide-beta coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                   P-glycoprotein; chemotherapy; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                   AAGCACTGTGCTAAAAAA 4819
                                                                                                                                                                                                                                                                                                                             AAGCACTGTGCTAATAACA 4828
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This sequence encodes a multidrug resistance-associated polypeptide (MRP-beta). MRP-beta is a transporter that can remove chemotherapeutic agents from cells and/or sequester such agents, and it probably accounts for multidrug resistant phenotypes that do not respond to treatments with reversal agents directed against P-glycoprotein or the known MRP. By inactivating MRP-beta, at nucleic acid or protein levels, cells should be rendered sensitive to chemotherapy agents. The MRP-beta coding sequence, or fragments of it, can be used to detect expression of the MRP-beta gene and thus multidrug resistant cells. Fragments of MRP-beta DNA are useful as primers and as antisense (therapeutic) agents for inhibiting expression of the MRP-beta gene. They can also be used for detecting mutations and to treat diseases associated with abnormal MRP-beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 CATGCATTCTCAGCTCAGAATCCTGGATGAGGAGCATCCCAAGGGAAAGTACCATCATGG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel nucleic acid encoding multidrug resistance-associated protein MRP-beta, useful for detecting and treating drug-resistant cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene expression, specifically cancer, particularly for potentiating chemotherapy of fluid or inoperable tumors, or in cases of regrowth after an initial course of chemotherapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TGATGTGAAACTAACAGTCTGTGAGCCCTGGAACCTCCACTCAGAGAAGATGAAGGATAT
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99.7%; Pred. No. 0;
ive 6; Mismatches
/product= "MRP-beta"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Fig 1; 41pp; English.
                                                                                                                                                                                                                                                                                                                                         (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                           97US-0843459
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Matches 4737; Conservative
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P-PSDB; AAB47021.
                                                                                                                                                                                                       .6-APR-1997;
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1816 2116 2176 1996 1980 2100 2236 2296 2356 2416 2400 2536 2460 2596 2716 CTTCGCTTATGTGGCCCAGCAGGCCTGGATCCTCAATGCTACTCTGAGAGACAACATCCT CAAGCACATCCACCTGGGCCACCTGCGCTTACAGAGGACACTGCACAGCATCGATCTGGA CATITICAGCCATITITAGGCCAGATGACGCTTCTAGAGGGCAGCATTGCAATCAGTGGAAC ACAGTACCTGGTTGACTGTGATGAAGTGATCTTCATGAAAGAGGGCTGTATTACGGAAAG GATCCAAGAGGGTAAACTGGTTGGAATCTGCGGCAGTGTGGGAAGTGGAAAAACCTCTCT CCTGAGCGGTGGGCAGCGCCAGAGGATCAGCCTTGCCCGGGGCCTTGTATAGTGACAGGAG CATCTACATCCTGGACGACCCCCTCAGTGCCTTAGATGCCCATGTGGGGCAACCACATCTT GAAGAAGTCACAAGACAAGGGTCCTAAAACAGGATCAGTAAAGAAGGAAAAAAGCAGTAAA GCCAGAGGAAGGCCAGCTTGTGCAGCTGGAAGAGAAAGGGCAGGGTTCAGTGCCCTGGTC

GCATTCCTGGTTATTATGGC 2640 TGGTGGTTGAGTTATTATGGC 2776 TGGTGGTTGAGTTACTGGAT 2776 TGGTGGTTGAGTTACTGGAT 2700 GAGACCTCGGTGGTGACAG 2836 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	qa .
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CCTGGTTATTATGGC GGTTGGTTATTATGGC GTTGACTTATTATGGAT GTTGACTTACTGGAT GCTCGTGAGTGACGAGT [3660 3796 3720
AGTATATGATCTACATCCAGGCTGCTGGGGGCCCCTTG CCTTTTCATGCTGAATGTAGGCAGCACCGCTTCAGCACC [01 CCCTGACTGGCCCCAGGAGGAGGAGGTGACCTTTGAGAACGCAGAGATGAGGTACCGAGA 37 AAACCTCCTCTTTGTCCTAAAGAAGTATCCTTCACGATCAACCTAAAGAGAAGATTGG 111111111111111111111111
258	Db 360; Qy 373; Db 366;

Oy do	3797	œ r
3	7	NITOTOGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
δλ	82	GAGTTATCTGGAGGCTGCATCAAGATTGATGGAGTGAGAATCAGTGATATTGGCCTTGC 391.
අ	78	GAGTTATCTGGAGGCTGCATCAAGATTGATGGAGTGAGAATCAGTGATATTGGCCTTGC 384
Qy d	3917	97
2 ,	* (GACCITCGAAAGCACICICIAICAIICCICAAGAGCCGGIGCIGIICAGIGGCACIGI 390
ZO GO	3901	CAGATCAAATTIGGACCCCTICAACCAGTACACIGAAGACCAGATTIGGGAIGCCCTGGA 4036
δy	4037	AGGACACACATGAAAGAATGTATTGCTCAGCTACCTCTGAAACTTGAATCTGAAGTGAT 409
qq	3961	02
δ	4097	GAGAATGGGGATAACTTCTCAGTGGGGAACGGCAGCTCTTGTGCATAGCTAGAGCCCT 41
qa	4021	SGGGATAACTICTCAGTGGGGGAACGCCAGCTCTTGTGCATAGCTAGAGCCCT 408
QY	4157	GCTCCGCCACTGTAAGATTCTGATTTTAGATGAAGCCACAGCTGCCATGGACACAGAGAC 4216
q	4081	CTCCCCACTGTAAGATTCTGATTTTAGATGAAGCCACAGGCCATGGACACAGAGAC 414
Qy	4217	CCATGCTGACCAT 427
С	4141	GACTTATTGATTCAAGAGACCATCCGAGAAGCATTGCAGACTGGTACCATGCTGACGT 420
δλ	4277	GACA 4
QQ	4201	GCCCATCGCCTGCACACGCTTCTAGGCTTCCGATAGGATTATGGTGCTGGCCCAGGGACA 426
Οy	4337	6
qq	4261	GTGGTGGAGTTTGACACCCCATCGGTCCTTCTGTCCAACGACAGTTCCCGATTTTATG
ογ	4397	CATGITIGCICCTGCAGAACAAGGICGCTGICAAGGGCIGACTCCTCCCTGITGACGA 4456
qq	4321	ATGITIGCICCICCAGAGAACAAGGICGCIGICAAGGGCIGACICCICCCIGIIGACGA 43
ΟŊ	4457	AGTCTCTTTCTTTAGAGCATTGCCATTCCTGCCTGGGGGGGG
qq	4381	GTCTCTTTTCTTTAGAGCATTGCCMYKGMMTKCCTGGGGCGGGCCCCTTCATCGCGTCC 444
Qy	4516	TTATCTTCGCACAGCAGTTCCGGATTGGCTT 457
qa	4441	CCTACCGAAACCTTGCCGTTTCTCGATTTTATCTTTCGCACAGCAGTTCCGGATTGGCTT 4
οy	4576	TAGGGAGAGTCAT
qq	4501	STGTTTCACTTTTAGGGAGAGTCATATTTTGATTATTGATTTATTCATATTCATGT 456
Qy	4636	TTTTGTTCTTAATTGCACTCTAAAAGGTTCAGGGAACCGTTA
qq	4561	CAAAATTTAGTTTTGTTCTTAATTGCACTCTAAAAGGTTCAGGGAACCGTTATT
Qy	4696	TTTATACGTGTAGCTATATCTATATATATTA
QQ	4621	
δλ	4756	GTACATAGCCTATATTTACAGTGAAAATGTAAGCTGTTTATTTTATATTAAAATAAGCAC 4815
Q	4681	ACATAGCCTATATTTACAGTGAAAATGTAAGCTGTTTATTTTATATTAAAATAAGC
δλ	4816	TGTGCTAATAACA 4828
Q .	4741	GTGCTAAAA

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These substrates are anotherwise comparations and anotherwise substrates are also transported by a novel canalicular multispecific organic anion transporter (cMOAT) protein. The ATP dependent comon transporter (cMOAT) protein. The ATP dependent comon anion transporter system mediates heptacobiliary excretion in the liver. cMOAT may be a liver-specific homologue of multidrug resistance-associated protein. The nucleic acids are used to provide cells with cMOAT protein activity, cMOAT protein activity in cells can be enhanced by increasing the level of glutathione, glucuronide and/or sulphate. Antisense constructs, especially derived from another multidrug resistance (MDR)-related protein, e.g. MDR-1, to the nucleic acids and vectors can be used to decrease the level of cMOAT in a cell. The nucleic acids and proteins can be used especially in diagnosis of Dubin-Johnson disease, Rotor disease or another disease involving cMOAT. The cMOAT gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present cDNA sequence encodes a human multidrug resistance-associated protein 5 (MRP5). The MRP5 gene has been localised to chromosome 3. The MRP5 protein is a member of the ATP-binding cassette (ABC) transporter family of anorganic anion transporters. MRP5 is a 4 domain protein, with 2 APP-binding domains, and 2 domains with transmembrane regions. The protein is a homologue of MRP1, which is involved in ATP-dependent transport of glutathione conjugates such as dinitrophenyl glutathione.
                                                                                                                                                                     Canalicular multispecific organic anion transporter protein; cMOAT protein; ATP-binding cassette transporter family; ABC transporter; hepatoblilary excretion; multidrug resistance-associated protein; MRP5; cMOAT protein activity; multidrug resistance-related protein; MDR-1; Dubin-Johnson disease; Rotor disease; ss.
                                                                                                                               Human multidrug resistance-associated protein 5 (MRP5) cDNA sequence 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encoding human and rat canalicular multispecific organic anion asporter proteins – useful for diagnosis and treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33.2%; Score 1936.4; DB 18; Length 2167; 96.7%; Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dubin-Johnson disease and Rotor disease
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HET NEDERLANDS KANKER INST.
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CDNA; 2167
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AAT94055 standard;
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ACAGGATCAGGGAAGTCCTCGCTGGGGATGGCCCTCTTCCGTCTGGTGAGTTATCTGGA
                                                         GGCTGCATCAAGATTGATGGAGTGAGAATCAGTGATATTGGCCCTTGCCGACCTCCGAAGC
                                                                                                      AAACTCTCTATCATCCTCAAGAGCCGGTGCTGTTCAGTGGCACTGTCAGATTTG
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10;

14; Gaps

47; Indels

9; Mismatches

Conservative

Local Similarity

Matches 2069;

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protein 5 (MRP5) cDNA sequence 1.

Human multidrug resistance-associated

(first entry)

Canalicular multispecific organic anion transporter protein; CMOAT protein; ATP-binding cassette transporter family; ABC transport hepatobiliary excretion; multidrug resistance-associated protein; MRC cMOAT protein activity; multidrug resistance-related protein; MDR-1; Dubin-Johnson disease; Rotor disease; Ss.

97WO-NL00079.

21-FEB-1997;

28-AUG-1997

W09731111-A2

Homo sapiens

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The present cDNA sequence encodes a human multidrug resistance-associated protein 5 (MRP5). The MRP5 gene has been localised to chromosome 3. The MRP5 protein is a member of the ATP-binding cassette (ABC) transporter family of anorganic anion transporters. MRP5 is a 4 domain protein, with comparing the anorganic anion transporters. MRP5 is a 4 domain protein, with comparing the protein is a homologue of MRP1, which is involved in ATP-dependent transport of glutathione conjugates such as dinitrophenyl glutathione. These substrates are also transported by a novel canalicular transporter comparing transporter system mediates hepatobilizary excretion in dependent cMOAT transporter system mediates hepatobilizary excretion in the liver. CMOAT may be a liver-specific homologue of multidrug resistance-associated protein. The nucleic acids are used to provide cells with cMOAT protein activity. cMOAT protein activity in cells can be enhanced by increasing the level of glutathione, glucuronide and/or sulphate. Antisense constructs, especially derived from another multidrug vectors can be used to decrease the level of cMOAT in diagnosis of Dubin-Johnson disease, Rotor disease or another disease involving cMOAT. The cMOAT gene compared as a selectable marker gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1979 CATTGCAATCAGTGGAACCTTCGCTTATGTGGCCCAGCAGGCCTGGATCCTCAATGCTAC 2038
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Dubin-Johnson disease and Rotor disease
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AAT94054 RESULT

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Human; transporter.related protein; metabolite transporter; organic cation transporter; multi-drug reasistance; MDR; gene therapy; cellular transporter; sodium-glucose cotransporter; diagnosis; screening; symptomatic; phenotypic manifestation; biological condition; ss.
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The present sequence is a human transporter-related protein cDNA. The human transporter-related protein share structural similarity with mammalian metabolite or organic cation transporters, multi-drug resistance (MDR) proteins, mammalian sodium-glucose cotransporters and other cellular transporters. The transporter-related protein DNA may be used for the detection of mutant sequences or inappropriately expressed sequences for the diagnosis of disease. They may also be used to screen for drugs effective in the treatment of the symptomatic or phenotypic manifestations of perturbing the normal functions of the sequences of the invention in the body. They may also be used in gene therapy for treating biological conditions. Novel polynucleotides encoding novel human proteins with structural similarity to cellular transporters for the diagnosis of disease and Claim 4; Page 60-61; 91pp; English. WPI; 2001-514599/56. P-PSDB; AAE08075. in gene therapy

Sequence 4101 BP; 1046 A; 1023 C; 1048 G; 983 T; 1 other;

8 1080 840 009 099 307 367 720 780 547 900 607 727 787 Gaps ACCCAGTGGACAATGCTGGGCTTTTTTCCTGTATGACTTTTTCGTGGCTTTCTTCTTCTGG 480 TGTTGATGGACATCGTGGCCAACATCCTGTGCATCATCGTGGCAGCCATAGGGCCGACAG 427 428 TTCTCATTCACCAAATCCTCCAGCAGACTGAGAGGACCTCTGGGGAAGTCTGGGTTGGCA 487 AAGTTGGGCCAGACGCTGCTTCCCTGCGAAGGGTTGTGTGGATCTTCTGCCGCACCAGGC CCCGTGTGGCCCCACAAGAAGGGGGAGCTCTCAATGGAAGACGTGTGGTCTCTGTCCAAGC TGGTGAAAGGCTACCGGCAAAG - - - GCTGACCGTAGACACCCTGCCCCCATTGTCGACAT ACGAGICTICTGACGIGAACTGCAGAGACTAGAGAGACTGTGGCAAGAGAGCTGAATG 308 GGGTGGGTCCTGAGAAGGCCTCTCTGAGCCACGTGTGTGGAAATTCCAGAGGACACGCG TCATCCTGTCCATCGTGTGCCTGATGATCACGCAGCTGGCTTGAGTGGACCAGCCT TCATGGTGAAACACCTCTTGGAGTATACCCAGGCAACAGAGTCTAACCTGCAGTACAGCT TGTTGTTAGTGCTGGGCCTCCTCCTGACGGAAATCGTGCGGTCTTGGTCGCTTGCACTGA TTGGACTGTGCATAGCCCTTTTTGCCACCGAGTTTACCAAAGTCTTCTTTTGGGCCCTTG 841 CTTGGGCATTGAATTACCGAACCGGTGTCCGCTTGCGGGGGGCCCATCCTAACCATGGCAT CCTGGGCCATCAACTACCGCACGGCCATCCGGTTGAAGGTGGCGCTCTCCACCTTGGTTT 901 TTAAGAAGATCCTTAAGTTAAAGAACATTAAAGAGAAATCCCTGGGTGAGCTCATCAACA GAGGACCCGTTGTTGCCATCTTAGGCATGATTTATAATGTAATTATTCTGGGACCAACAG CCATCCCGATCCTAATGGTCTTTTGTGCGGCGTACGCCTTTTTCATTCTGGGGCCCACAG 1081 GCTTCCTGGGATCAGCTGTTTTTATCCTTTTTACCCAGCAATGATGTTTGCATCACGGC Length 4101; 129; Pred. No. 1e-213; 0; Mismatches 1707; Indels 15.9%; 'Score 925.8; DB 22; 54.0%; Pred. No. 1e-213; Best Local Similarity 54.0 Matches 2159; Conservative Query Match 421 131 481 368 781 1021 191 541 109 199 721 488 961 g ò g õ g ŏ g à δ Ω δ g ò g à 8 ò q ŏ g ò 셤 ò

1790

qq

1327 1147 AAGCCTCAGTGGCTGTTGACAGATTTAAGAGTTTGTTTCTAATGGAAGAGGTTCACATGA 1560 1681 ACAAGAGGCTTCCAGGGGCAAGAAGAAGGTGAGGCAGCTGCAGCGCCACTGAGCATC 1740 ACAGCATCGATCTGGAGATCCAAGAGGGTAAACTGGTTGGAATCTGCGGCAGTGTGGGGAA 1920 CCGAAGAGGAAGAAGCAAAGCACATCCACCTGGGCCACCTGCGCTTACAGAGGACACTGC 1860 GGG-----GGCAGGAGCCAGGAAAGTA 1354 ATGAAGTTCTTACTTACATTAAATTTATCAAAATGTATGCCTGGGTCAAAGGATTTTCTC CTCTCATCGGGATATCAGTGTATGTCATATTCATACCCGTCCAGATGTTTATGGCCAAGC ATGAGTTTCTGACCTGCATCAGGCTGATCAAAATGTATGCCTGGGAGAAATCTTTACCA CTGTTCATATGACCCTGGGCTTCGATCTGACAGCACCACGGCTTTCACAGTGGTGACAG TAAAGAACAAACCAGCCAGTCCTCACATCAAGATAGAGATGAAAAATGCCACCTTGGCAT GGGACTCCTCCCACTCCAGTATCCAGAACTCGCCCAAGCTGACCCCCAAAATGAAAAAĠ AGAGTGTTCAAAAAATCCGCGAGGAGGAGCGTCGGATATTGGAAAAAGCCGGGTACTTCC TCTTCAATTCCATGACTTTTGCTTTGAAAGTAACACCGTTTTCAGTAAAGTCCCTCTCAG ACATCACCCAACCAGAAGACCCAGATACTGTTTTGCTTTTAGCAAATGCCACCTTGACAT TCACAGCATATTTCAGGAGAAAATGCGTGGCCGCCACGGATGAACGTGTCCAGAAGATGA GTGGAAAAACCTCTCTCATTTCAGCCATTTTAGGCCAGATGACGCTTCTAGAGGGCAGCA TGAGAGAAAACATACTCTTTGGAGAAAGTATGATCACCAAAGGTATCAGCACACAGTCC AGGGTATCACTGTGGGTGTGGCTCCCATTGTGGTGATTGCCAGCGTGGTGACCTTCT CCCCAAAGAAATTGCAGAACCAGAAAAGGCATTTATGCAAGAAACAGAGGTCAGAG----1741 AGGCGGTGCTGGCAGAGGCAGAAAGGCCACCTCCTGGACAGTGACGAGCGGCCCAGTC ----TTCTGC TTGCAATCAGTGGAACCTTCGCTTATGTGGCCCCAGCCGGCCTGGATCCTCAATGCTACTC TGGCAGTCAATGGAACTTTGGCCTACGTTTCACAGCAGGCATGGATCTTTCATGGAAATG GAGAGCGAGGAGCCAACCTGAGCGGTGGGCAGCGCCAGAGGATCAGCCTTGCCCGGGCCT ACAGCTGCTGCCTGAGGCCTGACCTGGCCATTCTTCCCAGCAGCGACCTGACGGAGATTG GCCCAGAGGAGCAAGTGACAGCCTCAAATCGG-848 806 1381 788 896 1501 1208 1561 1268 1201 1261 1321 1148 1621 1328 1411 1801 1451 1861 1490 1921 1550 1610 2101 2161 1028 1981 Ω g δ QΩ δ g Dp Qγ οy d ò δ g δy ò qq g Db δy Ω qq Dp οy q Q Qγ δ ò à δy g Q ò ŏ δ

Page 20

Qy Dp	OY 2221 TGTATAGTGACAGGAGCATCTACATCCTGGACGACCCCCTCAGTGCCTTAGATGCCCAT	CCTTAGATGCCCATG 2280 	
Qy Db	QY 2281 TGGGCAACCACTTCAATAGTGCTATCCGGAAACATCTCAAGTCCAAGACAGTTCTGT	CCAAGACAGTTCTGT 2340 	
Qy Dp	OY 2341 TTGTTACCCACCAGTTACAGTACCTGGTTGACTGATGAAGTGATCTTCATGAAAGAGG	TCTTCATGAAAGAGG 2400 	
Oy Db	OY 2401 GCTGTATTACGGAAGAGGCACCCATGAGGAACTGATGAATTTAAATGGTGACTATGCTA 	ATGGTGACTATGCTA 2460 	
Qy	QY 2461 CCATTTTTAATAACCTGTTGCTGGGAGACACCGCCAGTTGAGATCAATTCAAAAAGG D 2090 AACTGATTCACAACTGCGAGGATTGCAGTTCAAGGATCCTGAACACCTTTACAATGCAG	TCAATTCAAAAAGG 2520 	
Qy Db	2521 AAACCAGTGGTTCACAGAAGAAGTCAC	-AAGACAAGGTCCTAAAACAGGAT 2571 	
Oy Dp	2572 CAGTAAAGAAGGAAAAGCAGTAAAGCCAGAGGAA	2606 AATTTGTAGACACAA 2269	
Oy Dp	QY 2607GGGCAGCTTGTGCAGCTGGAAGAGAAAAGGGCAGGGTTCAGTGCCCTGGT 	STTCAGTGCCCTGGT 2655 SAACCGTGACCTGGA 2329	
Qy Db	QY 2656 CAGTATATGGTGTCTACATCCAGGCTGCTGGGGCCCCTTGGCATTCCTGGTTATTATGG	rccrggrrarrargg 2715 crcrrcacrgrgr 2389	
\$ B	Oy 2716 CCCTTTTCATGCTGAATGTAGGCAGCACCGCCTTCAGCACCTGGTGGTTGAGTTACTGGA	3GTTGAGTTACTGGA 2775 3GCTGGGTCTCTGGT 2449	
oy Db	OY 2776 TCAAGCAAGGAAGACACCACTGTGACTCGAGGGAACGAGACCTCGGTGAGT 	CCTCGGTGAGTG 2832 	
o da	2833	ACGCCCTCTCCATGG 2892 	
O.Y	2893	AGGCACGCTGCGAG 2952 AGACCACTGATGG 2629	
QY Db	OY 2953 CTTCCTCCGGCTGCATGACGAGCTTTTCCGAAGGATCCTTCGAAGCCCTATGAAGTTTTTD	30000 3012 3012 3012 3011	
og Op	QY 3013 TIGACACGACCACAGGGGGGGTTCTCAACAGGTTTTCCAAAGACATGGATGAAGTTG 	ACATGGATGAAGTTG 3072 ATATGGACGAGCTGG 2749	
Qy Dp	<pre>Qy 3073 ACGTGCGGCTGCCGAGGCCGAGATGTTCATCCAGAAGGTTATCCTGGTGTTCTTCT</pre>	CCTGGTGTTCTTCT 3132 TATGGTGGTGTTA 2809	
Oy Ob	QY 3133 GTGTGGGAATGATCGCAGGAGTCTTCCCGTGGTTCCTTGTGGCAGTGGGGCCCCTTGTCA	regeccccrrerca 3192 	
Oy Dp	Oy 3193 TCCTCTTTTCAGTCCTGCACATTGTCTCCAGGGTCCTGATTCGGGACCTGAAGCGTCTGG	GCTGAAGCGTCTGG 3252 GCTCAAGAAGGTGG 2929	

3372 3552 3229 3672 3792 3912 3529 3972 3649 4092 3769 4272 CCCTGCTCCGCCACTGTAAGATTCTGATTTTAGATGAAGCCACAGCTGCCATGGACACAG 4212 3050 AAAACTCCAGTCACCTCTACTTAACTGTGCTCTCAGGTGGTTTGCGCTGAGAATGG ACCTCATCACCATCGCCCTCATCACCACGGGCTGATGATCGTTCTTATGCACGGGC 3613 TCAATCACTACATTAAGACTCTGTCCTTGGAAGCACCTGCCAGAATTAAGAACAAGGCTC 3290 TCAGGGAATACATTTCGACCTGTGTTCCTGAATGCACTCATCCCCTCAAAGTGGGGACCT 3733 GAGAAAACCTCCCTCTTGTCCTAAAGAAAGTATCCTTCACGATCAAACCTAAAGAGAAGA 3853 TGGTGGAGTTATCTGGAGGCTGCATCAAGATTGATGGAGTGAGAATCAGTGATATTGGCC CCATCCACGCCTACAATAAAGGGCAGGAGTTTCTGCACAGATACCAGGAGCTGCTGGATG 2990 TCATTCACGCCTATGGCAAGAAGGAGGCTGCATCACCTAGTTTAAGACGCTAAAACGACG 3110 ATGICCICATGAACATCCTTACCTTCACTGIGGCCTTGTTGGTGACCCTGAGTTTCTCCT 3493 AGATTCCCCCAGCCTATGCGGGTCTCGCCATCTTATGCTGTCCAGTTAACGGGGCTGT TCCAGTTACGGTCAGACTGGCATCTGAGACAGAAGCTCGATTCACCTCGGTGGAGGAGI 3913 TTGCCGACCTCCGAAGCAAACTCTCTATCATTCCTCAAGAGCCGGTGCTGTTCAGTGGCA 4033 TGGAGAGGACACACATGAAAGAATGTATTGCTCAGCTACCTCTGAAACTTGAATCTGAAG 3673 CCTCCCTGACTGGCCCCAGGAGGAGGTGACCTTTGAGAACGCAGAGATGAGGTACC 3793 TTGGCATTGTGGGGCGGACAGGATCAGGGAAGTCCTCGCTGGGGGATGGCCCTCTTCCGTC AGACAGACTTATTGATTCAAGAGCATCCGAGAAGCATTTGCAGACTGTACCATGCTGA 4333 GACAGGTGGTGGAGTTTGACACCCCATCGGTCCTT 4367 3313 (3433 3553 3770 4153 3830 4213 3890 4093 Dp g Qγ da QY QQ Oy Db δλ o do δy dd \dot{Q} Q δ qq g Db qq ρp qq Ω δ ŏλ ÓΥ Q_{Y} Ωÿ $\overset{\circ}{\partial}$ qq qq Ωÿ Qγ q Qγ δ CCCGTGTGGCCCACACAAGAAGGGGGAGCTCTCAATGGAAGACGTGTGGTCTCTGTCCAAGC 540

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Human; transporter-related protein; metabolite transporter; organic cation transporter; multi-drug resistance; MDR; gene therapy; cellular transporter; sodium-qlucose cotransporter; diagnosis; screening; symptomatic; phenotypic manifestation; biological condition; ss.
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/transl_except= (pos:3370..3372, aa:Xaa)
/note= "Xaa can be any amino acid"
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GGAAGGTGATTGACAAGCCTGAAGTCCTT 4044
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2000US-0182422.
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14-FEB-2000;
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                                                                                                                        TGGTGAAAGGCTACCGGCAAAG - - GCTGACCGTAGACACCCTGCCCCCATTGTCGACAT
                                    ACGAGTCTTCTGACGTGAACTGCAGAAGACTAGAGAGACTGTGGCAAGAAGAGCTGAATG
                                                                  248 ATGACTCATCTGACACCAATGCCAAAGATTTCGAGTCCTTTGGGATGAAGAGGTAGCAA
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421 ACCCAGTGGACAATGCTGGGCTTTTTTCCTGTATGACTTTTTCGTGGCTTTCTTCTGG 480

Pred. No. 6.3e-181; 0; Mismatches 1669; Indels

Matches 2104; Conservative

Similarity

Local

Query Match

13.5%; Score 790.6; DB 22;

2715 2775 2449 2835 2892 2569 2629 3012 2689 3072 2749 3132 3192 2869 3252 2929 3312 2989 3372 1990 TCATTCACGCCTATGGCAAGAAGAAGCTGCATCACTAGTTTAAGACGCTAAACGACG 3049 3432 3109 3169 3672 3229 3612 3289 3732 ACCTCATCAGCATCGCCCTCATCACCACGGGGCTGATGATCGTTCTTATGCACGGGC 3492 CAGTATATGGTGTCTACATCCAGGCTGCTGGGGGCCCCTTGGCATTCCTGGTTATTATGG 2690 TIGACACGACTCCCACTGGCAGGCTAATGAACCGTTTTTCCAAGGATATGGACGACGACGG 3133 GIGIGGGAATGATCGCAGGAGTCTTCCCGTGGTTCCTTGTGGCAGTGGGGCCCCTTGTCA 2930 AGAATGTCAGCCGGTCACCCTGGTTCACCCACATCACCTCCATGCAGGGCCTGGGCA CCCTTTTCATGCTGAATGTAGGCAGCACCGCCTTCAGCACCTGGTGGTTGAGTTACTGGA 2836 GCA---TGAAGGACAATCCTCATATGCAGTACTATGCCAGCATCTACGCCCTCTCCATGG 2510 GCGCGGTGCTGGCAGCATCGCTCAGCATGTGTACCAGTGGGTGTACACTGCAAGCATGG 2893 CAGTCATGCTGATCCTGAAAGCCATTCGAGGAGTTGTCTTTGTCAAGGGCACGCTGCGAG 2953 CTTCCTCCCGGCTGCATGACGAGCTTTTCCGAAGGATCCTTCGAAGCCCTATGAAGTTTT 3013 TTGACACGACCCCCACAGGGAGGATTCTCAACAGGTTTTCCAAAGACATGGATGAAGTTG 3073 ACGIGCGGCIGCCGTICCAGGCCGAGAIGITCAICCAGAACGITAICCIGGIGIICIICI 3193 TCCTCTTTTCAGTCCTGCACATTGTCTCCAGGGTCCTGATTCGGGAGCTGAAGCGTCTGG 3313 CCATCCACGCCTACAATAAAGGGCAGGAGTTTCTGCACAGATACCAGGAGCTGCTGGATG 3493 AGATICCCCCAGCCTATGCGGGTCTCGCCATCTCTTATGCTGTCCAGTTAACGGGGCTGT TCCAGTTTACGGTCAGACTGGCATCTGAGACAGAAGCTCGATTCACCTCGGTGGAGGGA CCTCCCCTGACTGGCCCCAGGAGGAGGGAGCTTTGAGAACGCAGAGATGAGGTACC 2870 TAGGCTICTICATICTGTTACGCATITTCCACAGAGGAGTCCAGGAGCTCAAGAAGGTGG 3253 ACAATATCACGCAGTCACCTTTCCTCTCCCACATCACGTCCAGCATACAGGGCCTTGCCA 3170 CCATCAGTACTTCATCCAAAGGCCTGTCATTGTCATACATCATCACCAGCTGAGCGGACTGC TCAATCACTACATTAAGACTCTGTCCTTGGAAGCACCTGCCAGAATTAAGAACAAGGCTC 2270 2716 2656 2330 3433 3553 3230 3613 3290 3673 ò a q Dp qq òγ ολ g δŽ ò g οy Óγ q δy qq QQ Db QQ qq δy Ω ò g ò οy δ Q δ g Ω g Qγ g ŏ

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/note= "the amino acid residues encoded by the above 3
codons are not indicated in the correponding
protein sequence"
3350 GTCCCAAGGACTGGCCCAGCYGTGGGGAGATCACCTTCAGAGACTATCAGATGAGATACA 3409
                 GAGAAAACCTCCTCTTGTCCTAAAGAAAGTATCCTTCACGATCAAACCTAAAGAGAAGA 3792
                                                                                                                                                                                                           -----TATAATGAAACTCCCAGAAAATTACAGGCAGAAG 3676
                                                                                                                                                                                                                                     CIGICAGAICAAAITIGGACCCCTTCAACCAGIACACTGAAGACCAGAITIGGGAIGCCC 4032
                                                                                                                                                                                                                                                             CCCTGCTCCGCCACTGTAAGATTCTGATTTTAGATGAAGCCACAGCTGCCATGGACACAG 4212
                                                                                                                                                                                                                                                                                               AGACAGACTTATTGATTCAAGAGCCATCCGAGAAGCATTTGCAGACTGTACCATGCTGA 4272
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                           TGGTGGAGTTATCTGGAGGCTGCATCAAGATTGATGGAGTGAGAATCAGTGATATTGGCC
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                                                    TTGGCATTGTGGGGCGGACAGGATCAGGGAAGTCCTCGCTGGGGGATGGCCCTCTTCCGTC
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                                                                                                                                                                                                                                                                                                                                                     Novel isolated human polynucleotide sequences encoding polypeptides that share sequence similarity with mammalian multidrug resistance proteins and cellular transporter proteins, useful as probe or primer
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Pred. No. 4.7e-175;
0; Mismatches 1901;
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31-OCT-2000; 2000WO-US29852.
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P-PSDB; AAB62555.
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Sands AT;
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GTCGCTTGCACTGGCGTTGGGCATTGAATTACCGAACCGGTGTCCGCTTGCGGGGGGCCAT	7 CCTAACCATGGCATTTAAGAAGATCCTTAAGTTAAAGAACATTAAAGAGAAATCCCTGGG 	7 IGAGCTCATCAACATITGCTCCAACGATGGGCAGAAATGTTTGAGGCAGCAGCAGCGTTGG	7 CAGCCTGCTGGAGGACCCGTTGTTGCCATCTTAGGCATGATTATAATGTAATTATA	7 TCTGGGACCAACAGGCTTCCTGGGATCAGCTGTTTTTATCCTCTTTTACCCAGCAATGAT	7 GTTTGCATCACGGCTCACAGCATATTTCAGGAAAAATGCGTGGCCGCCACGATGAACG	7 IGTCCAGAAGATGAAGTTCTTACTTACATTAATTTATCAAAATGTATGCCTGGGT 	7 CAAAGCATTTTCTCAGAGTGTTCAAAAATCCGCGAGGAGGAGGAGGGGCGTCGGATATTGGAAAA	7 AGCCGGGTACTTCCAGGGTATCACTGTGGGTGTGGGCTCCCATTGTGGGGGGGTGATTGCCAG	7 CGTGGTGACCTTCTCTGTTCATATGACCCTGGGCTTCGATCTGACAGCGGCCAGGCTTT	7 CACAGTGGTGACAGTCTTCAATTCCATGACTTTTGCTTTGAAAGTAACACCGTTTTCAGT	AAAGTCCCTCTCAGAAGCCTCAGTGGCTGTTGACAGATTTAAGAGTTTGTTT	* AGAGGTTCACATGATAAAGAAACCAGCCAGTCCTCACATCAAGATAGAGATGAAAAA 		'CAAAATGAAAAAAGACAAGAGGCTTCCAGGGGCAAGAAAGA		GCGCACT		7 CGAGGGCCCAGTCCCGAAGAGGAAGACACAAGACACATCCACCTGGGCCACCTGCGCGTTT	7 ACAGAGGACACTGCAGCATCGATCTGGAGATCCAAGAGGGTAAACTGGTTGGAATCTG
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1688 2206 2326 2386 2342 2686 2746 2462 CGGCAGTGTGGGAAGTGGAAAAACCTCTCATTTCAGCCATTTTAGGCCAGATGACGCT 1966 1809 CCTCCAGGGCTCCACTGCTGCTGCAATCGGGACCTGGAATTCTGCCCTTTGGAGA 1868 1928 2266 2222 2626 2402 CTTCAGCACCTGGTGGTTGAGTTACTGGATCAAGGAAGGGGAAGCGGGAACACCACTGTGAC 2806 2522 2506 2566 2282 2923 2642 2643 AGGGATTTTCACCAAGGTCACGAGGAAGGCATCCACGGCCCTGCACAACAACATCTTCAA 2702 2984 AAGGATCCTTCGAAGCCCTATGAAGTTTTTGACACGACCCCCACAGGGAGGATTCTCAA 3043 CCTGGCCGGCGCCGTCTATTCCGACCGTCAGATCTACCTGCTGGACCCCCTGTCTGC 2327 CAAGACAGTTCTGTTTGTTACCCACCAGTTACAGTACCTGGTTGACTGTGATGAAGTGAT 2583 CTACCAGCTGGTGTACGGGCTCAACGCCCTGCTCCTCTTGTGTGGGGGTCTGCTCCTC CAACTCTGTGCTGAACAGCTGCTGCCTGAGGCCTGACCTGGCCATTCTTCCCAGCAGCGA 2147 CCTGACGGAGATTGGAGAGCGAGGAGCCAACCTGAGCGGTGGGCAGCGCCAGAGGATCAG 2387 CTTCATGAAACAGGGTGTATTACGGAAAGACGCCACCCATGAGGAACTGATTTAAA 2507 CAATTCAAAAAAGGAAACCAGTGGTTCACAGAAGAAGTCACAAGACAAGGGTCCTAAAAC 2567 AGGATCAGTAAAGAAGGAAAAAAGCAGTAAAGCCAGAGGAAGGGCAGCTTGTGCAGCTGGA 2627 AGAGAAAGGGCAGGGTTCAGTGCCCTGGTCAGTATAGGTGTCTACATCCAGGCTGCTGG GGGCCCCTTGGCATTCCTGGTTATTATGGCCCCTTTTCATGCTGAATGTAGGCAGCACCGC CTATGCCAGCATCTACGCCCTCTCCATGGCAGTCATGCTGATCCTGAAAGCCATTCGAGG AGTIGICITIGICAAGGGCAĞGIGCGAGCITCCICCCGGCIGCAIGACGAGCITITICG CCTTGCCCGGGCCTTGTATAGTGACAGGAGCATCTACATCCTGGACGACCCCCTCAGTGC 2447 IGGIGACTAIGCTACCATITITAATAACCIGIIGCIGGGAGAGACACCGCCAGIIGAGAI 2463 2027 2087 2207 1929 2687 2747 2807 2523 2864 g g δ Pp δy QQ Qγ qq ò g qq qq pp qq qq qq В g ò ŏ δy Qγ δ δy οy $^{\circ}$ δy Q g Dp g ò à Qγ

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similarity to cellular
use in gene therapy -
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P-PSDB; AAE08076.
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                                                                                                                     present sequence is a human transporter-related protein cDNA. human transporter-related protein share structural similarity with
                                                                                                                                                                                                                                                                                                                                                                                                               Human; transporter-related protein; metabolite transporter; organic cation transporter; multi-drug resistance; MDR; gene therapy; cellular transporter; sodium-glucose cotransporter; diagnosis; screen: symptomatic; phenotypic manifestation; biological condition; ss.
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                CGATGAAGCCACAGCCTCCATTGACATGGAGACAGCACCCTGATCCAGCGCACAATCCG
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/transl_except= (pos:3025.3039, aa:Thr-Thr)
/transl_except= (pos:3370, .3372, aa:Xaa)
/note= "Xaa can be any amino acid"
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CC mammalian metabolite or organic cation transporters, multi-drug
Cresistance (MDR) proteins, mammalian sodium-glucose cotransporters and
Cother cellular transporters. The transporter-related protein DNA may be
CC used for the detection of mutant sequences or inappropriately expressed
CC sequences for the diagnosis of disease. They may also be used to screen
CC for drugs effective in the treatment of the symptomatic or phenotypic
C manifestations of perturbing the normal functions of the sequences of the
CC invention in the body. They may also be used in gene therapy for treating
XX Sequence 3660 BP: 920 A: 915 C: 943 G: 881 T: 1 other.

8; 1140 1020 1080 ATGAAGTTCTTACTTACATTTATCAAAATGTATGCCTGGGTCAAAGCATTTTCTC 1260 TCACAGCATATTTCAGGAGAAAATGCGTGGCCGCCACGGATGAACGTGTCCAGAAGATGA 1200 480 540 009 307 999 367 720 427 780 487 840 547 900 960 299 787 Gaps ACCCAGTGGACAATGCTGGGCTTTTTTCCTGTATGACTTTTTCGTGGCTTTCTTCTGG TGGTGAAAGGCTACCGGCAAAG---GCTGACCGTAGACACCCTGCCCCATTGTCGACAT GGGTGGGTCCTGAGAGGCCTCTCTGAGCCACGTGGTGGGAAATTCCAGAGGACACGCG CTTGGGCATTGAATTACCGAACCGGTGCCGCTTGCGGGGGCCATCCTAACCATGGCAT GAGGACCCGTTGTTGCCATCTTAGGCATGATTTATAATGTAATTATTATTCTGGGACCAACAG CCCGTGTGCCCCACAAGAAGGGGGAGCTCTCAATGGAAGACGTGTGGTCTCTGTCCAAGC AAGTTGGGCCAGACGCTGCTTCCCTGCGAAGGGTTGTGTGGGATCTTCTGCCGCACCAGGC TCATCCTGTCCATCGTGTGCTGATGATCACGCAGCTGGCTTCAGTGGACCAGCCT TGTTGATGGACATCGTGGCCAACATCCTGTGCATCATCATGGCAGCCATAGGCCCGACAG TCATGGTGAAACACCTCTTGGAGTATACCCAGGCAACAGAGTCTAACCTGCAGTACAGCT TGTTGTTAGTGCTGGGCCTCCTCCTGACGGAAATCGTGCGGTCTTGGTCGCTTGCACTGA TTGGACTGTGCATAGCCCTTTTTGCCACCGAGTTTACCAAAGTCTTCTTTTGGGCCCTTG CCATCCCGATCCTAATGGTCTTTTGTGCGGCGTACGCCTTTTTCATTCTGGGGCCCACAG GCTTCCTGGGATCAGCTGTTTTTATCCTCTTTTACCCAGCAATGATGTTTGCATCACGGC CTCTCATCGGGATATCAGTGTATGTCATACCGTCCGTCCAGATGTTTATGGCCAAGC **ACGAGTCTTCTGACGTGAACTGCAGAAGACTAGAGAGACTGTGGCAAGAAGAGCTGAATG** ATGACTCATCTGACACCCAATGCCAAAAGATTTCGAGTCCTTTGGGATGAAGAGGTAGCAA TTCTCATTCACCAAATCCTCCAGCAGACTGAGAGGACCTCTGGGAAAGTCTGGGTTGGCA CCTGGGCCATCAACTACCGCACGGCCATCCGGTTGAAGGTGGCGCTCTCCACCTTGGTTT TTAAGAAGATCCTTAAGTTAAAGAACATTAAAGAGAAAATCCCTGGGTGAGCTCATCAACA Score 759.4; DB 22; Length 3660; Pred. No. 2.2e-173; 0; Mismatches 1571; Indels 129; Sequence 3660 BP; 920 A; 915 C; 943 G; 881 T; 1 other; 13.0%; 52.9%; Best Local Similarity 52.9 Matches 1911; Conservative Query Match 131 191 421 481 248 1021 1081 541 308 488 899 1141 1201 601 199 368 721 428 781 548 901 809 961 788 848 g ά q g 셤 οg qq ò ò õ ò g ò ò ò g ò g ò οy g ŏ qq δ g δ g

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1440 1620 1410 1450 1860 2040 1560 1680 1354 1489 1669 2100 2220 2280 2400 TGGGGAAGCACGTCTTTGAGGAGTGCATTAAGAAGACGCTCAGGGGAAAGACAGTCGTCC 1969 CTGTTCATATGACCCTGGGCTTCGATCTGACAGCACCACAGGCTTTCACAGTGGTGACAG GGGACTCCTCCCACTCCAGTATCCAGAACTCGCCCAAGCTGACCCCCAAAATGAAAAAG AGGGTATCACTGTGGGTGTGGCTCCCATTGTGGTGGTGATTGCCAGCGTGGTGACCTTCT ccreccacarcercargacecaaacreacecaccergecarrragrergarrecea 1441 TCTTCAATTCCATGACTTTTGCTTTGAAAGTAACACCGTTTTCAGTAAAGTCCCTCTCAG AAGCCTCAGTGGCTGTTGACAGATTTAAGAGTTTGTTTCTAATGGAAGAGGTTCACATGA ACAAGAGGCCTTCCAGGGCCAAGAAGAAGAAGGTGAGGCAGCTGCAGCGCCACTGAGCATC CCCCAAAGAAATTGCAGAACAGAAAAGGCATTTATGCAAGAAACAGAGGTCAGAG----AGGCGGTGCTGGCAGAGGCAAAAGGCCACCTCCTCGAACAGTGACGAGCGGCCCAGTC AAGCGAATGTCTCTAAGGAGAATGAAGAAAATTCTCATAGATAAAAGCCCCCCATCTT ACATCACCCAACCAGAAGACCCAGATACTGTCTTGCTTTTAGCAAATGCCACCTTGACAT CCGAAGAGGAAGGCAAGCACATCCACCTGGGCCACCTGCGCTTACAGAGGACACTGC TIGITACCCACCAGTACAGTACCTGGTGACTGTGATGAAGTGATCTTCATGAAAGAGG GCCCAGAGGAGCAAAGTGACAGCCTCAAATCGG---------TTCTGC **ACAGCATCGATCTGGAGATCCAAGAGGGTAAAACTGGTTGGAATCTGCGGCAGTGTGGGAA** GTGGAAAAACCTCTCTCATTTCAGCCATTTTAGGCCAGATGACGCTTCTAGAGGGCAGCA ACAGCTGCTGCCTGAGGCCTGACCTGGCCATTCTTCCCAGCAGCGACCTGACGGAGATTG GAGAGCGAGGCCAACCTGAGCGGTGGGCAGCGCCAGAGGATCAGCCTTGCCCGGGCCT TGGGCAACCACATCTTCAATAGTGCTATCCGGAAACATCTCAAGTCCAAGACAGTTCTGT TAAAGAACAAACCAGCCAGTCCTCACATCAAGATAGAGATGAAAAATGCCACCTTGGCAT 999 1208 1561 1321 1381 1501 1268 1621 1681 1355 1741 1451 1490 2041 1850 1328 1411 1801 1861 1921 1550 1981 1610 1670 2101 1730 1790 2281 2161 2221 1910 2341 g δ g qq g qq q ò à ò Qγ δŽ Q g οy Dp φ Ω δý Ωp δy Ω Qγ a οy qq δy g δ qq δλ q ò g δ

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ACCTCATCAGCATCGCCCTCATCACCACCACGGGGCTGATGATCGTTCTTATGCACGGGC 3492
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                          3110 ATGTCCTCATGAACATCCTTACCTTCACTGTGGCCTTGTTGGTGACCTTGTTCTCCT
                                                                                                                                CCATCAGTACTTCATCCAAAGGCCTGTCATTGTCATACATCCAGCTGAGCGGACTGC
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CAGTAAGATAA 3660
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KX XX XX Krasnow RE, Baughn MR;
XX WPI: 2002-394129/42.
DR P-PSDB; AAE22722.
XX Mammalian adenosine triphosphate-bi CDNA, useful for diagnosis and tree broast proliferative fibrocystic diax XX The invention relates to adenosine CC Sequences of the invention are useful breast adenocarcinoma and drug resi breast adenocarcinoma and drug resi breast adenocarcinoma and drug resi companion are useful are model systems for human breast companion are useful breast companion are useful are model systems for human breast therapy. ABCP sequences are useful B-lymphocyte immunosplobulin library CC specificity. They are also useful are breasent sequence is a cDNA encompanion.

Mammalian adenosine triphosphate-binding cassette protein, and encoding cDNA, useful for diagnosis and treatment of breast disorders, e.g. breast proliferative fibrocystic disease and breast adenocarcinoma - Claim 2; Fig 1; 80pp; English.

The invention relates to adenosine triphosphate (ATP)-binding cassette (ABC) proteins (ABCP) and nucleic acid molecules encoding such proteins

The invention relates to adenosine triphosphate (ATP)-binding cassette (ABC) proteins (ABC) proteins (ABC) proteins (ABC) proteins and uncleic acid molecules encoding such proteins. Sequences of the invention are useful for the diagnosis and treatment of breast disorders, particularly breast proliferative fibrocystic disease, breast adenocarcinoma and drug resistance. Polynucleotides of the invention are used to produce transgenic cell lines or organisms which are model systems for human breast disorders. They are also used in gene therapy. ABCP sequences are useful in screening assays of phagemid or brymphocyte immunoglobulin library to identify antibodies having desired specificity. They are also useful as chemoprotectants and as vaccines. The present sequence is a CDNA encoding human ABC protein.

Sequence 4074 BP; 961 A; 1050 C; 1080 G; 983 T; 0 other;

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421 ACCCAGTGGACAATGCTGGCCTTTTTTCCTGTATGACTTTTTCGTGGCTTTCTTCTTGG 480 CCCGTGTGGCCCACAAGAAGGGGGAGCTCTCAATGGAAGA-CGTGTGGTCTCTGTCCAAG 539 213 273 629 453 839 AGGCGAGGGATTGAAAAAGCTTCAGTGCTTCTGGTGATGCTGAGGTTCCAGAGAACAAGG 333 CTCATCCTGTCCATCGTGTGCTGATGATCACGCAGCTGGCTTGGCTTCAGTGGACCAGCC 719 334 TIGATITICGATGCACTICTGGGCATCTGCTTCTGCATTGCCAGTGTACTCGGGCCCAATA 393 779 ACTIGGGCAITGAATTACCGAACCGGTGTCCGCTTGCGGGGGGCCATCCTAACCATGGCA 899 Gaps GAAGTTGGGCCAGACGCTGCTTCCCTGCGAAGGGTTGTGTGGATCTTCTGCCGCACCAGG 98 ATCCCTGGACAATGCTGGCCTGTTCTCCTACCTCACGTGTCATGGCTCAC----CCCG CACGAGTCTTCTGACGTGAACTGCAGAAGACTAGAGAGACTGTGGCAAGAAGAGCTGAAT TTCATGGTGAAACACCTCTTGGAGTATACCCAGGCAACAGAGTCTAACCTGCAGTACAGC TTGATTATACCAAAGATCCTGGAATATTCAGAAGAGCAGTTGGGGAATGTTGTCCATGGA TTGTTGTTAGTGCTGGGCCTCCTCGTGACGGAAATCGTGCGGTCTTGGTCGCTTGCACTG GIGGGACTCTGCTTTGCCCTTTTTCTCTCCGAATGTGTGAAGTCTCTGAGTTTCTCCTCC ATTTGCTCCAACGATGGGCAGAATGTTTGAGGCAGCAGCCGTTGGCAGCCTGCTGGCT GGAGGACCCGTTGTTGCCATCTTAGGCATGATTTATAATGTAATTATTCTGGGACCAACA AGTIGGATCATCAACCAACGCACAGCCATCAGGTICCGAGCAGCTGTTTCCTCCTTTGCC TTTAAGAAGATCCTTAAGTTAAAGAACATTAAAGAGAAAATCCCTGGGTGAGCTCATCAAC 634 INCINCACCGGTGATGTAAACTACCTGTTTGAAGGGGTGTGCTATGGACCCCTAGTACTG DB 24; Length 4074; 119; Query Match
13.0%; Score 757.8; DB 24; Length
Best Local Similarity 51.0%; Pred. No. 5.7e-173;
Matches 2039; Conservative 0; Mismatches 1837; Indels 274 481 154 540 009 099 720 394 780 454 840 514 900 574 096 g g ģ ò ò g δ g g οy δŽ β ά g g Q õ ò ò g ò

694 ATCACCTGCGCATCGCTGGTCATCTGCAGTTTCTTCCTACTTCATTATTGGATACACT 753

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1259 1319 GGCTTCCTGGGATCAGCTGTTTTATCCTCTTTTACCCAGCAATGATGTTTGCATCACGG 1139 1499 1488 GAAGCCTCAGTGGCTGTTGACAGTTTTAAGAGTTTGTTTCTAATGGAAGAGGTTCACATG 1559 1799 1383 CACAGCATCGATCTGGAGATCCAAGAGGGTAAACTGGTTGGAATCTGCGGCAGTGTGGGA 1919 1548 CACTGCTGCTCCCTGAATCGGGACCTGGAACTTCTGCCCTTTGGAGACATGACAGAGATT 1728 994 CAGAGCCIGACAAGTATAACCTIGITCAICAICCCCACAGIGGCCACAGGGGITT 1054 CTCATCCACACCTTAAAGCTGAAACTCGCAGCGTCAATGGCCTTCAGCATGCTGGCC CTCACAGCATATTTCAGGAGAAAATGCGTGGCCGCCACGGATGAACGTGTCCAGAAGATG 1200 AATGAAGTICTTACTTACATTAAATTTATCAAAATGTAIGCCTGGGTCAAAGCAITTTCT 1260 CAGAGTGTTCAAAAATCCGCGGGGGGGGGGGTCGGATATTGGAAAAAGCCGGGTACTTC 1320 CAGGGTATCACTGTGGGTGTGGCTCCCATTGTGGTGGTGATTGCCAGCGTGGTGACCTTC 1440 GICTTCAATTCCATGACTTTTGCTTTGAAAGTAACACCGTTTTCAGTAAAGTCCCTCTCA 1114 TCCTTGAATCTCCTTCGGCTGTCAGTGTTCTTTGTGCCTATTGCAGTCCAAAGGTCCCACG 814 ATGGTTGTGAAGGCTCAGCATCACACATCTGAGGTCAGCGACCAGCGCATCCGTGTGACC 934 AAAATCATIGAAGACCTAAGAAGGAAAGGAAACTATIGGAGAAGIGCGGGCTIGTC 1174 AATTCTAAGTCTGATGAGGGTTCAAGAAGTTTTTCCTCCAGGAGCCCTGTTTTC 1380 TCTGTTCATATGACCCTGGGCTTCGATCTGACAGCAGCACAGGCTTTCACAGTGGTGACA ATAAAGAACAAACCAGCCAGCCTCACATCAAGATAGAGATGAAAAATGCCACCTTGGCA 1740 CAGGGGGTGCTGGCAGAGAGAAGGCCACCTCCTCGACAGTGACGAGGGGGCCCAGT CACAAGATCAACCTGGTGGTGTCCAAGGGGATGATAAGGGGTCTGCGGCAACACGGGG AGTGGTAAGAGCAGCCTGTTGTCAGCCATCCTGGAGGAGATGCACTTGCTCGAGGGCTCG 1234 TATGICCAGACATTACAAGACCCCAGCAAAGCTCTGGTCTTTGAGGAGGCCACCTTGTCA 1680 GACAAGAGGGCTTCCAGGGGCAAGAAGAAGGTGAGGCAGCTGCAGCGCACTGAGCAT **AGTGGAAAAACCTCTCTCATTTCAGCCATTTTAGGCCCAGATGACGCTTCTAGAGGGCAGC** 1324 GGGCACTGGAGCTGGAGGAACGGCCATGCTTCTGAGGGGATGACCAGGCCTAGAGAT CCCGAAGAGGAAGGCAAGCACATCCACCTGGGCCACCTGCGCTTACAGAGGACACTG ATTGCAATCAGTGGAACCTTCGCTTATGTGGCCCAGCAGGCCTGGATCCTCAATGCTACT AACAGCTGCTGCCTGAGGCCTGACCTGGCCATTCTTCCCAGCAGCGACCTGACGGAGATT 1294 TGGCAACAGACCTGTCCCGGGATC---1560 1500 1620 1318 1800 1429 1920 1489 1980 1549 2040 2100 1860 g δλ g g g δ ŏλ 임 δy οy Q Óγ g Qγ g ά QQ φ Q Qγ g δ q ó Op δy g ŏ qq op Qγ ŏλ qq δ g

GGAGAGCGAGCAACCTGAGCGGTGGGCAGCGCCAGGGATCAGCCTTGCCCGGGCC
TITGITACCCACCAGITACAGTACCIGGITGACIGAIGAAGIGAICITCAIGAAAGAG
GGCTGTATTACGGAAGAGGCACCCATGAGGAACTGATGATTTAAATGGFGACTATGCT
accatttttaataacctgttgctgggagagacaccgccagttgagatcaattcaaaaag
GAAACCAGTGGTTCACAGAAGACAAGACAAGGGTCCTAAAACAGGATCAGTAAAG
AAGGAAAAAAGCAGTAAAAGCCAGAGGAAGGCAGCTTGTGCAGCTGGAAGAGAAAGGGCAG
GGTTCAGTGCCTGGTCAGTATATGGTGTCTACATCCAGGCTGCTGGGGGCCCCTTGGCA
TTCTGGTATATTATGGCCTTTTCATGCTGAATGTAGGCAGCACCGCCTTCAGCACCGGG 1
GGTTGAGTTACTGGATCAAGCAAGGAAGCGGAACACCACTGTGACTCGAGGGAACGAG
ACCTCGGTGAGTGACAGCATGAAGGACAATCCTCATATGCAGTACTATGCCAGCATC
TACGCCCTCTCCATGCCAGTCATGCTGATACGAAAGCCATTCGAGGAGTTGTCTTTGTC
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GACATGGATGAAGTTGACGTGCGGTCCAGGCCGAGATGTTCATCCAGAACGTT
ATCCTGGTGTTCTTCTGTGTGGGAATGATCGCAGGGTCTTCCCGTGGTTCCTTGTGGCA
GTGGGCCCCTTGTCATCTTTTCAGTCCTGCACATTGTCTCCAGGGTCCTGATTCGG
GAGCTGAAGCGTCTGGACAATATCACGCAGTCACCTTTCCTCTCCCACATCACGTCCAGC

3416 2982 3716 3776 3342 3162 3836 4016 4136 3102 3596 3402 3462 3956 4196 3762 4256 4316 2803 GTGTTCAAGAGACTGGAGAACTATAAGCCGGTCTCCTTTATTCTCCCACATCCTCAATTCT 2862 ATACAGGGCCTTGCCACCATCCACGCCTACAATAAAGGGCAGGAGTTTCTGCACAGATAC 3356 GTTCTTATGCACGGCAGATTCCCCCCAGCCTATGCGGGTCTCGCCATCTCTTATGCTGTC 3536 ACCTCGGTGGAGGATCAATCACTACATTAAGACTCTGGTCCTTGGAAGCACCTGCCAGA 3656 ATGGCCCTCTTCCGTCTGGTGGAGTTATCTGGAGGCTGCATCAAGATTGATGGAGTGAGA 3896 CAGATITIGGGATGCCCTGGAGGACACACATGAAAGAATGTATTGCTCAGCTACCTCTG 4076 ATGGTGCTGGCCCAGGGACAGGTGGAGTTTGACACCCCATCGGTCCTTCTGTCCAAC 4376 CAGTTAACGGGGGCTGTTCCAGTTTACGGTCAGACTGGCATCTGAGACCAGAAGCTCGATTC GTGCTGTTCAGTGGCACTGTCAGATCAAATTTGGACCCCTTCAACCAGTACACTGAAGAC AAACCTAAAAGAGAAGATTGGCCATTGTGGGGCGGACAGGATCAGGGAAGTCCTCGCTGGGG CGCGGCCACGAAGTGGTGGGCATCGTGGGAAGGACGGCTCTGGGAAGTCCTCCTTGGGC ATCAGTGATATTGGCCTTGCCGACCTCCGAAGCAAACTCTCTATCATTCCTCAAGAGCCG AAACTTGAATCTGAAGTGATGGAGAATGGGGATAACTTCTCAGTGGGGGAACGGCAGCTC TIGIGCATAGCTAGAGCCCTGCTCCGCCACTGTAAGATTCTGATTTTAGATGAAGCCACA GCTGCCATGGACACAGACATTATTGATTCAAGAGACCATCCGAGAAGCATTTGCA GACTGTACCATGCTGACCATTGCCCATCGCCTGCACACGGTTCTAGGCTCCGATAGGATT 3717 3297 3357 2923 3417 2983 3163 3657 3223 3777 3343 3837 3403 3463 3523 3583 4137 4257 4317 3477 3537 3597 3897 3957 4017 4077 3643 4197 3763 3823 Qy Db οy Db Qγ QQ ογ Dp Ω g Ωy qq Q g Qγ Oy Ob QΫ́ QQ S S QY Db QΥ q οy g δy g Qγ qq δ Ωp ò

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                                                                                                                                                                                                                                                                                                                       Human; transporter-related protein; metabolite transporter; organic cation transporter; multi-drug resistance; MDR; gene therapy; cellular transporter; sodium-glucose cotransporter; diagnosis; screening; symptomatic; phenotypic manifestation; biological condition; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       used for the detection of mutant sequences or inappropriately expressed sequences for the diagnosis of disease. They may also be used to screen for drugs effective in the treatment of the symptomatic or phenotypic manifestations of perturbing the normal functions of the sequences of the invention in the body. They may also be used in gene therapy for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         other cellular transporters. The transporter-related protein DNA may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The human transporter-related protein share structural similarity with mammalian metabolite or organic cation transporters, multi-drug resistance (MDR) proteins, mammalian sodium-glucose cotransporters and
3883 CTGGTTATGGGCAATGGGAAGGTGGTAGAATTTGATCGGCCGGAGGTACTGCCGGAAGAAG 3942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel polynucleotides encoding novel human proteins with structural similarity to cellular transporters for the diagnosis of disease and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zambrowicz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is a human transporter-related protein cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product "Human transporter-related protein"
/transl_except= (pos:3025.3039, aa:Thr-Thr)
/transl_except= (pos:3370..3372, aa:Xaa)
/note "Xaa can be any amino acid"
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                                                                        3943 CCTGGGTCATTGTTCGCAGCCCTCATGGCCACAGC 3977
                                                                                                                                                                                                                                                                                   Human transporter-related protein #24 cDNA.
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                                   4377 GACAGTICCCGATICTATGCCATGTTTGCTGCTGC
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14-FEB-2000; 2000US-0182422.
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P-PSDB; AAE08077.
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                                        131 ACCCGGTGGATGATGCCGGGCTACTCTCCTTCGCCACATTTTCCTGGCTCACGCCGGTGA
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	1561 TAAAGAACAAACCAGCCAGTCCTCACATCAAGATGAGATGAAAATGCCACCTTGGCAT 	1621 GGGACTCCTCCCACTCCAGTATCCAGAACTCGCCCAAGCTGACCCCCAAAATGAAAAAG 	1681 ACAAGAGGGTTCCAGGGGCAAGAAAGAAGGAGGTGAGGCAGCTGCAGCGCACTGAGCATC	1741 AGGCGGTGCTGCCAGAACAAAGGCCACCTCCTCGACAGTGACGAGCGGCCCAGTC	1801 CCGAAGGAAGAAGGAAGCACATCCACCTGGGCCACCTGCGCTTACAGAGGACACTGC	1861 ACAGCATCGATCTGGAGATCCAAGAGGGTAAACTGGTTGGAATCTGCGGCAGTGTGGGAA 	1921 GTGGAAAAACCTCTCATTTCAGCCATTTTAGGCCAGATGACGCTTCTAGAGGGCAGCA 	1981 TIGCAATCAGTGGAACCTTGGCTTATGTGGCCCAGCAGGCCTGGATCCTCAATGCTACTC	2041 TGAGAGACAACATCCTGTTTGGGAAGGAATATGATGAAGAAGAAAGA	2101 ACAGCTGCTGACGCCTGACCTGGCCATTCTTCCCAGCAGCGACCTGACGAGATTG	2161 GAGAGCGAGGAGCCAACCTGAGCGGTGGGCAGCGCCCAGAGGATCAGCCTTGCCCGGGCCTT	2221 TGTATAGTGACAGGAGCATCTACATCCTGGACGACCCCCTCAGTGCCTTAGATGCCCATG	2281 TGGGCAACCACATCTTCAATAGTGCTATCCGGAAACATCTCAAGTCCAAGACAGTTCTGT	2341 TIGTTACCCACCAGTTACAGTACCTGGTTGACTGTGATGAAGTGATCTTCATGAAAGGG	2401 GCTGTATTACGGAAAGAGGCACCCATGAGGAACTGATGAATTTAAATGGTGACTATGCTA 	2461 CCATTTTAATAACCTGTTGCTGGGGGGGGGCCCGCCAGTTGGGTTCAAAAAAGG	2521 AAACCAGTGGTTCACAGAAGAAGTCACAAGACAAGGGTCCTAAAACAGGAT 111 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	
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2775 3012 2715 2389 2449 2892 2629 2689 3072 2749 2832 2509 2952 3132 3252 2929 3372 3432 3169 3552 3229 2210 CAGGAAATGAGAAAGATGAAGGAAAAGAATCTGAAACAGGCTCAGAATTTGTAGACACAA 2269 ACAATATCACGCAGTCACCTTTCCTCTCCCACATCACGTCCAGCATACAGGCCTTGCCA 3312 AGAATGTCAGCCGGTCACCCTGGTTCACCCACATCACCTCCTCCATGCAGGGCCTGGGCA 2989 2990 TCATTCACGCCTATGGCAAGAAGAAGCTGCATCACCTAGTTTAAGACGCTAAACGACG 3049 3433 ACCTCATCAGCATCGCCCTCATCACCACCACGGGGCTGATGATGGTCTTTTATGCACGGGC 3492 TCCAGITIACGGICAGACIGGCAICIGAGACAGAAGCICGAITCACCICGGIGGAGAGGA 3612 3613 TCAATCACTACATTAAGACTCTGTCCTTGGAAGCACCTGCCAGAATTAAGAACAAGGCTC 3672 2630 CATCCTCTCTGCATGACACGGTGTTTGATAAGATCTTAAAGAGCCCAATGAGTTTCT 2690 TIGACACGACTCCCACTGGCAGGCTAATGAACCGTTTTTCCAAGGATATGGACGAGCTGG ---CAGCTTGTGCAGCTGGAAGAGAAAGGGCAGGGTTCAGTGCCCTGGT CAGTATATGGTGTCTACATCCAGGCTGCTGGGGGCCCCTTGGCATTCCTGGTTATTATGG 2330 AAACATATCACACGTACATTAAGGCTTCTGGAGGGTACCTCTTCTTTCACTGTGT CCCTTTTCATGCTGAATGTAGGCAGCACCGCCTTCAGCACCTGGTGGTTGAGTTACTGGA 2390 TCCTCTTCCTCCTGATGATTGGCAGCGCTGCCTTCAGCAACTGGTGGCTGGGTCTCTGGT TCAAGCAAGGAAGCGGGAACACCACTGTGACTCGAGGGAACGAGACC---TCGGTGAGTG CAGTCATGCTGATCCTGAAAGCCATTCGAGGAGTTGTCTTTGTCAAGGGCACGCTGCGAG CTTCCTCCCGGCTGCATGACGAGCTTTTCCGAAGGATCCTTCGAAGCCCTATGAAGTTTT TTGACACGACCCCCACAGGGAGGATTCTCAACAGGTTTTCCAAAGACATGGATGAAGTTG ACGTGCGGCTGCCGTTCCAGGCCGAGATGTTCATCCAGAACGTTATCCTGGTGTTCTTCT TCCTCTTTTCAGTCCTGCACATTGTCTCCAGGGTCCTGATTCGGGAGCTGAAGCGTCTGG 3313 CCATCCACGCCTACAATAAAGGGCAGGAGTTTCTGCACAGGATACCAGGAGCTGCTGGATG ACAGCATGAAGGACAATCCTCATATGCAGTACTATGCCAGCATCTACGCCCTCTCCATGG 3493 AGATTCCCCCAGCCTATGCGGGTCTCGCCATCTTTATGCTGTCCAGTTAACGGGGCTGT 2270 2656 2450 3013 2750 2870 3253 2930 3373 3230 ' 2610 2716 2776 2833 2953 3193 3553 2893 3073 3110 g ò qq QYqq òγ qq QΩ δý 엄 à g Q Dp ΩŸ g ŏ qq Qγ g qq Dp qq qq δ QΥ Dp ογ δy δ δ òγ QQ Q Ω Οy qq

determining whether prostate cancer has metastasized in a patient, assessing the aggressiveness or indolence of prostate cancer in a

(I) is also useful as a pharmacodyanamic or pharmacogenomic marker

T; 2 other;

731 A; 765 C; 845 G; 712

Sequence 3055 BP;

pat:

88888

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Gaps

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Indels Length

Score 727; DB 23; Pred. No. 1.4e-165; 0; Mismatches 1120;

Query Match 12.5%; Best Local Similarity 55.8%; Matches 1428; Conservative

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TGCACAGCATCGATCTGGAGATCCAAGAGGGTAAACTGGTTGGAATCTGCGGGCAGTGTGG 1917

GAAGTGGAAAAACCTCTCTCATTTCAGCCATTTTAGGCCAGATGACGCTTCTAGAGGGCA 1977

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226 CGGTGGGGGTGCAGGGAAGCCTGGCCTATGTCCCCCAGCAGGCCTGGATCGTCAGCGGGA

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GCATTGCAATCAGTGGAACCTTCGCTTATGTGGCCCAGCAGGCCTGGATCCTCAATGCTA

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cancer; cytostatic; carcinogen; pharmacodyanamic marker;
marker; gene; ss.
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          1350 GTCCCAAGGACTGGCCCAGCYGTGGGGAGATCACCTTCAGAGACTATCAGATGAGATACA 3409
                                                3673 CCTCCCCTGACTGGCCCCAGGAGGGAGGTGACCTTTGAGAACGCAGAGATGAGGTACC
                                                                                      TGGTGGAGTTATCTGGAGGCTGCATCAAGATTGATGGAGTGAGAATCAGTGATATTGGCC
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                                      GAGAAAACCTCCCTCTTGTCCTAAAGAAAGTATCCTTCACGATCAAACCTAAAGAGAAGA
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25-MAY-2000;
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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate.

Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -

WPI; 2001-662795/76.

Claim 1; Page 3467; 11750pp; English.

(e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound;

(d) assessing the efficacy of a therapy in a patient;

cancer in a patient;

for inhibiting prostate cancer

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Novel isolated nucleic acid molecule associated with
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                                                                                               2260
                                                                                                                                                  4135
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marker; gene; ss.
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18-JUL-2000;
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cancerous state of

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prostate cells and correlating with presence of prostate cancer.

Ye createcting presence of prostate cancer. stage of prostate cancer.

Ye claim 1; Page 5435-5436; 11750pp; English.

Xi create cancer in the invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer;

(b) monitoring the progression of prostate cancer in a patient;

(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;

(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;

(e) salecting a composition for inhibiting prostate cancer in a patient;

(f) assessing the prostate cell carcinogenic potential of a compound;

(g) determining whether prostate cancer has metastasized in a patient;

(h) assessing the aggressiveness or indolence of prostate cancer in a patient;

(g) determining whether prostate cancer has metastasized in a patient;

(g) determining as a pharmacodyanamic or pharmacogenomic marker.

XX

Sequence 3055 BP; 731 A; 765 C; 845 G; 712 T; 2 other;
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5 2037 2097 2157 2217 2277 1858 TGCACAGCATCGATCTGGAGATCCAAGAGGGTAAACTGGTTGGAATCTGCGGCAGTGTGG 1917 GAAGTGGAAAAACCTCTCTCATTTCAGCCATTTTAGGCCAGATGACGCTTCTAGAGGGCA 1977 2337 2397 2457 2517 2577 285 345 465 705 CGTGGGGGTGCAGGGAAGCCTGGCCTATGTCCCCCAGCAGCCTGGATCGTCAGCGGGA ATGTGGGCAACCACATCTTCAATAGTGCTATCCGGAAACATCTCAAGTCCAAGACAGTTC GGAGTGGTAAGAGCAGCCTGTTGTCAGCCATCCTGGAGGAGATGCACTTGCTCGAGGGCT GCATTGCAATCAGTGGAACCTTCGCTTATGTGGCCCAGCAGGCCTGGATCCTCAATGCTA TGAACAGCTGCTGAGGCCTGACCTGGCCATTCTTCCCAGCAGCGACCTGACGGAGA TTGGAGAGCGAGCCAACCTGAGCGGTGGGCAGCGCCAGAGGATCAGCCTTGCCCGGG CCTTGTATAGTGACAGGAGCATCTACATCCTGGACGACCCCCTCAGTGCCTTAGATGCCC CCCAACTTATCCAGAAGATGCACAAGGAAGCCACTTCG-----GACATGTTGCAGGACA 2518 AGGAAACCAGTGGTTCACAGAAGAAGTCACAAGACAAGGGTCCTAAAACAGGATCAGTAA TGTTTGTTACCCACCAGTTACAGTACCTGGTTGACTGTGAAGTGAAGTCTTCATGAAAG AGGGCTGTATTACGGAAAGAGGCACCCATGAGGAACTGATGAATTTAAATGGTGACTATG CTACCATTTTTAATAACCTGTTGCTGGAGAGACACCGCCAGTTGAGATCAATTCAAAAA . 6 Ouery Match 12.5%; Score 727; DB 23; Length 3055; Best Local Similarity 55.8%; Pred. No. 1.4e-165; Matches 1428; Conservative 0; Mismatches 1120; Indels 9 1978 1918 2098 2158 2278 2338 2398 2458 166 286 346 406 2218 466 902 셤 δ g a g g ŏ ò g ŏ 8 ò δ οŽ g g õ g QΥ а ò Qγ

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Title: Perfect score: Sequence:	US-09-647-140A-3 5838 1 ccgggcaggtggctcatgctaaaaaaaaaaaaaa 5838
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Searched:	2054640 segs, 14551402878 residues
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ALIGNMENTS

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	5838 bp mRNA linear	OAT-C) mRNA						; Vertebrat	ni; Hominic		, Testa, J. F	new member	
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	5838	Homo sapiens ABC transporter MOAT-C (MOAT-C) mRNA, complete cds	ı	GI:4140697		· so	Ø	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	to 5838)	Belinsky, M.G., Bain, L.J., Balsara, B.B., Testa, J.R. and Kruh, G.D.	ation of MOAT-C an	subfamily of transporter proteins
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VSRVLIRELKRLDNITQSPFLSHITSSIQGLATIHAYNKGQFFLHRYQELLDDNQAPF
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/gene="MOAT-C"
/note="MRP/cMOAT-related ABC transporter"
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2 (bases 1 to 5838)

5 Belinsky,M.G., Baln,L.J. and Kruh,G.D.

Direct Submission

L Submitted (04-NOV-1998) Medical Oncology, Fox Cha

7701 Burholme Avenue, Philadelphia, PA 19111, USP

Location/Qualifiers
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/protein_id="AAD04169.1"
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                                                                     GAAAGTACCATCATGGCTTGAGTGCTCTGAAGCCCATCCGGACTACTTCCAAACACCAGC
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EKAGFFGSITVGVAPIVVIRSVYHMINKRFASPHIKIEFKNYTVPRSMTFALKYT

FRSYKSLGEASVAVDRFKSLEMBEVHHIKNKPASPHIKIEBERSSIGN

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ANGGGORORISLERARLYSTILDDPLGALDGOMTLUGSTARGHEKSKTVLFV

THQLQYTUCDCDEVTERREGGTTHEELMNILNGDYATIFNNILLGETPPVEINSKK
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NLPLVLKKVSFTIKPKEKIGIVGRTGSGKSSLGMALRRLVELSGGGCIKIDGVRISDIG
LADLRSKLSIIPQEPVLFSGTVRSNLDPFNQYTEDQIMDALERTHMKECIAQLPLKLE
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                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 5881)
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MCAleer,M.A., Breen,M., White,N. and Matthews,N.
Direct Submission
Submitsed (27-APR-1999) Yamanouchi Research Institute, Armstrong
Road, Oxford OX4 4SX, UK
Location/Qualifiers
                                   5701 ATGTCGTGACCAACTAGACATTCTGTCGCCTTAGCATGTTTGCTGAACACCTTGTGGAAG 5760
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Homo sapiens ABC protein mRNA, complete cds.
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/note="pabC11; MOAT-C; MRP5"
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2964. CAACCTGAGCGGTGGGCAGCGCCCAGAGGATCAGCCTTGCCGGGCCTTGTATAGTGACAG **AAGAGGCACCCATGAGGAACTGAATTTAAATGGTGACTATGCTACCATTTTTAATAA** TGTGGGAATGATCGCAGGAGTCTTCCCGTGGTTCCTTGTGGGCAGTGGGGCCCCTTGTCAT GAGGCCTGACCTGGCCATTCTTCCCAGCGACCTGACGGAGATTGGAGAGCGAGGAGC AAAGCCAGAGGAAGGGCAGCTTGTGCAGCTGGAAGAGAAAAGGGCAGGGTTCAGTGCCCTG GTCAGTATATGGTGTCTACATCCAGGCTGCTGGGGGCCCCTTGGCATTCCTGGTTATTAT GGCCCTTTTCATGCTGAATGTAGGCAGCACCGCCTTCAGCACCTGGTGGTTGAGTTACTG TGACACGACCCCCACAGGGAGGATTCTCAACAGGTTTTCCAAAGACATGGATGAAGTTGA g ò g q g Q ద gg ζ. Q q οy ά ζ à οŻ ŏ g δ q ΩŽ 셤 ζ qq g $\tilde{\zeta}$ ζ à Š q g $\frac{1}{2}$ à q à

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/protein_id="Baa76608.1"
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/tbanslaton="MKDIDIGKEYIIPSPGYRSVRERTSTSGTHRDREDSKFRRTRPL
ECOPALETAARAEGELDASHHSOLRILDEEHPKGKYHHGLSALKFITATSKHQHPVD
NAGLFSCMTFSWLSSLARVAHKKGELSMEDVWSLSKHESSDVNCRRLERLWOEBLNEV
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Suzuki,T., Kuh,H. and Nishio,K.
Suzuki,T., Kuh,H. and Nishio,K.
Direct Submission
Submitted (20-0CT-1998) Toshihiro Suzuki, National Cancer Center Research Institute, Pharmacology Division; Tsukiji 5-1-1, Chuo-ku, Tokyo 104-0045, Japan (E-mail:tssuzuki@ganZ.res.ncc.go.jp, Tel:81-3-3542-2511(ex.4451), Fax:81-3-3542-1886)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 GCCCTGGAGCCAACTGCTGTTTTTGAGGTGGCACTTTTTCATTTGCCTATTCCCACACC
                TCCACAGTTCAGTGGCAGGGCTCAGGATTTCGTGGGTCTGTTTTCCTTTCTCACCGCAGT
                                                                               CTGGTTGCTGTGTTGGTGTGTTCCCGCAAACCCCCTTTGTGCTGTGGGGCTGGTAG
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Suzuki,T., Sasaki,H., Kuh,H.J., Agui,M., Tatsumi,Y.,
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Detailed structural analysis on both human MRP5 and
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Pred. No. 0;
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1415 c 1472 g 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="MRP5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 97.9%;
Best Local Similarity 99.9%;
Matches 5720; Conservative
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ORIGIN
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oy op	674	CGTGTGCCTGATGATGACGCAGCTGGCTTCAGTGGACCAGCCTTCATGGTGAAACA 733
Oy Db	734	CCTCTTGGAGTATACCCAGGCAACAGTCTAACCTGCAGTACAGCTTGTTGTTAGTGCT 793
Qy Dp	794	GGGCCTCCTCCTGACGGAAATCGTGCGGTCGCTTGCACTGACTTGGGCATTGAA 853
Oy Db	854	TTACCGAACCGGTGTCCGCTTGCGGGGGCCATCCTAACCATGGCATTTAAGAAGATCCT 913
Qy Dp	914	TAAGTTAAAGAACATTAAAGAGAAATCCCTGGGTGAGCTCATCAACATTTGCTCCAACGA 973
Qy Db	974	TGGGCAGAGAATGTTTGAGGCAGCAGCCGTTGGCAGCCTGCTGGTGGAGGACCCGTTGT 1033
Oy Dp	1034 961	TGCCATCTTAGGCATGATTTATAATGTAATTATTCTGGGACCAACAGGCTTCCTGGGATC 1093
Qy	1094	AGCTGTTTTTATCCTCTTTTACCCAGCAATGATGTTTGCATCACGGCTCACAGCATATTT 1153
Oy Dp	1154	CAGGAGAAAATGCGTGGCCGCCACGGATGAACGTGTCCAGAAGATGAAGTTCTTAC 1213
Qy Dp	1214	TTACAFTAAATTTATCAAAATGTATGCCTGGGTCAAAGCATTTTCTCAGGGTGTTCAAAA 1273
Oy Dp	1274	AATCCGCGAGGAGCGTCGGATATTGGAAAAGCCGGGTACTTCCAGGTATCACTGT 1333
Qy Db	1334	GGGTGTGGCTCCCATTGTGGTGGTGATTGCCAGCGTGGTGACCTTCTCTGTTCATATGAC 1393
Oy Dp	1394	CCTGGGCTTCGATCTGACAGCACAGGCTTTCACAGTGGTGACAGTCTTCAATTCCAT 1453
Qy Dp	1454	GACTITIGCTITIGAAGTAACACGGTITICAGTAAAGTCCCTCTCAGAAGCCTCAGTGGC 1513
, yo	1514	TGTTGACAGATTTAAGAGTTTGTTTCTAATGGAAGGGTTCACATGATAAAGAACAAACC 1573
Qy Dp	1574	AGCCAGTCCTCACATCAAGATAGAGATGAAAAATGCCACCTTGGCATGGGACTCCTCCCA 1633
Oy Db	1634	CTCCAGTATCCAGAACTCGCCCAAGCTGACCCCCAAAATGAAAAAGACAAGAGGGCTTC 1693
QY	1694	CAGGGGCAAGAAAGAGAAGGTGAGGCAGCTGCAGCACTGAGCATCAGGGGGTGCTGGC 1753
οy	1754	SCAGAAAGGCCACCTCCTCGGACAGTGACGAGCGGCCCAGTCCCGAAGAGGAAGA

1740 1873 1933 1860 1993 1920 2053 1980 2113 2040 2173 2100 2233 2160 2293 2220 2353 2280 2413 2340 2473 2400 2533 2460 2593 2520 2653 2580 2713 2640 2773 2700 2833 2760 CAGCATGAAGGACAATCCTCATATGCAGTACTATGCCAGCATCTACGCCCTCTCCATGGC 2893 AAAGCCAGAAGGGCAGCTTGTGCAGCTGGAAGAGAAAAGGGCAGGGTTCAGTGCCCTG CAACCTGAGCGGTGGGCAGCGCCAGAGGATCAGCCTTGCCCGGGCCCTTGTATAGTGACAG GGCCCTTTTCATGCTGAATGTAGGCAGCACCGCCTTCAGCACCTGGTGGTTGAGTTACTG GGAGATCCAAGAGGGTAAACTGGTTGGAATCTGCGGCAGTGTGGGAAGTGGAAAAACCTC GAGCATCTACATCCTGGACGACCCCCTCAGTGCCTTAGATGCCCATGTGGGCAACCACAT ACAGAAGAAGTCACAAGACAAGGGTCCTAAAACAGGATCAGTAAAGAAGGAAAAAAGCAGT GTCAGTATATGGTGTGTACATCCAGGCTGCTGGGGGCCCCTTGGCATTCCTGGTTATTAT AGGCAAGCACATCCACCTGGGCCACCTGCGCTTACAGAGGACACTGCACAGCATCGATCT GAGGCCTGACCTGGCCATTCTTCCCAGCGACCTGACGGAGATTGGAGGAGGAGGAGC CCTGTTGCTGGGAGACACCGCCAGTTGAGATCAATTCAAAAAAGGAAACCAGTGGTTC 1981 2041 2341 1681 1814 1741 1801 1934 1861 1994 1921 2174 2101 2234 2161 2294 2221 2354 2281 2414 2534 2461 2594 2834 1874 2054 2114 2474 2401 2654 2581 2714 2641 2774 2701 2521 . g qq g Ωp qq QQ QQ Dp g qq QQ Ω q ογ Db ōλ Qγ Qγ Ω δ ò δŽ QQ οy δ ò οy δ q ò g Ω q ۵y g 6

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2820	2953	3013	3073	3133	3193	3253	3313	3373	3433	3493	3553	3613 3540 ·	3673 3600	3733	3793 3720	3853 3780	3913 3840	3973 3900
61 CAGCATGAAGGACAATCCTCATATGCAGTACTATGCCAGCATCTACGCCCTCTCCATGGC	94 AGTCATGCTGATCCTGAAAGCCATTCGAGGAGTTGTCTTTGTCAAGGGCACGCTGCGAGC	54 TTCCTCCCGGCTGCATGACGAGCTTTTCCGAAGGATCCTTCGAAGCCTATGAAGTTTTT	4 TGACACGACCCCCACAGGAGATTCTCAACAGGTTTTCCAAAGACATGGA 	CGTGCGGCTGCC	14. TGTGGGAATGATCGCAGGAGTCTTCCCGTGGTTCCTTGTGGCAGTGGGGCCCCTTGTCAT 14. 11.	04 CCTCTTTTCAGTCCTGCACATTGTCTCCAGGGTCCTGATTCGGGAGCTGAAGCGTCTGGA 	4 CAATATCACGCAGTCACCTTTCCTCTCCCACATCACGTCCAGATACAGGGCCTTGCCACACATACAGGGCCTTGCCACATCACGCACATACAGGCCTTGCCACATCACGTCCAGGATACAGGCCTTGCCACATCACGTCCAGGATACAGGCCTTGCCACATCACGTCCAGGATACAGGCCTTGCCACATCACGTCCAGGATACAGGCCTTGCCACATCAGGATACAGGATACAGGAATACAGGAATACAGGAATACAGGAATACAGGAATACAGGAATACAGGAATACAGGAATACAGGAATACAGGAATACAGGAATACAGGAATACAGGAATACAGGAATACAGGAATACAGAATACAGGAATACAAGAATACAAGAATACAGAATACAGAATACAGAATACAGAATACAGAATACAGAATACAGAATACAATACAGAATACAATA	4 CATCCACGCCTACAATAAAGGCAGGAGTTTCTGCACAGATACCAGGAGCTGCTGGATGA 	74 CAACCAAGCTCCTTTTTTTTTTACTGTGCGATGCGGTGGCTGGC	34 CCTCAPCAGCAPCGCCCTCAFCACCACGGGGCTGAFGATGGTCTTTATGCACGGGA	94 GATTCCCCCAGCCTATGCGGGTCTCGCATCTTATGCTGTCCAGTTAACGGGGCTGTT 	4 CCAGITTACGGICAGACIGGGAICTGAGACAGAAGCICGAI 	4 CAATCACTACATTAAGACTCTGTCCTTGGAAGCACCTGCCAAAATTAAGAACAAGGCTCC 	74 CTCCCCTGACTGGCCCCAGGAGGAGAGTGACCTTTGAGAACGCAGAGATGAGGTACCG 	4 AGAAAACCTCCTCTTGTCCTAAAGAAAGTATCCTTCACGATCAAACCTAAAGAGAAGAT 	4 TGGCATTGTGGGGCGGACAGGATCAGGAAGTCCTCGCTGGGGATGGCCTCTTCCGTCT	4 GGTGGAGTTATCTGGAGGCTGCATCAAGATTGATGGAGTGAGAATCAGTGATATTGGCCT 	4 TGCCGACCTCCGAAGCAAACTCTCTATCATTCCTCAAGAGCCGGTGCTGTTCAGTGGCAC
Ob 276	Oy 289 Db 282	29	y 301 b 294	y 3074 b 3001	у 313 b 306	y 319 b 312	у 325 b 318	331	33	34	34	355	354	367	373	379	385	391
Q	O D	QY Dp	Q Q	QY	Qy Db	QY Db	Qy Dp	0.y 0.b	Qy Dp	QY Db	S G	Qy Dp	δο qa .	QQ Dp	oy ap	Qy Db	Oy Dp	Oy Op

οy		TCAACCAGTACACTGAAGACCAGATTTGGGATGCCCT 403
QQ		GTCAGATCAAATTTGGACCCCTTCAACCAGTACACTGAAGACCAGATTTGGGATGCCCT 39
QY	4034	ATGAAAGAATGTATTGCTCAGCTACCTCTGAAACTTGAATCTGAAAGT
Ωp	3961	GAGAGGACACACATGAAAGAATGTATTGCTCAGCTACCTCTGAAACTTGAATCTGAAGT
Qy	4094	SAACGGCAGCTCTTGTGCATAGCTAGAG
Dp	4021	ATGGAGAATGGGGATAACTTCTCAGTGGGGGAACGCCAGCTCTTGTGTGTAGTGGTGGGG
Oy .	4154	TAAGATTCTGATTTTAGATGAAGCCACAGGCTGCCATGGACACAGA
Db	4081	CTGCTCCGCCACTGTAAGATTCTGATTTTAGATGAAGCCACAGCTGCCATGGACACAGA
Qy	4214	CAAGAGCATCCGAGAAGCATTTGCAGACTGTACCATGCTGAC
QQ		ACAGACTTATTGATTCAAGAGACCATCCGAGAAGCATTTGCAGACTGTACCTGCTGAA
Qy	4274	GCCCATCGCCTGCACACGGTTCTAGGCTCCGATAGGATTATGGTGCTGGCCCAGGG
qa		TTGCCCATGGCTGCACACGGTTCTAGGCTCCGATAGGATTATGGTGCTGGCCCAGGG
Qy	4334	GTGGTGGAGTTTGACACCCCATCGGTCCTTCTGTCCAACGACAGTTCCCGATTCTA
qq	4261	AGGTGGTGGAGTTTGACACCCCATCGGTCCTTCTGTCTCAACGACAGTTCCCGATTCTA
ΟY	4394	GTTTGCTGCTGCAGAACAAGGTCGCTGTCAAGGGCTGACTCCTCCTGTTGA
qq	4321	GCCATGTTTGCTGCAGAGAACAAGGTCGCTGTCTAGGGCTGACTCCTCCCTGTTGA
Qy	4454	CTCTTTTCTTTAGAGCATTGCCATTCCCTGGGGCGGGCGG
qq	4381	GAAGTCTCTTTTCTTTAGAGCATTGCCATTCCTGCGTGGGGGGGG
Óλ	4514	TACCGAAACCTTGCTCGATTTTATCTTTCGCACAGCAGTTCCGGATTGGC
рр	4441	CTCCTACCGAAACCTTGCTTTTTTTTTTTTTTTTCTTTTCGCACAGCAGTTCCGGATTGGC
Οy	4574	TGTTTCACTTTTAGGGAGAGTCATATTTTGATTATTGTATTTATT
qq	4501	TGTGTGTTTCACTTTTAGGGAGAGTCATATTTTGATTATTGTATTTATT
ΟŊ	4634	CAAAATTTAGTTTTGTTCTTAATTGCACTCTAAAAGGTTCAGGAACCGTTATT
qq	Ď	AAACAAATTTAGTTTTTGTTCTTAATTGCACTCTAAAAGGTTCAGGGAACCGTTATT
ΟŊ	4694	GAGGCCTATAATGAAGCTTTATACGTGTAGCTATATCTATATATT
Dp	4621	AATTGTATCAGAGGCCTATAATGAAGCTTTATACGTGTAGCTATATCTATATAATTA
Qy	4754	CIATATTTACAGTGAAAATGTAAGCTGTTTATTTTATATAAAATAAGC
QQ		STACATAGCCTATATTTACAGTGAAAATGTAAGCTGTTTATTTTATATTAAAATAAGC
δy	4814	TGCATATTCCTTTCTACATTTTTGTACAGTTTGCTGTACTAGA
QQ	4741	CTGTGCTAATAACAGTGCATATTCCTTTCTATCATTTTTGTACAGTTTGCTGCTGTACTAGA
Qy	4874	TTGCTATTAGACTGTAGGAAGAGTAGCATTTCATTCTTCTTAGCTGG
Db	4801	ATCTGGTTTTGCTATTAGACTGTAGGAGAGTAGCATTTCATTCTTCTCTAGCTGGGGG
Qy	4934	TTTCTGGGTGTCCAAAGGAAGACGTGTGGCCAATAGTGGGCCCTC
QQ	4861	TTCACGGTGCCAGGTTTTCTGGGTGTTCCAAAGGAAGACGTGTGGCAATAGTGGGCCCTC
Qy	4994	CGCCTCCCCACAGCCGCTCCAGGGTGGCTGGAGACGGGTGGGC
QQ	4921	GACAGCCCCCTTTTTTTTTTTTTTTTTTTTTTTTTTTTT

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INICSNDGQRMFBAAVGSLLAGGPVVAILGMINVIILGPTGFLGSAVFILFPPAMB
RASRLTAYFRRKCVAATDERVQKMEVLTYKFIKMYAWVRAFGGSAVFILFPPAMB
RASRLTAYFRRKCVAATDERVQKMEVLTYKFIKMYAWVRAFGSGVQKIREERRIL
EKAGFGOSITVGVAPIVVYTESHLAKEVTATAMDSHSSION
SPKLTPKMKKDRAATDERVGKTEHOAVLABOKGHLLLDSDERBSPEEEEKH
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RAYVAQOAMILMYTRASRGKKEKVROLQRTEHOAVLABOKGHLLLDSDERBSPEEEEKH
INIGGGRAFGATLSTDLETOGSTGGSKGRTSLISALLGOMTLLEGSIAISGT
RAYVAQOAMILMYTRANTKERVROLGSTAGGSKTSLISALTGOMTLLEGSIAISGT
RAYVAQOAMILMYTRAKGTERVERVERTAKTTDDPLGALDAHVGNHIFNSAITKHKSKTVLEV
THQLQYLVUDCDVIFMKEGCITERGTHEELMNLNGDYATIFNNLLLGGFTPVEINSKE
ETSGSOKKSODKGPRTGSYKKERAVKEPEGOLVQLEEKGGGSVPWSVYGYYLOAGGS
LAFLVIMALKYNGSTARSTWALSYNIKGGSGNTTVTRGNETSVSDKKDNPHMOYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASIYALSMAVMLILKAIRGVVFVKGTLRAŠSRIHDELFRRILRSPMKFFDTTPTGRIL
NRFSKDMDEVDVRLPFQAEMFIQNVILVFFCVGMIAGVFPWFLVAVGPLVILFSVLHI
VSRVLIRELKRLDNITQSPFLSHITSSIQGLATIHAVNKGGFFLHRYQELLDDNQAPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VELASETERRETSVERINHY KTLSLERPARIKNKAPSPDWPOEGEVTFENAEMRYRE
NLPLVLKKVSFTIRPREKIGTVGRTGSGKSSLGMALFRLVELSGGCKTIDOVRISDIG
TADLRSKKLSITYOEPVLFSGVYRSULDPROVYTEDOLWDALERTHMKECIAQLEKLE
SEVWRNGDNESVGEROCLLCTARALLHUCKILILDEATAAMOTETDLLIQETIREAFAD
CTMLTIAHRLHTVLGSDRIMVLAQGQVVEFDTPSVLLSNDSSRFYAMFAAABNKVAVK
        Upases 1 to 5826)
Wijnholds,J., Mol.C.A., van Deemter,L., de Haas,M., Scheffer,G.L., Baas,F., Beijnen,J.H., Scheper,R.J., Hatse,S., De Clercq,E., Balzarini,J. and Borst,P.
Multidrug-resistance protein 5 is a multispecific organic anion transporter able to transport nucleotide analogs
Proc. Natl. Acad. Sci. U.S.A. 97 (13), 7476-7481 (2000)
10840050
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NAGLFSCMTFSWLSSLARVAHKKGELSMEDVWSLSKHESSDVNCRRLERLWQEELNEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPDAASLRRVVWIFCRTRLILSIVCLMITQLAGFSGPAFWVKHLLEYTQATĒSNLQYS
LLLVLGLLLTEIVRSWSLALTWALNYRTGVRLRGAILTWAFKKILKLKNIKEKSLGEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FLFTCAMRWLAVRLDLISIALITTGLMIVLMHGQIPPAYAGLAISYAVQLTGLFQFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MKDIDIGKEYIIPSPGYRSVRERTSTSGTHRDREDSKFRRTRPL
                                                                                                                                                                                                                                                                                              Submitted (03-JAN-1997) Molecular Biology, Netherlands Cancer Institute, Plesmanlaan 121, Amsterdam 1066 CX, The Netherlands (bases 1 to 5826)
Wijhbolds, J., Mol.C.A.A.M., Ponne, N.J., Baas, F. and Borst, P. Direct Submission
Submitted (03-AUG-1999) Molecular Biology, Netherlands Cancer Institute, Plesmanlaan 121, Amsterdam 1066 CX, The Netherlands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps.
                                                                                                                                                                                                                                       Kool,M., Wijnholds,J., de Haas,M., Mol,C.A.A.M., Ponne,N.J.,
Baas,F. and Borst,P.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence update by submitter
On Aug 3, 1999 this sequence version replaced gi:2439973.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="ABC transporter protein; MOAT-C; pABC11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 5826;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="multidrug resistance protein
/protein_id="AAB71758.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /map="7.69 cR from WI-6365"
/tissue_type="brain"
/dev_stage="fetus"
1. .5826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 5671;
Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .5826
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="AAB71758
/db_xref="G1:5685864"
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Homo saplens multidrug resistance protein 5 (MRP5) mRNA, complete
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176 GCGGTGGGCAGCGCCAGAGGATCACCCTTGCCCGGGCCTTGTATAGTGACAGGAGCATCT 242 ACATCCTGGACGACCCCTCAGTGCCTTAGATGCCCATGTGGGCAACCACATTTAGATA 241 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	62 ACCTGGTTGACTGTGAAGTGATCTTCATGAAGGGGGTGTATTACGGAAGGGGG 11111111111111111111111111111	2 TGGGAGACACCGCCAGTTGAGATCAATTCAAAAAGGAAACCAGTGGTTCACAGAAGA [602 AGGAAGGGCAGCTTGTGCAGCTTGGAAGAGAAAGGGCAGGGTTCAGTGCCCTGGTCAGTAT [11] [1] [1] [1] [1] [1] [1] [1] [1] [1]			902 TGATCCTGAAAGCCATTCGAGGAGTTGTCAAGGGCACGCTGCGAGCTTCCTCCC	022 CCCCCACAGGGAGGATTCTCAACAGGTTTTCCAAAGACATGGATGAAGATGACGGGGCGGC	SCAGGAGTCTTCCCGTGGTTCCTTGTGGCAGTGGGGCCCCTTGTCATCTCTTTTTCCAGGGCCCCTTGTTGTTGTTTTTTTT	1100 111111111111111111111111111111111
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Qy	3671	TCCCTCCCCTGACTGGCCCCAGGAGGAGGTGACCTTTGAGAACGCAGAGATGAGGTA 3730
. Qy	3731	CCGAGAAAACCTCCCTCTTGTCCTAAAGAAAGTATCCTTCACGATCAAACCTAAAGAGAA 3790
QY	3791	GATTGGCATTGTGGGGGGACAGGATCAGGAAGTCCTCGCTGGGATGGCCCTCTTCCG 3850
QY Db	3851	TCTGGTGGAGTTATCTGGAGGCTGCATCAAGATTGATGGAGTGAGAATCAGTGATATTGG 3910
QY	3911	
QY	3971 3961	
ζΟ.	4031	CCTGGAGAGGACACACATGAAAGAATGTATTGCTCAGCTACCTCTGAAACTTGAATCTGA 4090
QY Db	4091	AGTGATGGAGAATGGGGATAACTTCTCAGTGGGGGAACGGCAGCTCTTGTGCATAGCTAG 4150
Qy Db	4151	
Qy	4211	
Qy	4271	GACCATIGCCCATCGCCTGCACACGGTTCTAGGCTCCGATAGGATTATGGTGCTGGCCCA 4330
Qy Db	4331	
Qy	4391	
Qy	4451	TGACGAAGTCTCTTTTCTTTAGAGCATTGCCATTCCCTGCCTG
Qy	4510	GCGTCCTCCTACCGAAACCTTGCCTTTCTCGATTTTAFCTTTCGCACAGCAGTTCCGGA 4569
. 0y. Db	4570	TGGCTTGTGTGTTTCACTTTTAGGAGAGTCATATTTGATTATTGTATTTATT
Qy	4630	TCATGTAAACAAAATTTAGTTTTTGTTCTTAATTGCACTCTAAAAGGTTCAGGGAACCGT 4689
Qy	4690	TATTATAATTGTATCAGAGGCCTATAATGAAGCTTTATACGTGTAGCTATATCTATATA 4749
QY	4750	AATTCTGTACATAGCCTATATTTACAGTGAAAATGTAAGCTGTTTATTTTATATAAAAT 4809

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qq	2821	ATGCTGATCCTGAAAGCCATTCGAGGAGTTGTCTTTGTCAAGGGCACGCTGCGAGCTTC 288
QY	6	GCTGCATGACGAGCTTTTCCGAAGGATCCTTCGAAGCCCTATGAAGTTTTTGA 301
qq	2881	TCCCGGCTGCATGAGGATCCTTCGAAGGATCCTTCGAAGCCCTATGAAGTTTTTGA 294
QY	3017	CAGGTTTTCCAAAGACATGGATGAAGTTGACGT 307
QQ	2941	ACGACCCCCACAGGGAGGATTCTCAACAGGTTTTCCAAAGACATGGATGAAGTTGACGT 30
Οy	3077	TGCCGTTCCAGGCCGAGATGTTCATCCAGAACGTTATCCTGGTGTTCTTCTGTGT 313
qα	3001	CGGCTGCCGTTCCAGGCCGAGATGTTCATCCAGAACGTTATCCTGGTGTTCTTCTGTGT 306
ΟŸ	3137	ATCGCAGGAGTCTTCCCGTGGTTCCTTGTGGCAGTGGGGCCCCCTTGTCATCCT 319
.qq	3061	SAATG
Οy	3197	TTTCAGTCCTGCACATTGTCTCCAGGGTCCTGATTCGGGAGCTGAAGCGTCTGGACA 325
QQ		TTCGGGAGCTGAAGCGTCTGGACAA 318
ΟŊ	3257	ICACGCAGTCACCTTTCCTCTCCCCACATCACGTCCAGCATACAGGGCCTTGCCACCAT 331
qa	3181	ATCACGCAGTCACCTTTCCTCTCCCACATCACGTCCAGCATACAGGGCCTTGCCACCAT 324
٥y	3317	ACCCTACAATAAAGGGCAGGAGTTTCTGCACAGATACCAGGAGCTGCTGGATGACAA 337
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δy	3497	CTGTCCAGTTAACGGGG
QQ	4	CCCCCAGCCTATGCGGGTCTCGCCATCTCTTATGCTGTCCAGTTAACGGGGCTGTTCCA
Qŷ	3557	GTCAGACTGGCATCTGAGACAGAAGCTCGATTCACCTCGGTGGAGAGGATCAA
qq	3481	TTTACGGTCAGACTGGCATCTGAGACAGAAGCTCGATTCACCTCGGTGGAGGGATCAA
δy	3617	ATTAAGACTCTGTCCTTGGAAGCACCTGCCAGAATTAAGAACAAGGCTCCCTC
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qq		CTGACTGGCCCCAGGAGGGAGGGAGGTGACCTTGAGAACGCAGAGATGAGGTACCGAGA 36
Qy	3737	TTCCTCTTGTCCTAAAGAAAGTATCCTTCACGATCAAACCTAAAGAGAAGATTGG 3
QQ	3661	CTCTCGTCCTAAAGAAAGTATCCTTCACGATCAAACCTAAAGAGAAGATGG
Qy	3797	GACAGGATCAGGGAAGTCCTCGCTGGGGATGGCCCTCTTCCGTCTGGT 3
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Qy	3857	CTGGAGGCTGCATCAAGATTGATGGAGTGAGAATCAGTGATATTGGCCTTGC 3
qa	7	AGTTATCTGGAGGCTGCATCAAGATTGATGGAGTGAGAATCAGTGATATTGGCCTTGC 3
Ολ	3917	GAAGCAAACTCTCTATCATCCTCAAGAGCCGGTGCTGTTCAGTGGCACTGT
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TITLE Multidrug resistance-associ	FEAURES SOUCÇE BASE COUNT 1217	Query Match Best Local Similarity 99:7%; Pred. No. 0; Matches 4737; Conservative 6; Mismatches 9; Indels 1; Gaps	OY 77 TGATGTGAAACTAACAGTCTGTGAGCCTCGGAACCTCGGGAGAAGATGAAGGATAT 136	9y 137 CGACATAGGAAAAGAGTATATCATCCCCGGTCCTGGGTATAGAAGTGTGGGGAGAGAAC 196	9y 197 CAGCACTÍCTGGGACGCACAGAGACCGTGAAGATTCCAAGTTCAGGAGAACTCGACCGTT 256	. Qy 257 GGAATGCCAAGATGCCTTGGAAACAGCAGCCGAGGCCGAGGGCCTCTCTTGATGCCTC 316	OY 317 CATGCATTCTCAGGTCAGAATCCTGGATGAGGAATCCCCAAGGGAAAGTACCATCATGG 376	Oy 377 CTTGAGTGCTCTGAAGCCCATCCGGACTACTTCCAAACACCCAGTGGACAATGC 436	Qy 437 TGGGCTTTTTTCTGTATGACTTTTTCGTGGCTTTCTTCTGGCCCGTGTGGCCCACAA 496	QY 497 GAAGGGGAACTCTCAATGGAAGACGTGTGGTCTCTGTCCAAGCACGATCTTCTGACGT 556 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	QY 557 GAACTGCAGAAGACTAGACAGACTGTGCCAAGAAGACTGAATGAA	0y 617 TGCTTCCCTGCGAAGGGTTGTGGAACTCTTCTGCCGCACCAGGCTCATCGTGTGT 676	Qy 677 GTGCCTGATGATCACGCAGCTGGCTTCAGTGGACCAGCCTTCATGGTGAAACACCT 736	OY 737 CTTGGAGTATACCCAGGCAACAGAGTCTAACCTGCAGTACAGCTTGTTAGTGTGGGG 796	QY 797 CCTCCTCGAAATCGTGGGGTCTTGGTCGCTTGCACTGGCATTGGGCATTGAATTA 856	Qy 857 CCGAACCGGGGTCCGCTTGCGGGGGCCATCCTAACCATGGCATTTAAGAAGATCCTAA 916	QY 917 GTTAAAGAACATTAAAGAGAAATCCCTGGGTGAGCTCATCAACATTGCTCCAACGATGG 976 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	GCAGAGAATGTTTGAGGCAGCCGTTGGCAGCCTGCTGGCTG
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Submitted (10-JUJ-1997) Toshihiro Suzuki, National Cancer Center
Submitted (10-JUJ-1997) Toshihiro Suzuki, National Cancer Center
Research Institute, Pharmacology Division; Tsukiji 5-1-1, Chuo-ku,
Tokyo 104, Japan (E-mall: Issuzuki@gan2.res.ncc.go.jp,
Tel:03-3542-2511, Fax:03-3542-1886)
Location/Qualifiers
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Ikeuchi,T., Tanabe,S., Terada,M. and Saijo,N.

CDNA cloning of a short type of multidrug resistance protein homologue, SMRP, from a human lung cancer cell line
Biochem. Biophys. Res. Commun. 238 (3), 790-794 (1997)
                                                TGCCCATCGCCTGCACACGGTTCTAGGCTCCGATAGGATTATGGTGCTGGCCCAGGGACA
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DPLSALDAHVGNHIFNSAIRKHLKSKTVLFVTHQLQYLVDCDEVIFMKEGCITERGTH
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EROGLVOLEERGOGSYPWSYTGYY I QAAGGPLAFLY I NALLEMLNYGSTRFSTWMLSSYN
I KOGSGNTYYTRGRETS VSDSMKNDPHMOY YAS I YALSWAVMLILKAI RGVVFVKGTL.
RASSRLHDELFRRILRSPMKFFDTT PTGRILNRFSKDDMDEVDVRLPFQARMFIONYIL
                                                                                                                                                                                                                                                                                                                                                               MIVLMHGQIPPAYAGLAISYAVQLTGLFQFTVRLASETEARFTSVERINHYIKTLSLE
APARIKNKAPSPDWPQEGEVTFENAEMRYRENLPLVLKKVSFTIKPKEKIGIVGRTGS
                                                                                                                                                                                                                                                                                                                           VFFCVGMIAGVFPWFLVAVGPLVILFSVLHIVSRVLIRELKRLDNITQSPFLSHITSS
IQGLATIHAYNKGQEFLHRYQELLDDNQAPFFLFTCAMRWLAVRLDLISIALITTTGL
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CKILILDEATAAMDTETDLLIQETIREAFADCTMLNIAHRLHTVLGSDRIMVLAQGQV
                                                                                                                                                                           PHOAVLAEOKGHLLLDSDERPSPEEEGKHIHLGHLRLQRTLHSIDLEIQEGKLVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="SMRP"
737. .3577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTAAATTTATCAAAATGTATGCCTGGGTCAAAGCATTTTCTCAGAGTGTTCAAAAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGCTTCGATCTGACAGCAGCATTTCACAGTGGTGACAGTCTTCAATTCCATGACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 80.4%; Score 4691.6; DB 9; Length 4939; Best Local Similarity 97.6%; Pred. No. 0; Matches 4819; Conservative 0; Mismatches 4; Indels 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        VEFDTPSVLLSNDSSRFYAMFAAAENKVAVKG
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1224 c 1249 g 129
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Dp	541	CAGATTTAAGCTTCCTTCCACT	009
Οy	1528		1527
οp	601	TAGGCTTGTCTCCCTGGTCTTGATCCAGTGTCTCATCTTTG	099
δ δ	1528	STTTGTTTCTAATGGAAGAGGTTCACATGATAAAGAACAAACCAGCAG	1582
Qy Qy		CAGAGATT GOTTO CLAMIGGAAGAGGITCACATGATGAAGAACAAACCAGCCAGTC ATCAAGATAGAGATGAAAAATGCCACCTTGGCATGGGACTCCTCCCACTCCAGTA	/20 1642
qq	721	SAAGATAGATGAAAATGCCACCTTGGCATGGGACTCCTCCCACTCTAFTI	780
Oy B	1643	SCTGACCCC	1702
δy		SAAGGTGAGGCAGCGCACTGAGCATCAGGCGGTGCTGGCAGAGCAG	
qa	841	TGCAGGGCACTGAGCAT	Ō
Qy	9	ACCTCCTCCTGGACAGTGACGAGGGGCCCAGT	1822
QQ	0	GGCCACCTCCTCGACAGTGACGGGCCCCAGTCCCGAAGAGGAAGAGGCAAGC	096
Qy Dp	1823	$\tilde{n} - \tilde{n}$	1882
Οy	1883	GAGGGTAAACTGGTTGGAATCTGCGGCAGTGTGGGAAGTGGAAAAACCTCTCTCATTT	1942
QQ	1021	AGAGGGTAAACTGGTTGGAATCTGCGGGAGTGTGGGAAAAACCTCTCTCATTC	1080
O. O.	1943	ITTAGGCCAGATGACGCTTCTAGAGGCAGCATTGCAATCAGTGGAAC 	2002
Qy .	0	CTG	2062
QQ		TATGTGGCCCAGCAGGCCTGGATCCTCAATGCTACTCTGAGAGACAACATCCTGTTTG	1200
Qy	2063	ATATGATGAAGAAAGATACAACTCTGTGCTGAACAGCTGCTGCTG. 	2122
ΟŸ	2123	TGGCCATTCTTCCCAGCAGCACCTGACGAGATTGGAGAGCGAGGAGCCAACCTGA	-
qq	1261	CCTGGCCATTCTTCCCAGCACCTGACGGAGATTGGAGAGCGAGGAGCCAGCTGAG	1320
Qy	2183	TGGGCAGCGCCAGAGGATCAGCCTTGCCCGGGCCTTGTATAGTGACAG	2242
qq	1321	GGTGGGCAGCCCAGAGGATCAGCCTTGCCCGGGCCTTGTATAGTGACAGGAGCATCT	1380
δŏ	4	CCTGGACGACCCCCTCAGTGCCTTAGATGCCCATGTGGGCAACCACTTT	2302
QQ	38	ATCCTGGACGCCCCCCAGTGCCCTTAGATGCCCATGTGGGCAACCACATCTTCAATA	44
δλ.	0	ACATCTCAAGTCCAAGACAGTTCTGTTTGTTACCCACCAG	2362
Q	44	GCTATCCGGAAACATCTCAAGTCCAAGACAGTTCTGTTTGTT	1500
ος C	2363	IGAA	
3 6		201100C101001001001C11C4104440600C1014114C0C44440400CC	'n
දු දු	1561	CCATCAGGAACTGATGAATTTAAATGGTGACTATGCTACCATTTTTAITAATAACTGGTTGGT 	2482
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	3623 C	2761 C	3683 C	2821 C	3743 C	2881 C	3803 G	2941 G	3863 A	3001 A	3923 C	3061 C	3983 A	3121 A	4043 A	3181 A	4103 T	3241 T	4163 C	3301 C	4223 A	3361 A	4283 T	3421 T	4343 G	3481 G	m	3541 T	4463 T	3601 T	4523 G	3661 G	4583 TC	_	4643 AT	3781 A
	Óγ	qa .	ΟŻ	qq	ΟŊ	qq	Qy	qq	Οy	qq	ΟŊ	qa	. Qy	QΩ	ογ	qq	οy	qq	Qy	qq	QY	QQ	QY	QQ	QY	qq	ΟŊ	qq	δλ	qq	ΟŊ	QΩ	ΟY	qa	δĀ.	qq
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GAAGAA	GCCAGA	GCCAGA	AGTATA	AGTATA	CTTTT	CCTTTT			CATGAA	CATGAA	CATGCT	CATGCT	TCCCG									CCTCTTTTC														
GITCACA	CAGTAAA	CAGTAAA	CTGGTC	CTGGTC	PTATGGG	TATEGE	ACTGGAT	ACTEGRAT	STGACAG	IIIIII STGACAGO	rescaeto		SAGCTTC	AGCTTC	TTTTGA	TTTTGAC	TGACGTO	TGACGTC	CTGTGTG	CTGTGTC	OHOUTEO.	Greatecte	GGACAAT	GGACAAT	CACCATO	CACCATO	TGACAAC	TGACAACCAAGC	GGACCTC	GGACCTC	GCAGATT	GCAGATT	GTTCCAG	GTTCCAG	GATCAAT	GATCAAT
ACCAGIG	GAAAAAG	SAAAAAG	rcagigo	I I I I I I I I	CTGGTTA	TILLILL	PTGAGTT	TGAGTT	rcggrga	CGGTGA	TCTCCA	TCTCCA	ACGCTGC	ACCCTCC	TGAAGT		ATGAAGI		TGTTCT	FGTTCT	CCCTTGT	CCCTTGT	AGCGTC1	AGCGTCT	GCCTIGC		TGCTGGA	TGCTGGA	TGCGGCT	GIGCGCCIGGACCICAICAG	TGCACGG	TGCACGG	CGGGGCT	CGGGGCT	TGGAGAG	 TGGAGAG
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ATTCAAA	SATCAGT.	IIIIII SATCAGI	AGAAAGG	IIIIIII AGAAAGG	SCCCCTT	SCCCTT	CAGCAC	CAGCAC	3AGGGAA(BAGGGAAG	CAGCATO	CAGCATO	CTTTGT	CTTTGT	CCTTCG	CCTTCGZ	TTCCAA	TTCCAA	GAACGTI	GAACGT	TGTGGCA	TGTGGC	GATTCGG	GATTCG	GTCCAGC	GICCAGO	CAGATAC	CAGATAC	GCGGTGG		GATGATC		TGCTGTC	TGCTGTC	TCGATTC	TCGATTC
SAGATCA	AAAAÇAG	AAAACAG	TGGAAG	HIIIII TGGAAG	CTGGGGG	CTGGGGG	CCGCCT	CCGCCT	TGACTCC	TGACTCC	ACTATGO	ACTATGO	GAGTTG	GAGTTGT	GAAGGAT	GAAGGAT	ACAGGTI	ACAGGTI	TCATCCA	TCATCCA	GGTTCCT	GGTTCCT	GGGTCCI	GTCCTGCACATTGTCTCCAGGGTCCTGATT	ACATCAC	ACATCAC	TTCTGCA	TTCTGCA	GTGCGAT		CGGGGCT	CGGGGCT	TCTCTTA	ILLILL	CAGAAGC	CAGAAGC
GCCAGTTC	GGTCCT	GGTCCTA	GTGCAGG	GEGCAGO	CAGGCTG	CAGGCTC	GGCAGCA	GGCAGCA	ACCACTG	ACCACTG	ATGCAGT	ATGCAGI	ATTCGAG		CTTTTCC		ATTCTCA		GAGATGT	GAGATGT	TTCCCGT	TCCCGT	STCTCCA	STCTCCA	CTCTCCC	TOTOCC	CAGGAGT	CAGGAGT	FTTACGT	FTTACGT	ACCACCA	ACCACCA	CTCGCCA	TCGCCA	rctgaga	FI I I I I I I I
BACACC	AGACAAG	AGACAAG	GCAGCTI	GCAGCTI	CTACATC	CTACATO	GAATGTA	GAATGTA	CGGGAAC	CGGGAAC	TCCTCAT		GAAAGCC	SAAAGCC	FGACGAG	 GACGAG	AGGGAGG	AGGGAGG	CAGGCC	CAGGCC	AGGAGTC	AGGAGTC	CACATT	SCACATE	ACCTTTC	ACCTTTC	PAAAGGG	AAAGGG	TTTTTG	TTTTTC	CTCATC	CTCATC	GCGGGT	GCGGGT	CTGGCA	CTGGCA
GGGAGA				GGAAGG		TGGTGTC	CATGCT	CATGCTGAATG	4	— «	GGACAA	GGACAA	GATCCT	GATCCTC	GCTGCA	GCTGCA!	CCCCAC	CCCCAC	GCCGTTC	GCCGTTC	GATCGCA	GATCGC	AGTCCTG	AGTCCTG	GCAGTCA	GCAGTCA	CTACAAT	CTACAAT	TCCTTT	TCCTTTT	CATCGCC	CATCGCC	AGCCTAT	AGCCTAT	GGTCAGA	GGTCAGA
1621	. 2543	1681	2603	1741	2663	1801	2723		2783	1921	2843	1981	2903	2041	2963	2101	3023	2161	3083	2221	3143	2281	3203	2341	3263	2401	3323	2461	3383	2521	3443	2581	3503	2641	3563	2704
Ωp	Οy	QQ	δ	Ob	Qy	g	δy	QQ	ΟŸ	q	δλ	qq	δ	q	δŏ	qq	δλ	QQ	ò	g	ô	g	οχ	οg	δÿ	qq	οy	g	οy	qq	ογ	Op	οy	Dp	δy	qq

CCGAAGCAAACTCTCTATCATTCCTCAAGAGCCGGTGCTGTTCAGTGGCACTGTCAGATC CTGGCCCCCAGGAGGAGGAGGTGACCTTTGAGAACGCAGAGATGAGGTACCGAGAAAACCT CCCTCTTGTCCTAAAGAAAGTATCCTTCACGATCAAACCTAAAGAGAGATGGCATTGT GGGGCGGACAGGATCAGGGAAGTCCTCGCTGGGGATGGCCCTCTTCCGTCTGGTGGAGTT TGGGGATAACTICTCAGTGGGGAACGGCAGCTCTTGTGCATAGCTAGAGCCCTGCTCCG CCACTGTAAGATTCTGATTTTAGATGAAGCCACAGCTGCCATGGACACAGAGACTT IGCTGCTGCAGAGAACAAGGTCGCTGTCAAGGGCTGACTCCTCCTCCTGTTGACGAAGTCTC TTTTCTTTAGAGCATTGCCATTCCCTGCGTGGGGGGGCCCCCTCATCGCGTCCTCCTACC SAAACCTTGCCTTTCTCGATTTTATCTTTCGCACAGCAGTTCCGGATTGGCTTGTGTTT CACTTTTAGGGAGAGTCATATTTGATTATTGTATTTATTCCATATTCATGTAAACAAA ITTAGTTTTTGTTCTTAATTGCACTCTAAAAGGTTCAGGGAACCGTTATTATAATTGTA

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AB020209 5744 bp mRNA linear ROD 07-JAN-2000 Rattus norvegicus mRNA for multidrug resistance protein (MRP5),
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Ecodaletarregiscldisyhshiolideeprkgkyhhgisalkpfrttrhohpvd
Bagefsymtpsmlspladyhkkgellembdwybtskyrssobvcrrlerragenev
Gpdaserrwwhicktrytlsivchaftolagesgpafvykhlileytogatesnloys
Lilvigilltevvrswslallymafvrgvrlrgavilmafkkilikknikeksigel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INICSNDGQRNFEAAAVGSLLAGGPVVAILGMIYNVIILGPTGFLGSAVFILFYPAMM
FVSRLTAFRRKCVAATDDRVQKMBYLTAIRFRWAVAWFSBCVCVGKTBEBERIL
FVSAGYFOSITVGVAPTPVVAIASVYFESYHMTLGFDLTAAQAFTVVTVRNSMTFALKVT
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IHAGSBHKLQPFLYFUTDLEIEBEKLVGITGSCYGSGKFSLISAILGQMTLLEGSIRAVGGT
FAYVAQQAMILNATLRDNILEGKEFDEERNNSVLNSCCLRPDLAILPNSDLTEIGERGKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANLSGGGQRQRISLARALYSDRSIYILDDPLSALDAHVGNHIFNSAIRKRLKSKTVLFV
THQLQYLVDCDEVIFMKEGCITERGTHEELMNLNGDYATIFNNLLLGETPPVEINSKK
EASGSQKSQDKGPKPGSVKKEKAVKSEEGQLVQVEEKGGGSVPWSVYWYIQAAGGPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AFLVIMVLEMLNVGSTAFSTWALSYNIKQGSGNSTVFEGNRSSYSDSMRDNPFLQYYA
SIYALSMAVMLILKAIRGVVFVKGTLRASSRLHDELFRRILKSPMKFFDTTPTGRILN
RFSKDMDEVDVRLPFQAEMFIQNVILVFFCVGMIAGVFPWFLVAVGFLLILFSVLHIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SRVLIRELKRLDNITQSPFLSHITSSIQGLATIHAYNKRQEFLHRYQELLDDNQAPFF
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EVMENGDNFSVGERQLLCIARALLRHCKILILDEATAAMDTETDLLIQETIREAFADC
TMLTIAHRLHTVLGSDRIMVLAQGQVVEFDTPSVLLSNDSSRFYAMCAAAENKVAVKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LFTCAMRWLAVRLDLISIALITTTGLMIVLMHGQIPSAYAGLAISYAVQLTGLFQFTV
RLASETEARFTSVERINHYIKTLSLEAPARIKNKAPPHDWPQEGEITFENAEMRYREN
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                                                                                                                                                                                                                                               to mRNA.
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Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (17-NOV-1998) Masashi Homma, Graduate School of Pharmaceutical Sciences, University of Tokyo, Department of Biopharmaceutics; 7-3-1 Hongo, Bunkyo-ku, Tokyo 113-0033, Japan (E-mail: homma@seizai.f.u-tokyo.ac.jp, Tel:81-3-5802-2045,
                                                                                                                                                         complete cds.
AB020209
AB020209.1 GI:6682826
multidrug resistance protein (MRP5); MRP5.
Rattus norvegicus (strain:Sprague-Dawley) male brain cDNA
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                                                                                                                                                                                                                                                                                                                                                        Homma, M., Suzuki, H. and Sugiyama, Y. Rat MRP5 complete cDNA sequence Published Only in DataBase (2000)
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Suzuki,T., Kuh,H. and Nishio,K.
Direct Submission
Submitted (20-607-1998) Toshihiro Suzuki, National Cancer Center
Research Institute, Pharmacology Division; Tsukiji 5-1-1, Chuo-ku,
Tokyo 104-0045, Japan (E-mail:tssuzuki@gan2.res.ncc.go.jp,
Tel:81-3-3542-2511(ex.461), Fax:81-3-3542-1886)
Location/Qualifiers
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Suzukl,T., Sasaki,H., Kuh,H.J., Agui,M., Tatsumi,Y., Tanabe,S.,
Terada,M., Saijo,N. and Nishio,K.
Detailed structural analysis on both human MRP5 and mouse mrp5
transcripts
Gene 242 (1-2), 167-173 (2000)
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/db_xref="taxon:10090"
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EKAGYFQSITVGVAPIVVVIASVVTFSVHWTLGFHLTAAQAFTVVTVFNSMTPALKVT
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FAYYAQOMILLMATRADNILFGKEEDEERYNSVLNSCCLRPDLAILDNSDITEIGERG
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THQLQYLVDCOPETEMREGGITERGTHBELANILNGDYATIRFNLLLGETPPPVEINSK
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LFTCAMMWLPVRLDIISLATISTSJGGLATHATNATRYCBLLHDRYCBLLDDNQAPFF
LFTCAMMWLPVRLDIISLTSSTGGLATHATNATRYCBLCHRARY
RLASETEARFTSVERINHYIKTLSLEAPARIKNKAPPHDWPOGGEVTFENAEMRYREN
LADLTSTGLALITSTGGLATUSGWARSLSAY AGLAISY SAVOLIGLFOFFVV
RLASETEARFTSVERINHYIKTLSLEAPARIKNKAPPHDWPOGGEVTFENAEMRYREN
LADLKKVSFTIRFRKENIGTYGRTGSGKSSIGMALERTHMKECIAQLPLKLES
EVWENGDNFSVGEROLLCIARALLRHCKILLDEATAANADPETDLLIQELYLKLES
EVWENGDNFSVGEROLLCIARALLRHCKILLLDEATAANADPETDLLIQUPLKLES
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Oude, E.R., Paulusma, C.C.,
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          Patent: WO 9731111-A 62 28-AUG-1997;
INTROGENE BV (NL)
Other publication AU 1736697 19970910.
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Other publication AU 1736697 19970910.
Location/Qualifiers
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Oude, E.R., Paulusma, C.C., Bosma, P.J.,
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. D AGAGGGCTGTATTACGGAAAGAGCCACCATGAGGAACTGATGAATTTAAATGGTGACT	6 TGCTACCATTTTTAATAACCTGTTGCTGGGAGAGACACCGCCAGTTGAGATCAATTCAAA 	AAAGGAAACCAGTGGTTCACAGAAGAAGTCACAAGACAAGGGTCCTAAAACAGGATCAGT	6 AAAGAAGGAAAAACAGTAAAGCCAGAGGAAGGGCAGCTTGTGCAGCTGGAAGAGAAAGG 	6 GCAGGGTTCAGTGCCCTGGTCAGTATAGGTGTCTACATCCAGGCTGCTGGGGGCCCCTT	6 GGCA-TICCTGGTTATTATGGCCCTTTTCATGCTGAATGTAGGCAGCACCGCCTTCAG	3 CACCTGGTGGTTGAGTTACTGGATCAAGCAAGGGGGAACACCACTGTGACTCGAGG 	3 GAACGAGACCTCGGTGAGTGACAGCATGAAGACAATCCTCATATGCAGTACTATGCCAG 	3 CATCTACGCCCTCTCCATGGCAGTCATGCTGATACGTGAAAGCCATTCGAGGAGTTGTCTT	3 TGTCAAGGGCACGCTGCGAGCTTCCTCCCGGCTGCATGACGAGCTTTTTCCGAAGGATCCT	3 TCGAAGCCTATGAAGTTTTTGACACGACCCCCACAGGAGGATCTCAACAGGTTTTC	3 CAAAGACATGGATGAAGTTGACGTGCGGCTGCCGTTCCAGGCCGAGATGTTCATCCAGAA 	3 CGTTATCCTGGTGTTCTTCTGTGGGAATGATCGCAGGAGTCTTCCCGTGGTTCCTTGT	3 GGCAGTGGGGCCCCTTGTCATCTCTTTTCAGTCCTGCACATTGTCTCCAGGGTCCTGAT	3 TCGGGAGCTGAAGCGTCTGGACAATATCACGCAGTCACCTTTCCTCTCCCACATCACGTCC	3 CAGCATACAGGGCCTTGCCACCATCCACGCTACAATAAAGGGCAGGAGTTTCTGCACAGG	a ataccaggagctgctggatgacaaccaagctcctttttttt	3 GTGGCTGGCTGTGCGGCTGGACCTCATCAGCATCGCCCTCATCACCACCACCGGGGCTGAT	GATCGTTCTTATGCACGGCAGATTCCCCCAGCCTATGCGGGTCTCGCCATCTTATG
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Mammallas Eutherlas) Primates; Catarrhini; Hominidae; Homo.

I (bases I to 15907)

Muzny, D. M., Adama, C., Adio-Odola, B., Ali-Osman, F. R., Allen, C., Alabrooks, S. L., Amaratunge, H. C., Are, J. R., Ayele, M., Bonnin, D., Balbaroaks, S. Bricken, M., Brown, E., Brown, M., Barks, T., Balbaroaks, S. Bricken, M., Brown, E., Brown, M., Baryalt, N. P., Balbay, C., Burchl, P., Burkett, C., Burrell, K. L., Dayrd, N. C., Carron, T. E., Carron, M., Dayrd, N. C., Chen, R., Chen, S., Chowdry, I. Christopoulos, C., Chen, R., Chen, C., Coyle, M. D., Dathone, S. R., Dayrd, R., Dayrd, C., Dayrd, M. D., Delaney, K. R., Deladoco, Denn, A. L., Ding, Y., Duth, H. H., Delaney, K. R., Deladoco, Denn, A. L., Ding, Y., Duth, H. H., Delaney, K. R., Derger, H., Dayan Rocha, S., Durbin, K. J., Earnhart, C., Edgar, D., Edwards, C. C., Elhaj, C., Escotto, M., Falls, T., Edwards, C. C., Elhaj, C., Escotto, M., Falls, T., Gorrell, J. H., Guevara, W., Gunarathe, P., Hale, S., Hamilton, K., Harrandez, O., Hodgson, A., Hogues, M., Holles, M., Harrandez, J., Harrandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Harriss, K., Harrandez, O., Hodgson, A., Hogues, M., Holloway, C., Hamilton, K., Jacobson, B., Jia, Y., Johnson, R., Johlivet, S., Joudah, S., Kally, S., Khan, U., King, L., Kovrah, J., Kovar, C., Krafsvor, E., Kelly, S., Khan, U., King, L., Kovrah, J., Kovar, C., Kratovt, J., Kureshi, A., Mann, U., King, L., Kovrah, J., Maylen, B., Martinez, E., Machell, A., Martin, R., Massey, E., Mawhiney, R., Machill, T., Mathage, M., Mayle, P., Mattin, R., Massey, E., Mawhiney, R., Mattin, R., Massey, E., Mawhiney, R., Mayler, P., Markson, J., Lu, J., Liu, J., Liu, R., Mayler, P., Markson, J., Moster, M., Nayen, R., Massey, E., Mathiney, R., Mathiney, R., Noldew, R., Nelle, M., Mayler, R., Parkson, L., Sodet, G., Many, S., Stone, R., Mang, C., Many, S., Stone, R., Wall, Man, M., K., Wu, Y., Wa
                                                                                                                                                                                                                                                                                                                                                                                                                                      ACL31160 159070 bp DNA linear HTG 17-AUG-2002 HOMO Sapiens clone RP11-449K6, *** SEQUENCING IN PROGRESS ***, 13
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Submitted (17-AUG-2002) Human Genome Sequencing Center, Department
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                         3593 ATTCACCTCGGTGGAGAGGATCAATCACTACATTAAGACTCTGTCCTTGGAAGCACCTGC
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     Medicine,
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                                                                                                                                          Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 150858 bases at least Q40
Consensus quality: 122515 bases at least Q30
Consensus quality: 153446 bases at least Q20
  Baylor College of USA
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unknown length
                                                                 Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
------ Project Information
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 and Human Genetics,
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standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URE: http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annot
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Muzny, D.M., Adams, C., Adio-Oddola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, Enenton, J., Binge, K., Blankenburg, K., Bonnin, D., Burbaria, Benton, J., Binge, K., Blankenburg, K., Bonnin, D., Burbaria, Eneton, J., Binge, K., Brown, E., Brown, M., Bryant, N.P., Burbaria, E., Barter, M., C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Charce, D., Carron, T.F., Chen, S., Chodhry, I., Christopoulos, C., Carron, T.F., Chen, C., Coyle, M.D., Dathorne, S.R., David, R., David, M.L., Davy, Carroll, L., Dederich, D.A., David, M.L., Draper, H., Duyan Rocha, S., Durbin, K.J., Douthwaite, K.J., Draper, H., Duyan Rocha, S., Durbin, K.J., Douthwaite, K.J., Draper, H., Duyan Rocha, S., Durbin, K.J., Erlagado, O., Denn, A.L., Ding, Y., Dinh, H. H., Douthwaite, K.J., Brander, P., Hales, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hakes, M., Hell, M., Harris, C., Howarz, M., Guneratne, P., Hales, S., Hamilton, K., Harris, C., Howarz, M., Guneratne, P., Hales, S., Hamilton, K., Harris, C., Howarz, M., Guneratne, J., Hang, M., Johnson, R., Johnson, R., Johlson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Locier, R., Luda, M., Louise, R., Luna, R., Louise, R., Luna, M., Louise, R., Luna, R., Martin, R., Shogan, J., Martin, R., Shogan, J., Martin, R., Shogan, R., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens 3 BAC RP11-315J22 (Roswell Park Cancer Institute Human BAC Library) complete sequence.
Db 127525 GTTGCTGTGTGTTTGGTGTTTCCCGCAAACCCCCTTTGTGCTGTGGGGCCTGGTAGCTC 127466
                                                                                                                                                                                                                                                              Db 127465 AGGTGGGCGTGGTCACTGCTGTCATTGAATGGTCAGCGTTGCATGTCGTGACCAAC 127406
                                                                                                                                                                                                                                                                                                                                                                                           Db 127405 TAGACATTCTGTCGCCTTAGCATGTTTGCTGAACACCTTGTGGAAAGCAAAAATCTGAAAA 127346
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Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                      5714
                                                                                                                                                                                                                                                                                                                                                             5715 TAGACATTCTGTCGCCTTAGCATGTTTGCTGAACACCTTGTGGAAGCAAAAATCTGAAAA 5774
                                                                                                                                                                                                                            5655 AGGIGGCGTGCTCACTGCTCATCAGTTGAATGGTCAGCGTTGCATGTCGTGACCAAC
                                                                                                  GTTGCTGTGTGTTTGGTGTGTTCCCGCAAACCCCCTTTGTGCTTTGGGGCTGGTAGCTC
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Mammalia; Eutheria;
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                                 Db 127585
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KEYWORDS
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Location/Qualifiers

1. .178688

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CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STSS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of Sequence similarity are identified by BLAST (Nuc. Acids Res. 25:338)-3402) similarity (expect < 1e-34) to the EST and CDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (21-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 178688)
                                                                                                                                                                                                                             Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (14-ANG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                   Submitted (06-MXY-2000) Human Genome Sequencing Center, Departmen of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               On Aug 14, 2002 this sequence version replaced gi:21490042. INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email gc-help@bcm.tmc.edu
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Direct Submission
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Direct Submission
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1 (bases 1 to 4101)
Turner,C.A., Mathur,B., Wang,X., Abuin,A., Friedrich,G.B., Zambrowitzcz,B. and Sands; A.T.
Human transporter proteins and polynucleotides encoding the same Patent: WO 0157214-A 43 09-AuG-2001;
Lexicon Genetics Incorporated (US)
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                                                 TGGTGGAGTTATCTGGAGGCTGCATCAAGATTGATGGAGTGAGAATCAGTGATATTGGCC 3912
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BH795205 K-EST0076
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BM795207 K-EST0076
BM79607 K-EST0076
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Allikmets, R., Gerrard, B., Hutchinson, A. and Dean, M.
Characterization of the human ABC superfamily: isolation and mapping of 21 new genes using the expressed sequence tags database Hum. Mol. Genet. 5 (10), 1649-1655 (1996)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Allkmets, R., Gerrard, B. and Dean, M.
Direct Submission
Submitted (12-AUG-1996) Human Genetics Section, National Cancer Institute, NCI-FCRDC, Frederick, MD 21702, USA
                                                                                                                                                                                                                              BI524575 (BO575809 IBG328614 (
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Homo sapiens clone EST90757 mRNA sequence.
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1. .1977

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BASE COUNT 450 a 537 c 513 g 469 t 8 others ORIGIN	Query Match (34.4%; Score 1749.4; DB 11; Length 1977; Best Local Similarity 96.7%; Pred. No. 0; Matches 1889; Conservative 0; Mismatches 49; Indels 15; Gaps 10;	3134 TTGCACCAGGCACTGCTGCACAACAAGATACGCTCGCCACAGTCCTTTTGACACCACCACACACA	3194 CCATCAGGCCGCATCCTGAACTGCTTCTCCAAGGACATCTATGTCGTTGATGAGGTTC 3251	3252 TGGCCCTGTCATCCTCAT-GCTGCTCAATTCCTTCAACGCCATCTCCACTCTTGTG 3310	3311 GTCATCATGGCCAGCACGCCGCTCTTCACTGTGGTCATCCTGCCCCTGGCTGTGCTC 3367 11111111111111111111111111111111111	3368 -TACACCTTAGTGCAGCGCTTCTATGCAGCCACATCACGGCAACTGAAGCGGCTGGAATC 3426	3427 AGTCAGCCGCTCACCTATCTACTCCCACTTTTCGGAGACAGTGACTGGTGCCAGTGTCAT 3486	7. 3487 CCGGCCTACACCGCAGCCGGATTTTGAGATCATCAGTGATACTAAGGTGGATGCCAA 3546 	3547 CCAGAGAAGCTGCTACCCCTACATCATCTCCAACCGGTGGCTGAGCATCGGAGTGGGATT 3606 11111111111111111111111111111111111	3607 CGTGGGGAACTGCGTGGTGCTCTTTGCTGCACTATTGCCGTCATCGGGAGGAGCAGCCT 3666	3667 GAACCCGGGGCTGGTGGGCCTTTCTGTGTCCTACCTGCAGGTGACATTTGCTCTGAA 3726	3727 CTGGATGATACGAATGATGTCAGATTTGGAATCTAACATCGTGGCTGTGGAGGGTCAA 3786 	3787 GGAGTACTCCAAGACAGAGACAGAGGCGCCCTGGGTGGAAGGCAGCCGCCCTCCGA 3846	3847 AGGTTGGCCCCACGTGGGGAGGTGGAGTTCCGGAATTATTCTGTGCGCTACCGGCCGG	3907 CCTAGACCTGGTGCTGAGACCTGAGTCTGCATGTGCACGTGGCGAGAAGGTGGGGAT 3966 	3967 CGTGGGCCGCACTGGGGCTGGCAAGTCTTCCATGACCCTTTGCCTGTTCCGCATCCTGGA 4026	4027 GGCGGCAAAGGGTGAAATCCGCATTGATGGCCTCAATGTGGCCAGACATCGGCCTCCATGA 4086 	4087 CCTGCGCTCTCAGCTGACCATCATCCCGAGGACCCCATCCTGTTCTCGGGGACCCTGCG 4146
B7		Qy Db	S S	S G	Oy Db	Oy Db	cy Ga	oy Op	Qy Dp	Oy Op	64 Pp	QZ	QY Db	oy Op	Q D	Oy Db	O _Y	δλ

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BO941613 920 bp mRNA linear EST 21-AUG-2002 AGENCOURT_8826379 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:6421421

5', mRNA sequence BQ941613

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BM924812
AGENCOURT_6653905 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5761266
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1 (bases 1 to 1098)

NIH-MGC http://mgc.nci.nih.gov/.

National institutes of Health, Mammalian Gene Collection (MGC)

LOnpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: pooled colon, kidney, stomach; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); source anonymous pool of 3 colons, age 26 yo male, 49
            3250 TCTGGCCCCTGTCATCCTCATGCTGCTCAATTCCTTCTTCAACGCCATCTCCACTTGT
                                                                                                                                                         3310 GGTCATCATGGCCAGCACGCCGCTCTTCACTGTGGTCATCCTGCCCCTGGCTGTGTCTA
                                                                                                                                                                                                                                CAGCCGCTCACCTATCTACTCCCACTTTTCGGAGACAGTGACTGGTGCCAGTGTCATCCG
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BM924812.1 GI:19375191
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TITLE
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GGCACGAG(G). Library constructed by ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC_Library."
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                                                 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 920)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                              Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLCM556 row: m column: 06
High quality sequence stop: 742.
Location/Qualifiers
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Pred. No. 3.7e-184;
0; Mismatches 7;
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Homo
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/db_xref="taxon:9606"
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5', mRNA sequence.
BQ227366
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Best Local Similarity 98.7%;
Matches 849; Conservative (
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female, 71 yo male colon; 46 yo male kidney, and pool of stomachs, 62 yo male and 70 yo female. Library is oligo-dr primed and directionally cloned (BcoRv site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and carriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH,MGC Library."
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                                                                                                                  Score 843.6; DB 14;
Pred. No. 1.1e-177;
0; Mismatches 44;
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                                                                                                                                                                                                                                                                                                                                                                                                     Euteleostomi;
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13327 row: m column: 01
GGCCTCCCGCGAGGACCAGGTGCTGGGGGCCCCGGGCCCCAGGCCCCGGAAGCCCCTCC
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/clone_lib="NH_MGC_68"
/lisque_type="large cell carcinoma"
/lab_host="DH108 (phage-resistant)"
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Pred. No. 1e-172;
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60275456F1 NIH_MGC_19 Homo sapiens CDNA clone IMAGE:4891237 5',
mRNA sequence.
BI196662
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NHF-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammallan Gene Collection (MGC) Unpublished (1999)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incytte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCN1769 row: o column: 14
High quality sequence stop: 799.
Location/Qualifiers
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                                                                                         CTGCTTCAGGGAGAAACCTCCATTTTTCTCGGCAAAGAATGTCGACCCTAACCCTACCC
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
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/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_19"
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/lbl.nost-branch neuroblastoma"
//lbl.nost-branch hyll B (phage-resistant)"
//note-"Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2: BcoRI; cDNA made by oligo-dr priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIL_MGC Library."
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                            Site_2:
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98.8%;
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AGENCOURT_10032885 NIH_MGC_40 homo sapiens cDNA clone IMAGE:6481379 5', mRNA sequence. BQ936868 BQ936868 1 GI:22352251 EST.
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1 (bases 1 to 96).

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999).

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLCM2662 row: k column: 12
High quality sequence stop: 565.
Location/Qualifiers
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                                                                                                         GGCCCCTGCCCCTGTTTTCTTTGTCACCCCCTTGGTGGTGGGGGGGTCACCATGCTGCTGGC
                              GCTGTGGTGCGTCTCCTGGGCGGACCTTTTTTACTCCTTCCATGGCCTGGTCCATGGCCG
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                                                                                                                                                                               BI761935 959 bp mRNA linear EST 25-SEP-2001 603048767F1 NIH_MGC_116 Homo saplens cDNA clone IMAGE:5188984 5',
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                                                                                                                                                                                                                                                                                                                                                                                                      Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I. M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMINI.gov
Ecolomics top: 832.
Location/Qualifiers
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 959)
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5188984"
/clone_lib="NHFMGC_ll6"
/lab_host="DH108"
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1. 969

/ Organism="Homo sapiens"
//db_xref="taxon:966"
//db_xref="taxon:966"
//clone="InAGE:648179"
//clone=lib="NIH_MGC_40"
//tissue_type="carcinoma" cell line"
//lab_host="DBLOB (phage-resistant)"
//lab_host="DBLOB (phage-resistan
                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4326 TCCGCAAGAGCCGCATCCTGGTTTTAGACGAGGCCACAGCTGCCATCGACCTGGAGACTG 4385
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                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                         Length 969;
                                                                                                                                                                                                                                                                                                                                                                                                                                   13; Indels
                                                                                                                                                                                                                                                                                                                                                                                         15.3%; Score 779.2; DB 14; 98.3%; Pred. No. 2.6e-163;
                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                   798; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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BQ687464 888 bp mRNA linear EST 15-JUL-2002
AGENCOURT_8058516 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6206756
5', mRNA sequence.
BD687464.1 GI:21812780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI; Site_2: ECORI; CDNA made by oligo-dT priming.

Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH_MCC Library."
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                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 888)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGAGGGTCAAGGAGTACTCCAAGACAGAGACAGAGGCGCCCTGGGTGGTGGAAGGCAGCC 3836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: McC.clone distribution information can l
found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLCM2361 row: 1 column: 21
High quality sequence stop: 707.
I. 9888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AGAGGGTCAAGGAGTACTCCAAGACAGAGACAGAGGCGCCCTGGGTGGTGGAAGGCAGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone='InAGE:6206756"
/clone='InH_WGC_IIO"
/tissue_type="ductal carcinoma, ce}
/lab_host="DHIOB (phage-resistant)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 773; DB 14;
Pred. No. 6.2e-162;
0; Mismatches 31;
                        5046 TAAAAATGGGAGTACTGATGAAATAAAACTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.2%;
95.6%;
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/clone="INAGE:625004"
/clone="INAGE:625004"
/clone_lib="NIH_MGC_110"
/tissue_type="ductal carcinoma, cell line"
/lab_host="ductal carcinoma; cell line"
/lab_host="DH108 (phage-resistant)"
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAGCAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
76 a 264 c 268 g 190 t
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                                                                                                                                                                                                                                                                                                Length 898;
                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                            Score 708.2; DB 14;
Pred. No. 1.9e-147;
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                                                                                                                                                                                                                                                                                                                            0; Mismatches
1. .898
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                            13.9%;
98.8%;
                                                                                                                                                                                                                                                                                           Query Match 13.9
Best Local Similarity 98.8
Matches 724; Conservative
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                                                                                                                                                                                                                                             176
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I (bases 1 to 898)

NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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                                                               TGACCATCGCACCGCCTTAACACTATCATGGACTACACGGGTCCTGGTCCTGGACA
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
AGENCOURT_8171427 NIH_MGC_110 Homo sapiens 5', mRNA sequence.
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DEFINITION

RESULT 9 BQ690370

ACCESSION

VERSION KEYWORDS SOURCE

ORGANISM

AUTHORS TITLE JOURNAL

COMMENT

FEATURES

REFERENCE

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KEYWORDS
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sapiens cDNA clone IMAGE:5212832 5',
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Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostoo
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 776)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMIS34 row: g column: 09
High quality sequence stop: 775.
I. 776/Qualifiers
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Pred. No. 1,3e-143;
0; Mismatches 5; Indels (
                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                                                                                              Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
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/clone="IMAGE:5212832"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="leukocyte"
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                                                                       603063536F1 NIH_MGC_118 Homo
                                                                                                                   BI907445.1 GI:16170278
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99.3%;
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Matches 694; Conservative
                                                                                        mRNA sequence.
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/organism="Homo.sapiens"
/db.xref="taxon:9606"
/clone="InAGE:6480462"
/clone="InAGE:6480462"
/clone="InAGE:6480462"
/clone="InAGE:6480462"
/clone="InAGE:6480462"
/lab_host="blul0b" (phage-resistant)"
/note="Organ: prostate; Vector: pOTB): Site_1: XhOI;
Site_2: EcoRI; cDNA made by oligo-dT.priming.
Directionally cloned into EcoRIXXhOI sites using the following 5' adaptor: GGACAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library." 6 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BQ944733 956 bp mRNA linear EST 21-AUG-2002
AGENCOURT_10038014 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:6480462
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                       CACCCTGCTGATACAGTATGAGCGGCTGCAGGGCGTACAGTCTTCGGGGGGTCCTCATTAT
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GGCCCCTGCCCCTGTTTTCTTTGTCACCCCTTGGTGGTGGGGGGTCACCATGCTGGT
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High quality sequence stop: 591.
Location/Qualifiers
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Contact: Robert Strausberg, Ph.D.
Emall: cgapbs-rémail.nih.gov
Tissue Procurement: DCTD/DTP
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UI-HED1-axx-m-22-0-UI.s1 NCI_CGAP_ED1 Homo sapiens cDNA clone
BQ009190
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                           4146
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                             4027 GGCGGCAAAGGGTGAAATCCGCATTGATGGCCTCCAATGTGGCAGACATCGGCCTCCATGA 4086
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                                                          1 GGGGGAAAGGGTGAAATCCGCATTGATGGCCTCAATGTGGCAGACATCGGCCTCCATGA
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                                                                                                                                        CATGAACCTGGACCCCTTCGGCAGCTACTCAGAGGAGGACATTTGGTGGGCTTTGGAGCT
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 Length 956;
                        Indels
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Pred. No. 5.8e-143;
0; Mismatches 4;
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tch 13.5%;
al Similarity 99.3%;
701; Conservative
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Unpublished (1997)
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 Query Match
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/dev_stage="Adult"
//dev_stage="Adult"
//dev_stage="Adult"
//dev_stage="Adult"
//dev_stage="Adult"
//dev_stage="Adult"
//dote="Organ: Left Pubic Bone; Vector: pT7T3-Pac
//note="Organ: Left Pubic Bone; Vector: pT7T3-Pac
(Pharmacia) with a modified polylinker; Site_1: EcoR I;
Site_2: Not I; NCI_GGAP_EDI is a normalized cDNA library
containing the following tissue(s): Chondrosarcoma cell
line CS5. The library was constructed according to Bonaldo
/ Lennon and Soares Genome Research, 6:791-806, 1996.
First strand CDNA synthesis was primed with an oligo-dr
primer containing a Not I site. Double stranded cDNA was
ligated to an EcoR I adaptor, digested with Not I, and
cloned directionally into pT7T3-Pac vector: The
oligonuciacotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT18 tail. The
sequence tag for this library is GCTCAAGGCT.
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                        Tissue Procurement: Dr. Jöse Mercuende
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
POLYA-Yes.
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Pred. No. 1.7e-142;
                                                                                                                                                                                                                                                                                                                                                                           /clone="IMAGE:5835069"
/clone_lib="NCI_CGAP_ED1"
/tissue_type="Chondrosarcoma"
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TAG_SEQ=CGTCAAGGCT"
148 c 171 g 201
                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                 Location/Qualifiers
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AUTHORS
TITLE
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SOURCE
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/ Organism="Homo saplens"

/ Organism="Homo saplens"

/ Clone="InACE:484036"

/ Clone="InACE:484036"

/ Clone="Ib="NIH_MGC_43"

/ Lissue="Ype="normal pigmented retinal epithelium"

/ Lab_host="BH108 (phage-resistant)" ite_1: XhoI; Site_2:
ECORI: CDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAGGO, Library constructed by Ling
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. | " (Life Technologies).
                                                                                                                                                                                                                                                                                                                BG750831 680 bp mRNA linear EST 15-MAY-2001 602707348F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4844026 5',
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: Arcc

cDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLCM1680 row: p column: 11

High quality sequence stop: 677.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 680)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                   4990
 TCAAATAACGATTTTATGAAATGACCTCTGTCCTCCTCTGATTTTTCATATTTTTTAAA 4930
                                                                                                                               GTCAGGCCACCCTAGGAACTCAGTCCTGTACTCTGGGGTGCTGCCTGAATCCATTAAAA 5050
                    3465 CAGTGACTGGTGCCAGTGTCATCCGGGCCTACAACCGCAGCCGGGATTTTGAGATCATCA
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                                                                GTTTCGTTTCTGTTTTTAATAAAAGCTTTTTCCTCCTGGAACAGAAGACAGCTGCTGG
                                                                                                                                              Length 680;
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100.0%; Pred. No. 1e-140;
iive 0; Mismatches 0;
                                                                                                                                                                                               ATGGGAGTACTGATGAAATAAAACTACA 5078
                                                                                                                                                                                                                mRNA sequence.
BG750831
BG750831.1 GI:14061484
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AUTHORS
TITLE
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KEYWORDS
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602726915F1 NIH_MGC_15 Homo sapiens CDNA clone IMAGE:4866603 5', BG803723 SER 22-MAY-2001 BG803723 GI:14171310 EST.
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I (bases I to 1047)

S NIH-MGC http://mgc.nci.nih.gov/.

I (bases I to 1049)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: Arc.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: NIH Intramural Sequencing Center

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
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TGCAGGTGACATTTGCTCTGAACTGGATGATACGAATGATGTCAGATTTGGAATCTAACA
                                                                                                                                                                                                                                              GGCTGAGCATCGGAGTTCGTGGGGAACTGCGTGGTGCTCTTTGCTGCACTATTTG
                                                                                                                                          CCGTCATCGGGAGGAGCAGCCTGAACCCGGGGCTGGTGGGGCCTTTCTGTGTCCTACTCCT
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High quality sequence stop: 712.
Location/Qualifiers
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us-09-647-140a-5.rst

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10;
                                          /tissue_type="adenocarcinoma cell line"
/lab_host="NH10B (phage-resistant)"
/note="Organ: colon; Vector: porPB; Site_1: XhoI; Site_2:
/note="Organ: colon; Vector: porBB; Site_1: XhoI; Site_2:
/note_"Organ: colon; Vector priming. Directionally
cloned into EcoRI/XhoI sites using the following 5/
cloned into EcoRI/XhoI sites using the following 5/
adaptor: GGCAGGAG(G). size-selected >SODbp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"
258 C
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                                                                                                                                                                                                                                                              Score 664.4; DB 12;
Pred. No. 1.3e-137;
0; Mismatches 151;
                                 /clone_lib-"NIH_MGC_15"
/db_xref="taxon:9606"
/clone="IMAGE:4866603"
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83.8%;
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Matches 873; Conservative
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BI524575 793 bp mRNA linear EST 29-AUG-2001
603051980T1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5201898 3',
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                                                                                    4285
                                                                                                                                                                                                                                                                                 GTGGGCCAGAGGCAGCTCGTGTGCCTGGCCC--GAGCCCTGCTCCGCAAGAGCCGCATCC 4343
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                                                                                                                                                                                               Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoston
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 79)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11505 row: o column: 19
                        GCTACTCAGAGGAGACATTTGGTGGGCTTTGGAGCTGTCCCACCTGCACGTTTGTGA
                                                                                    GCTCCCAGCCGGCAGGCCTGGACTTC----CAGTGCTCAGAGGGCGGGGAGAATCTCAGC
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Pred. No. 2.1e-137;
0; Mismatches 23;
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/clone_lib="NIH_MGC_122"
/lab_host="DH10B"
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High quality sequence stop: 783.
Location/Qualifiers
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                                      .398 AGGCTACCACCACCCACTTTGATACCTGCACTGTCCTGACCATGCACACGGCTTA
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/cgn2_6/ptodata/1/pubpna/PCT_ Database :

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES	
		dР				
Result		Query	1	2	ç	
	acor e	March	acca bengua be	97	TD	Description
. 1	1749.4	34.4	1977	10	US-09-954-456-804	Sequence 804, App
7	1749.4	34.4	1977	10	US-09-880-107-3407	Sequence 3407, Ap
٣	1749.4	34.4	1977	10	.US-09-967-768A-190	Sequence 190, App
4	1408.6	27.7	1448	10	US-09-925-299-157	Sequence 157, App
2	1094.8	21.6	5300	10	US-09-880-107-3373	Sequence 3373, Ap
9	1034	20.4	4918	10	US-09-917-800A-1578	Sequence 1578, Ap
7	1030.2	20.3	5728	10	US-09-917-800A-479	
80	982	19.3	1019	10	US-09-925-297-247	Sequence 247, App
٥ ص	418	8.2	418	10	US-09-998-598-2049	_`
10	407	8.0	419	10	US-09-998-598-175	Sequence 175, App
11	386	7.6	1936	10	US-09-880-107-3832	Sequence 3832, Ap
12	354	7.0	4551	9	US-09-938-842A-1674	Sequence 1674, Ap
13	335.2	9.9	418	φ	US-10-042-125A-32	Sequence 32, Appl
14	326	6.4	4872	6	US-09-938-842A-436	Sequence 436, App
15	311	6.1	329	10	US-09-864-761-16892	Sequence 16892, A
16	297.2	5.9	4545	σ	US-09-938-842A-55	Sequence 55, Appl
17	280	5.5	496	10	US-09-864-761-51	Sequence 51, Appl
.18	279.4	5.5	3786	φ	US-10-012-896-1006	Sequence 1006, Ap

Sequence 1007, Ap

US-10-012-896-1007

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Sequence 536, App Sequence 536, App Sequence 536, App Sequence 1392, App Sequence 535, App Sequence 535, App Sequence 535, App Sequence 964, App Sequence 964, App Sequence 1375, App Sequence 12655, App Sequence 11775, App Sequence 11775, App Sequence 11775, App Sequence 11771, App Sequence 11771, App Sequence 11771, App Sequence 824,	Sequence 824, App Sequence 824, App Sequence 1, Appli Sequence 3, Appli Sequence 603, App Sequence 1560, Ap
9 US-10-012-896-536 10 US-09-759-143-536 10 US-09-82-827-536 9 US-09-938-842A-1392 9 US-10-12-896-535 10 US-09-938-842A-1392 10 US-09-789-143-535 10 US-09-789-143-535 10 US-09-802-827-535 10 US-09-804-761-585 10 US-09-864-761-585 10 US-09-864-761-585 10 US-09-864-761-585 10 US-09-864-761-13775 10 US-09-864-761-13775 10 US-09-864-761-13775 10 US-09-864-761-13775 10 US-09-864-761-13775 10 US-09-864-761-13775 10 US-09-864-761-13775 10 US-09-864-761-13775 10 US-09-864-761-13775 10 US-09-954-456-1571 10 US-09-954-456-1571 10 US-09-954-456-1571 10 US-09-959-138-447	10 0S-09-822-827-824 10 0S-09-822-827-824 10 0S-09-769-097-1 10 0S-09-560-863-603 10 0S-09-917-800A-1560
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ALIGNMENTS

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GENERAL INFORMATION:

APPLICANT: Young, Paul
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-76
CURRENT FILING DATE: 2001-09-18
PRIOR FILING DATE: 2001-09-18
PRIOR FILING DATE: 2000-09-18
                                                                                                                                                                                                                                                                                                                                                                   PRIOR PLLING DATE: 2000-09-10
PRIOR PELING DATE: 2000-09-20
PRIOR PELING DATE: 2000-09-20
PRIOR PLLING DATE: 2000-09-25
PRIOR PILING DATE: 2000-09-25
PRIOR PELING DATE: 2000-09-25
PRIOR PELING DATE: 2000-09-26
PRIOR PELING DATE: 2000-09-27
US-09-954-456-804
; Sequence 804, Application US/09954456
; Patent No. US20020115057A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
; OTHER INFORMATION: n=a,t,g or c
US-09-954-456-804
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SOFTWARE: Patentin version 3.0
SEQ ID NO 804
LENGTH: 1977
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               49;
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0; Mismatches
 1749.4;
 Score
34.4%;
96.7%;
         Matches 1889; Conservative
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US/09880107 Sequence 3407, Application US/C Patent No. US20020142981A1 GREMAL INFORMATION: APPLICANT: Horne, Darci T. APPLICANT: Scherf, Joseph G: APPLICANT: Scherf, Uwe APPLICANT: Gene Logic, Inc. Ö US-09-880-107-3407

Gene Logic, Inc.

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TITLE OF INVENTION: Gene Expression Profiles in FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: U.S/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR APPLICATION NUMBER: US 60/237,054
SPINGR APPLICATION NUMBER: US 60/237,054
SPINGR PILING DATE: 2000-10-02
SOFTURE: Patentin Ver: 2.1
SOFTURE: Patentin Ver: 2.1
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                                                                                                                                                                                                          34.4%; Score 1749.4; 96.7%; Pred. No. 0;
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Matches 1889; Conservative
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; LOCATION: (1).(1968)
; OTHER INFORMATION: n = a
US-09-880-107-3407
                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
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	RESULT 3 US-09-967-768A-190 ; Sequence 190, Application US/09967768A ; Patent No. US20020150877A1 ; Fatent INFORMATION: ; APPLICANT: Augustus, Meena	; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu; TITLE OF INVENTION: Sets; FILE REFERENCE: 689290-72; CURRENT APPLICATION NUMBER: US/09/967,768A; CURRENT FILING DATE: 2001-09-28; PRIOR APPLICATION NUMBER: US/60/236,109; PRIOR FILING DATE: 2000-09-28	PRIOR FILING DAMER: US/60/236,034	; TYPE: DNA ; ORGANISM: Homo sapiens ; FRATURE; ; NAME/KEY: misc_feature ; LOCATION: (1)(1977) ; OTHER INFORMATION: n=a,t,g or c US-09-967-768A-190	Query Match 34.4%; Score 1749.4; DB 10; Length 1977; Best Local Similarity 96.7%; Pred. No. 0; 0.0 </td <td>TTC - - -</td> <td>Qy 3311 GTCATCATGGCCAGCACGCCGCTCTTCACTGTGGTCATCCTGCCCCTGGCTGTGGTC 3367 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII</td> <td>6 6 E 4</td>	TTC - - -	Qy 3311 GTCATCATGGCCAGCACGCCGCTCTTCACTGTGGTCATCCTGCCCCTGGCTGTGGTC 3367 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	6 6 E 4

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JEDELICANT: Rosen et al.

TILLE OF INVENTION: Nucleic Acids, Proteins is FILE REPERENCE: PAIO2

CURRENT APPLICATION NUMBER: US/09/925,299

CURRENT FILING DATE: 2001-08-08

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR PILING DATE: 2000-03-08

PRIOR PILING DATE: 1999-03-12

NUMBER: OF SEQ ID NOS: 1556

SEQ ID NO 157

LENGTH: 1448
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Patent No. US20020055627A1
GENERAL INFORMATION:
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; LOCATION: (456)
; OTHER INFORMATION: n equals
US-09-925-299-157
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
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           1020 AAAICCIGGIIGAAGGCICIGIICAAAACTIICIACAIGGIGCICCIGAAAICAIIC 1079
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                                           GCTGCTGGGTCAGGCCACCCCTAGGAACTCAGTCCTGTACTCTGGGGTGCTGCCTGAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1080 CTACTGAAGCTAGTGAATGACATCTTCACGTTTGTGAGTCCTCAGCTGCTGAAATTGCTG
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Sequence 3737, Application US/09880107
Sequence 1873, Application US/09880107
Setent No. US20020142981A1
SEDERAL INFORMATION:
APPLICANT: Wockley, Joseph G.
APPLICANT: Scherf, Uwe
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
STIOR APPLICATION NUMBER: US 60/211,379
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
SOFTWARE PARENT NOS: 3950
SOFTWARE PARENT NOS: 3950
SEQ ID NO 3373
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US-09-880-107-3373
                                                                                    CATTAAAAATGGGAGTACTGATGAAATAAAACTACA 5078
                                                                                                 Query Match
Best Local Similarity 56.81
Matches 2105; Conservative
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                                                                    1500 GTTGGGGTGATGGTGCTTGTAATCCCAATTAATGCGATACTGTCCACCAAGAGTAAGACC
                                                                                                                                                       1490 AACGGCATCAAGGTGCTGAAGCTGTACGCCTGGGAGCCCCAGCTTCCTGAAGCAGGTGGAG
                                            GTCGCTTTCATGGTCTTGCTGATTCCACTCAACGGAGCTGTGGGCCGTGAAGATGCGCGCC
                                                                                                1680 AACCTCCGGAAGAAAGACTCAAGAACCTGCTGGCCTTTAGTCAACTACAGTGTAATA
                                                                                                                                                                                                                                                                                                                                               1800 CTGGTGGATAGCAACAATATTTGGATGCACAAAAGGCCTTCACCTCCATTACCCTCTTC
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ATAGCATGCACTTTCTT 2576	CTGAGATGGGCCCGTAC 2509	TAGAGAAGGATCCTAC 2636	256	269	GIGCAGAGAGAG 2529 GTGAAGAGAGAT 2750	268		TGTCCTCAGATGGGGAG 2749	GGTCCAATGGCAGGCAT 2870	AGAAGGTGCAGGTGACA 2809 				CGATATTCTTCATCATC 3050	### ##################################		 STCAGAGGGACATGAGA 3170	TGATGCTGGCAGCCATG 3097 			SCCGCATCCTGAACTGC 3217 			CAGCACGCCCTTC 3337	34	339	GATGTTTATGTGTCT 3530	TATCTACTCCCACTTT 3457 		
CCCAATGGCCTGTTGAAAGGCAAGACTCGACTCTTGGTTACACATAGCAIGCACTTTCT			CCAGCCCTGCTGCAGCGCAACGGCTCCTTTGCCAACTTTCTCTGCAACTATGCCCCGGAT CAGCCTCTCTCTCTGCAACGCCTCCTTTGCCAACTTTCTCTGCAACTATGCCCCCGAT ACTCCTCTTCTCTCTCTCTTTTCTCTCTTTTCTTT		11 1 1 1 1 1 1 1 1 1			ACCTATGTGGTCCAGAAGCAGTTTATGAGACAGCTG	GAAAGAGAACAGCTTTCGTCGAACACTTAGCCGCAGTTCTAGGTCCAATGGCAGGCA	GGACAGGGTCGGCCTGTACCCCGGAGGCACCTGGGTCCATCAGAGAGGTGCAGGTGACA				TTCTCCATCTACCTGGAGTACCTACAAGCAATAGGATTGTTTTCGATATTCTTCATCATC	CTCCTGTATGTGGGTCAAAGTGGGGCTGCCATTGGAGCCAATGTGTGGCTCAGTGCCTGG	ACAAATGATGCCATGGCAGACAGTAGACAGAACAACATTC		CTGGGCGTCTATGCTTTAGGAATTCTGCAAGGTTCTTGGTGATGCTGGCGCCATG	GCCATGGCAGCGGGGGGCATCCAGGCTGCCCGTGTGTTGCAC		AAGATACGCTCGCCACAGTCCTTCTTGACACCACATCAGGCCGCATCCTGAACTGC	TTCTCCAAGGACATCTATGTCGTTGATGAGGTTCTGGCCCCT		AATTCCTTCTAACGCCATCTCCACTCTTGTGGTCATCATGGCCAGGCGCGCTCTTC	ACATGCTTCCTGGGGATAATCAGCACCCTTGTCATGATCTGC;	ACTGTGGTCATCCTGCCCCTGGCTGTGCTCTACACCTTAGTGCAGCGCTTCTATGCAGCC	ACCATCATCGTCATTCCTTGGCATTATTTATGTATCTGTT(ACATCACGGCAACTGAAGCGGCTGGAATCAGTCAGCCGCTCACCTATCTACTCCCACTTT	TCGGAGACAGTGACTGGTGCCAGTGTCATCCGGGCCTACAACC	ACCGAGACCGTATCAGGTTTGCCAGTTATCCGTGCCTTTGAGCACCAGCAGTTTTTGTG
2517	2450	2577	2510	2570	2697	2630	2751	2690	2811	2750	2810	2931	2870	1662	2930	2990	3111	3038	3098	3231	3158 3291	3218	3351	278				3398 2	3458	3591
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3637 3697 3830 3757 3817 3950 3877 4007 4067 3997 3878 CGGAATTATTCTGTGCGCTACCGGCCGGGCCTAGACCTGGTGCTGAGAGACCTGAGTCTG 3937 4127 ATGACCCTTTGCCTGTTCCGCATCCTGGAGGCGGCAAAGGGTGAAATCCGCATTGATGGC 4057 4117 4247 4307 4367 4297 4427 4177 4237 4298 CAGCTCGTGTGCCTGGCCCGAGCCCTGCTCCAAGAGCCGCATCCTGGTTTTAGACGAG 4357 4487 4417 4547 AACCGGTGGCTGAGCATCGAGTGGAGTTCGTGGGGAACTGCGTGGTGCTCTTTGCTGCA CATGTGCACGGTGGCGAGAAGGTGGGGATCGTGGGCCGCACTGGGGCTGGCAAGTCTTCC ATCATCAGTGATACTAAGGTGGATGCCAACCAGAGAAGCTGCTACCCCTACATCATCTCC TACTCCTTGCAGGTGACATTTGCTCTGAACTGGATGATACGAATGATGTCTGGAA TGGGTGGTGGAAGGCAGCCGCCCTCCCGAAGGTTGGCCCCCACGTGGGGAGGTGGAGTTC CTATTTGCCGTCATCGGGAGGAGCAGCCTGAACCCGGGGCTGGTGGGCCCTTTCTGTGTCC TCTAACATCGTGGCTGTGGAGGGTCAAGGAGTACTCCAAGACAGAGACAGAGGGGGCCCC GAGGAGGACATTTGGTGGGCTTTGGAGCTGTCCCACCTGCACGTTTGTGAGCTCCCAG CTCAATGTGGCAGACATCGGCCTCCATGACCTGCGCTCTCAGCTGACCATCATCCCGCAG CCGGCAGGCCTGGACTTCCAGTGCTCAGAGGGCGGGGAGAATCTCAGCGTGGGCCAGAGG AGGGTCCTGGTCCTGGACAAAGGAGTAGTAGCTGAATTTGATTCTCCAGCCAACCTCATT GCCACAGCTGCCATCGACCTGGAGACTGACCATCCAGGCTACCATCCGCACCCAG TITGATACCTGCACTGTCCTGACCATCGCACGCGCTTAACACTATCATGGACTACACC GCAGCTAGAGGCATCTTCTACGGGATGGCCAGAGATGCTGGACTTG 4583 3698 3518 3651 3578 3638 3771 3758 3818 3998 3938 4068 41.88 4118 4248 4058 4178 4368 4238 4428 4358 4488 4418 4548 4478 4608 4538 Q οq δý Db Ω Q οy q δ Ω Qγ g ŏ qq ŏ g Qγ qq δ qq g ò ò qq ò qq Qγ QΩ g ò ŏ g Qγ qq δ g

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM_012833 US-09-917-800A-1578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24;
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                                                                                                                                                                                        APPLICANT: Elashoff, Aichael
APPLICANT: Elashoff, Michael
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5038-US
CURRENT FILING DATE: 2001-07-31
PRIOR PAPLICATION NUMBER: US 60/222,040
PRIOR FILING DATE: 2000-07-31
PRIOR PAPLICATION NUMBER: US 60/222,040
PRIOR FILING DATE: 2000-11-02
PRIOR FILING DATE: 2001-05-11
PRIOR FILING DATE: 2001-05-12
PRIOR FILING DATE: 2001-05-13
PRIOR FILING DATE: 2001-05-15
PRIOR FILING DATE: 2001-05-15
PRIOR FILING DATE: 2001-05-22
PRIOR FILING DATE: 2001-06-13
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55.8%; Pred. No. 5.5e-250;
iive 0; Mismatches 1615;
Sequence 1578, Application US/09917800A
Patent No. US20020119462A1
                                                                                                                                                Johnson, Kory
Castle, Arthur
Elashoff, Michael
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Best Local Similarity 55.8*
Matches 2067; Conservative
                                                       GENERAL INFORMATION: APPLICANT: Mendrick, Donna
                                                                                                                        Porter, Mark
                                                                                                                                          APPLICANT:
APPLICANT:
                                                                                                                    APPLICANT:
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Oy Dp	2450 C 1 2558 C	CCCCAGACAGACTICATCATTGIGGTAGCIGACAGGIGTCIGAGAIGGGCCGTAC 25:	2509
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δy	2990 A	ACAAATGATGCCATGGCAGACAGTAGACAGACACTTCCCTGAGG 303	37
QQ	3092 A	AGGGACATGAGA 31	51
Qy Db	3038 C	CIGGECGICTAIGCIGCTITAGGAATICIGCAAGGGITCTIGGIGAIGCIGGCAGCCAIG 3097	97 11
Qy Dp	3098 G	GCCATGGCAGCGGGTGGCATCCAGGCTGCTGCTGCACCAGGCCACTGCTGCACAAC 3157	57
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2 8		ACCTCCGGGCACCCATGAGGTTTTTTGACACCACAGGCCGGATTGTGAGCCGC 321/	31
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g ,	332	TTTCTGGTGATATTCTACTGTGGACGACTTGCTCCCCCAGACACTTCGAAGCTGGATG 3391	9.1
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3577 3691 3637 3697 3811 3988 3458 TCGGAGACAGTGACTGGTGCCAGTGTCATCCGGGCCTACAACCGCAGCCGGGATTTTGAG 3517 3751 3871 3817 3931 3877 3997 4108 4057 4228 4297 4408 3698 TACTCCTTGCAGGTGACATTTGCTCTGAACTGGATGATACGAATGATGTCAGATTTGGAA 3757 CGGAATTATTCTGTGCGCTACCGGCCCGGCCTAGACCTGGTGCTGAGAGACCTGAGTCTG 3937 4117 GAGGAGGACATTTGGTGGGCTTTTGGAGCTGTCCCACCTGCACGTTTGTGAGCTCCCAG 4237 4357 3638 CTATTIGCCGTCATCGGGAGGAGCAGCCTGAACCCGGGGCTGGTGGGCCTTTTCTGTGTCC 3818 TGGGTGGAAGGCAGCCGCCCTCCCGAAGGTTGGCCCCCCACGTGGGGAGGTGGAGTTC ATCATCAGTGATACTAAGGTGGATGCCAACCAGAGAAGCTGCTACCCCTACATCTCC AACCGGTGGCTGAGCATCGGAGTTCGTGGGGAACTGCGTGGTGCTCTTTGCTGCA 3812 AACGCCCTCAATATCACACAAACCTTGAACTGGCTAGTGAGGATGACGTCAGAAGCAGAG TCTAACATCGTGGCTGTGGAGGGTCAAGGAGTACTCCAAGACAGAGACAGAGGCGCCC CATGTGCACGGTGGCGAGAAGGTGGGGATCGTGGGCCCGCACTGGGGCTGGCAAGTCTTCC ATGACCCTTTGCCTGTTCCGCATCCTGGAGGCGGCAAAGGGTGAAATCCGCATTGATGGC CTCAATGTGGCAACATCGGCCTCCATGACCTGCGCTCTCAGCTGACCATCATCCCGCAG CCGGCAGGCCTGGACTTCCAGTGCTCAGAGGGCGGGGAGAATCTCAGCGTGGGCCAGAGG CAGCTCGTGTGCCTGGCCCGAGCCCTGCTCCGCAAGAGCCGCATCCTGGTTTTAGACGAG GCCACAGCTGCCATCGACCTGGAGACTGACAACCTCCAGGCTACCATCCGCACCCAG TTTGATACCTGCACTGTCCTGACCATCGCACACCGGCTTAACACTATCATGGACTACACC AGGGTCCTGGTCCTGGACAAAGGAGTAGTAGCTGAATTTGATTCTCCAGCCAACCTCATT 3518 3758 3878 3989 3938 3998 4109 4058 4238 4349 (4298 (4178 4169 4478 4589 4409 4358 4469 4418 4529 qq οy Ω Dp ò Qγ ΩŸ β Q, ρp ŏ qq Qγ QQ δ qq δy qq Qy dd δλ οp a δ ò Ωp οχ Op δy qq ò qq Qγ qq a δ

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Best Local Similarity 53.4%; Pred. No. 5.5e-249;
Matches 2420; Conservative 0; Mismatches 2013; Indels 102;
GCAGCTAGAGGCATCTTCTACGGGATGGCCAGAGATGCTGGACTTG 4583
                 APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Molecular Toxicology Modeling
                                                                                                                                                                                                                                                                                                    CURRENT PEPLICATION NUMBER: US/09/917,800A
CURRENT PELING DATE: 2001-07-31
PRIOR PEPLICATION NUMBER: US 60/222,040
PRIOR PELING DATE: 2000-07-31
PRIOR PELING DATE: 2000-10-3
PRIOR APPLICATION NUMBER: US 60/222,880
PRIOR PELING DATE: 2000-11-02
PRIOR PELING DATE: 2000-11-02
PRIOR PELING DATE: 2001-05-11
PRIOR PELING DATE: 2001-05-11
PRIOR PELING DATE: 2001-05-12
PRIOR PELING DATE: 2001-05-15
PRIOR PELING DATE: 2001-05-15
PRIOR PELING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: US 60/292,336
PRIOR PELING DATE: 2001-06-06
PRIOR PELING DATE: 2001-06-06
PRIOR PELING DATE: 2001-06-06
PRIOR PELING DATE: 2001-06-06
PRIOR PELING DATE: 2001-06-07
PRIOR PELING DATE: 2001-06-19
PRIOR PELING DATE: 2001-07-09
                                                                                                                     Sequence 479, Application US/09917800A Patent No. US20020119462A1
                                                                                                                                                                                                                                       Elashoff, Michael
                                                                                                                                                                                                                                                                                            FILE REFERENCE: 44921-5038-US
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 479
LENGTH: 5728
                                                                                                                                                                                                                         Castle, Arthur
                                                                                                                                                     GENERAL INFORMATION: APPLICANT: Mendrick, Donna
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APPLICANT: Johnson, Kory
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2719 2675 2779 2600 ACCGCGTTGGAAGGTGCAGAGGATAAGGAGGCACTGCTGATTGAAGACACACTCAGCAAC 2659 2573 ATGGAGCCAGACAGCCTGCAGGCGAAGGAGAAGGAAG------CACATGCTGCAGC 2624 2780 CTGGGTCCATCAGAGAAGGTGCAGGTGACAGGCGAAGGCAAGATGGGGCACTGACCCAG 2839 2899 2959 2904 2960 ATTGGAGCCAATGTGTGGCTCAGTGCCTGGACAAATGATGCCATGGCAGACAGTAGACAG 3019 2964 3020 AACAACATTCCCTGAGGCTGGGGGTCTATGCTGCTTAGGAATTCTGCAAGGGTTCTTG 3079 2844 CAGGCACTGCTGCACAACAAGATACGCTCGCCACAGTCCTTTTGACACCACACCATCA 3199 3260 GTCATCCTCATGCTGCTCAATTCCTTCTTCAACGCCATCTCCACTCTTGTGGTCATCATG 3319 3320 GCCAGCACGCCGCTCTTCACTGTGGTCATCCTGCCCTGGCTGTGTGTCTACACCTTAGTG 3379 3205 AAGATGAGGACCCTGCTGACCTATGGACTCCTGGAGGTTGGCCTGGCAGTGTCG 3264 3265 ATGCCCACACCACTGCTATTGTGGCCATCCTACTCTTATGCTCGGTTT 3324 3440 CCTATCTACTCCCACTTTTCGGAGACAGTGACTGGTGCCAGTGTCATCCGGGCCTACAAC 3499 3325 CAGAGCCTCTACGTGGCCACATGTTGCCAGCTGAGACGCCTGGAGTCGGCCAGTTACTCC 3384 3445 GCCCAGGGGCCCTTCACAGCTCAGCATGCATGGATGAGAACCAGAGGATCAGT 3504 3620 GTGGTGCTCTTTGCTGCACTATTTGCCGTCATCGGGAGGAGCAGCCTGAACCCGGGGCTG 3679 CACACGGATCTGACAGACAATGATCCAGTCACCTATGTGGTCCAGAAGCAGTTTATGAGA 111 | 1 | 1 | 1 | 2625 CACCAGTGATGACTTTGGAGGTGGGACGCCCACGCGCAG------CAGCTGAGTGCCCTGTCCTCAGATGGGAGGGACAGGGTCGGCCTGTACCCCGGAGGCAC 2840 GAGGAGAAAGCAGCCATTGGCACTGTGGAGCTCAGTGTGTTTCTGGGATTATGCCAAGGCC 2735 AGATGG------AGCCTTCTCTGGATGACGTTGAGGTCACTGACTGACAGGA 2785 GAGGACAGTGTGCAGTATGGCCGGGTGAAGAGGGCCACATACCTGAGCTACCTGCGGGCG GTGGGGCTCTGTACCACGCTGGCCATCTGTCTCTCTGTATGTGGGGTCAAAGTGCGGCTGCC GIGATGCTGGCAGCCATGGCCAGCGGGTGGCATCCAGGCTGCCCGTGTTGCAC 3500 CGCAGCCGGGATTTTGAGATCATCATGATACTAAGGTGGATGCCAACCAGAGAAGCTGC 3560 TACCCCTACATCATCTCCAACCGGTGGCTGAGCATCGGAGTGGAGTTCGTGGGGAACTGC 2720 2660 2900 3080 3140 δ QQ δy qq ò do. οy QQ ò qq δ ρp οy QQ ολ Dp οχ α δy g g οy οy QQ ò qq δý qq ŏ g δy q ŏ ò

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Pred. No. 2.8e-237;
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CURRENT APPLICATION NUMBER: US/09/925,297
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05989
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 928
SOFTWARE: PatentIn Ver. 2.0
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Sequence 247, Application US/09925297
Patent No. US20020081659A1
GENERAL.INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies; FILE REFERENCE: PA105

US-09-925-297-247

RESULT 8

59

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CTAAAGITICGTTTCTGTTTTTAATAAAAGCTTTTTCCTCCTGGAACAGAAGACAG 4983
          GCCAGTTAGACTAGTCCCCGGTCTCCCGATTCCCAACTGAGTGTTATTTGCACACTGCAC
                                                       TGTTTTCAAATAACGATTTTATGAAATGACCTCTGTCCTCCCCTCTGATTTTTCATATTT
                                                                     8.0%; Score 407;
99.8%; Pred. No. 8
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US-09-998-598-175
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
es 418; Conserv
                                                                                                                                                                 RESULT 10
US-09-998-598-175
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100.0%; Pred. No. 1.4e-95;
ilve 0; Mismatches 0;
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Patent No. US2002015092A1
GENERAL INFORMATION:
APPLICANT: Stolk, John A.
APPLICANT: Chenault, Ruth A.
TITLE OF INVENTION: DIAGNOSTIONS AND METHODS FOR TITLE OF INVENTION: DIAGNOSTIONS OF COLON CANCER.
FILE REFERENCE: 210121.561
CURRENT APPLICATION NUMBER: US/09/998,598
CURRENT FILING DATE: 2001-11-16
NUMBER OF SEQ ID NOS: 2606
SOFTWARE: COTIXA INVENTION Disclosure Database
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US-09-998-598-2049/c
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; ORGANISM: HOMO :
US-09-998-598-2049
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                                                                                                                                               AND METHODS FOR THE THERAPY
Sequence 175, Application US/09988598
Patent No. US2002015092A1
GENERAL INFORMATION:
APPLICANT: Stolk, John A.
APPLICANT: Chenault, Ruth A.
APPLICANT: Maagher, Madelein Joy
TITLE OF INVENTION: DIAGNOSITIONS AND METHODS FOR TITLE OF INVENTION: DIAGNOSITIONS OF COLON CANCER:
FILE REFERENCE: 210121.561
CURRENT FILING DATE: 2001-11-16
NUMBER OF SEQ ID NOS: 2606
SOFTWARE: COFIXA INVENTION DISCLOSURE Database
SECURAL OF SEQ ID NOS: 2606
SOFTWARE: COFIXA INVENTION DISCLOSURE DATABASE
                                                                                                                                                                                                                                                                                                                                                                                                Score 407; DB 10;
Pred. No. 8.2e-93;
0; Mismatches 0
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Patent No. US20020142981A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                         0
                                      APPLICAMY: Gene Logic, Inc.
TILLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILLE REPERENCE: 4491-5028-W0
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILLING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILLING DATE: 2000-06-14
PRIOR FILLING DATE: 2000-06-14
PRIOR FILLING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PALEATIN VET. 2.1
SEQ ID NO 3832
LENGTH: 1936
                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Genbank Accession No. US20020142981A1 X95715
US-09-880-107-3832
                                                                                                                                                                                                                                                                                                                                                           Length 1936;
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Pred. No. 3.8e-87;
0; Mismatches 420;
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Horne, Darci T.
Vockley, Joseph G.
Scherf, Uwe
                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 60.39
Matches 638; Conservative
                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
                              APPLICANT:
                                                                                                                                                                                                                                                                                           FEATURE:
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APPLICANT: Harper, Jeff
APPLICANT: Harper, Jeff
APPLICANT: Rreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: SAME, AND METHODS OF DEANTS, TRANSGENIC PLANTS CONTAININ
TITLE OF INVENTION: SAME, AND METHODS OF USE
CURRENT APPLICATION NUMBER: US 60/227,866
PRIOR PELING DATE: 2000-08-24
PRIOR PELING DATE: 2001-01-16
PRIOR PELING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-06-22
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4276 GAATCTCAGCGTGGGCCAGAGGCAGCTCGTGTGCCTGGCCCGAGCCCTGCTCCGCAAGAG 4335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 354; DB 9;
Pred. No. 6.9e-79;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1674, Application US/09938842A
Patent No. US20020160378A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Arabidopsis thaliana
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Matches 1671; Conservative
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SEQ ID NO 1674
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US-09-938-842A-1674
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1233 1252 ACTGGGGTGAAGTTTCGTACTGGGATCATGGGTGTCATCTACAGGAAGGCTCTGGTTATC 1192 GCCCAGCGCTTCATGGACCTTGCCCCCTTCCTCAATCTGCTGTGGGTCAGCACCCCTGCAG 1312 1432 1612 1653 1713 1414 ATTGGGCTGACTGGAGTGTTCGTCTTCATCCTCGGGGACTCAGAGAACAACGGTAC 1473 GGCATCAAGGTGCTGAAGCTGTACGCCTGGGGGCCCAGCTTCCTGAAGCAGGTGGAGGGC 1552 1792 1852 1887 2007 2086 2266 TACATGCGAGTCATCAAGTTTCAGGCTTGGGAGAATCATTTTAACAAGAGGATCCTCAAA 1593 TGGGCCC---AGGACCTGCCCCCACTCTGCACACCTAGACATCCAGGTCCCGAAAGG 1966 GAGCTCACTGGGATAGTTGGAACCGTTGGTTCAGGGAAATCTTCTCTGTTAGCTTCGGTT 2067 GCTCAGACGTCGTGGATTGAAAACGGGACGGTTCAAGACAACATCTTGTTTGGTCTTCCA, 2187 GCACAACAGCTCTCTGACATGCTTCAGCTCCACGCAATCTGGCTCATGCCTTTGCAA GAAAGAAAGACCATCCCCCAGGCTATGCCATCACCATACAG---TGGCACCTTCACC GAGAGGCCCTGGGTTGTGATGGTAATACTGCCGTGGAGGTCAGAGATGGAAGCTTTAGT **ACCAACTCAGTCAAACGTGCGTCCACTGTGGGGGAAATTGTCAACCTCATGTCAGTGGAT** GCTTTCATGGTCTTGCTGATTCCACTCAACGGAGCTGTGGCCGTGAAGATGCGCGCCTTC ATCAGGCAGGGTGAGCTCCAGCTGCGCACGGCGGCCTACCTCCACACCACAACCACC TTCAGGGACATGGAGTTTGGTTGGCTATCCAAGTTTCTTTACTCCATTGCTGGCAATATT TTCACCTGGATGTGCAGCCCCTTCCTGGTGACCCTGATCACCCTCTGGGTGTACGTGTAC ATTGTCCTCTGGAGCACGCCAGTGCTTATCTCTGCTCTCACCTTCGCCACCGCCCTTGCC GTGGACCCAAACAATGTGCTGGACGCCGAGAAGGCCTTTGTGTCTGTGTCCTTGTTTAAT ATCTTAAGACTTCCCCTCAACATGCTGCCCCAGTTAATCAGCAACCTGACTCAGGCCAGT GTGTCTCTGAAACGGATCCAGCAATTCCTGAGCCAAGAGGAACTTGACCCCCAGAGTGTG TGGGATGATGAGGACAACGAACCTGCTCTCAGTGATATCAACTTCAAGGTTAAGAAAGGT CTGAACCCCAAGCGCTACCAGCAGACTCTGGAGGCCTGTGCCTTGCTAGCTGACCTGGAG GCACTGGTGGCCGTGGGGCCTGTGGGCTGTGGGAAGTCCTCCCTGGTGTCTGCCCTG CTGGGAGAGATGGAGAAGCTAGAAGGCAAAGTGCACATGAAGGGCTCCGTGGCCTATGTG CCCCAGCAGGCATGGATCCAGAACTGCACTCTTCAGGAAAACGTGCTTTTCGGCAAAAGC 1174 1193 1133 1234 1313 1534 1594 1253 1294 1373 1433 1474 1493 1613 1654 1673 1733 1768 1828 1888 1910 1948 2087 1714 1793 1853 1961 2008 2027 2068 2128 2147 2188 2207 õ g ò g à Q δ g op g qq g ò δ οy ò g δ à g δ g ò g 셤 ŏ οy g δ g a p ò ò 셤 QY ò

CCAAGAACACCAACGTCTCCCCATGCAAGCTCTCCGAGAACGTCAATGGAGTCTCCTCAC 2712 3106 3226 ACAGAGGCGAAGGCAGATGGGGCACTGACCCAGGAGGAGAAAGCAGCCATTGGCACTGTG 2866 3287 TTCAACGCCATCTCCACTCTTGTGGTCATGGCCAGCACGCGCCTCTTCACTGTGGTC 3346 GATGACCACTGTCCGGGTGGACTCTCATGTGGCCAAGCACATCTTTGACCACGTCATCT CAGCGGCAGCGGGTCAGTCTGGCTCGAGCTGTTACAGTGATGCCGATATTTTCTTGCTG GACGATGTTTTTAGCGCAGTGGATGCTCATACCGGTTCAGATATATT-----CAAGAAA TACCCAGCCCTGCTGCAGCGCAACGGCTCCTTTGCCAACTTTCTCTGCAACTATGCCCCC GATGAGGACCAAGGGCACCTGGAGGACAGCTGGACCGCGTTGGAAGGTGCAGAGATAAG GTCACCTATGTGGTCCAGAAGCAGTTTATGAGACAGCTGAGTGCCCTGTCCTCAGATGGG GAGGGACAGGGTCGGCCTGTACCCCGGAGGCACCTGGGTCCATCAGAGAAGGTGCAGGTG GAGCTCAGTGTTCTGGGATTATGCCAAGGCCGTGGGGGCTCTGTACCACGCTGGCCATC CTGTTCTTCTCTGACGTGGCAGGGATCTCTAATGGCCAGCGATTACTGGCTTGCATAC TGGACAAATGATGCCATGGCAGACAGTAGACAGAACAACACTTCCCTGAGGCTGGGCGTC TATGCTGCTTTAGGAATTCTGCAAGGGTTCTTGGTGATGCTGGCAGCCATGGCCATGGCA TATGTAATTATTGCACTTGTTTCCATCGTTTTGGTGAGCATCCGGTCATATTACGTCACC GCGGGTGGCATCCAGGCTGCCCGTGTTGCACCAGGCACTGCTGCACAACAAGATACGC TCGCCACAGTCCTTCTTTGACACCACCATCAGGCCGCATCCTGAACTGCTTCTCCAAG 2927 TGTCTCCTGTATGTGGGTCAAAGTGCGGCTGCCATTGGAGCCAATGTGTGGCTCAGTGCC GACATCTATGTCGTTGATGAGGTTCTGGCCCCTGTCATCCTCATGCTGCTCAATTCCTTC AAACCGGACAGGTTAGCTTAGGAGTTTACAAA------2248 2267 2308 2368 2507 2542 2567 2627 2653 2687 2747 2881 3047 2327 2807 2713 2804 2987 2995 3167 3115 2769 2867 2836 3107 3055 3227 3175 g ò Db Ω q οy qq δy β Q Dp ò Db QY Dρ ò g ŏ g δ g οp δ ò g Qγ q οy g QΥ Q g ò δy ö

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                                                                                             3407 CAACTGAAGCGGCTGGAATCAGTCAGCCGCTCACCTATCTACTCCCACTTTTCGGAGACA
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                               ATCCTGCCCCTGGCTGTGCTCTACACCTTAGTGCAGCGCTTCTATGCAGCCACATCACGG
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APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
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                    4424 ACCTGCACTGTCCTGACCATCGCACACCGGCTTAACACTATCATGGACTACACCAGGGTC 4483
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                                                                                                                                                                                                           Sequence 32, Application US/10042125A
PRECENT NO. US20020164345A1
GENERAL INFORMATION:
APPLICART: Jiang, Yuqiu
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REPERENCE: 210121.557
CURRENT APPLICATION NUMBER: US/10/042,125A
CURRENT FILING DATE: 2001-10-18
NUMBER OF SEC ID NOS: 58
SOFTWARE: FastSEQ for Windows Version 4.0
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6.6%; Score 335.2; DB 9
Best Local Similarity 98.8%; Pred. No. 9.5e-75;
Matches 337; Conservative 0; Mismatches 4
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                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 32
LENGTH: 418
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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                                                                                                                                                                                                                                                                         Score 326; DB 9; Length 4872;
Pred. No. 8e-72;
0; Mismatches 1740; Indels 153;
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: U$/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: U$ 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-06-22
PRIOR FILING DATE: 2001-06-22
SEQ ID NO 436
                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                         Query Match 6.4%;
Best Local Similarity 46.6%;
Matches 1653; Conservative
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                                                                                                                                                                                        LENGTH: 4872
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                                           GGCTATGCCATCACCATACACAGTGGCACCTTCACCTGGG----CCCAGGACCTGCCCCCC
                                                                     ACTCTGCACAGCCTAGACATCCAGGTCCCGAAAGGGGCCACTGGTGGCCGTGGTGGGCCCT
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                             2948 AGTGCGGCTGCCATTGGAGCCAATGTGTGGCTCAGTGCCTGGACAAATGATGCCATGGCA
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APPLICANT: Hanzel, bavid K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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                          TTCCGCATCCTGGAGGCGCCAAAGGGTGAAATCCGCATTGATGGCCTCAATGTGCCAGAC
                                                                                                                            TCGGGGACCCTGCGCATGAACCTGGACCCCTTCGGCAGCTACTCAGAGGAGGACATTTGG
                                                                                             ATCGGCCTCCATGACCTGCGCTCTCAGCTGACCATCATCCCGCAGGACCCCCATCCTGTTC
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PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR PLICATION NUMBER: US 60/207,456
PRIOR PELING DATE: 2000-08-03
PRIOR PELING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR PLING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR PLING DATE: 2001-01-30
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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Patent No. US20020048763A1
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                                   PRIOR PELICATION NUMBER: PCT/USO1/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00653
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR APPLICATION NUMBER: PCT/USO1/00662
PRIOR PELING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: US 06/234,687
LICATION NUMBER: PCT/US01/00665
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PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
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ORGANISM: Homo sapiens
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84 278 144	338 204 398	264	324	384	444	504	564 758	624 818	684	744	788 998	840 1058	885 1118	945 1178	1005	1065
25 CGGGAGCTCGACTTCTGGGACTCCAACCTGTCTGTGCACACACA	279 CTICACCAAGICTITITITICAGACACGGTCCTCGTGTGGGTCCCTTTTTTTTTT	205 CCACCTGTCCAAGGTCAAGATGGTCCTGGGTGCTGCTGGTGCGTCCTCTGGGCGGA	265 CCTTTTTTACTCCTTCCATGCCTGGTCCATGGCCGGCCCCTGCCCCTGTTTTCTTGT	325 CACCCCCTTGGTGGTGGGGTCACCATGCTGGCCACCCTGCTGATACAGTATGAGCG	385 GCTGCAGGGCGTACAGTCTTCGGGGGTCCTCATTATCTTCTGGTTCCTGTGTGTG	445 CGCCATCGTCCCATTCCGCTCCAAGATCCTTTTAGCCAAGGCAGGGTGAGATCTCAGA	505 CCCTTCCGCTTCACCACCTCTACATCCACTTTGCCCTGGTACTCTCTGCCCTCATCTT	565 GGCCTGCTTCAGGGAGAAACCTCCATTTTCTCCGCAAAGAATGTCGACCCTAACCCCTA	625 CCCTGAGACCAGCGCTGTTTCTCCCCGCCTGTTTTCTGGTGGTTCACAAAGATGGC	685 CATCTATGGCTACCGGCATCCCCTGGAGGAGGACCTCTGGTCCCTAAAGGAAGG	745 CAGATCCCAGATGGTGGTGCAGCTGCTGGAGGATGGAGGA	789AGCAGGAAAAGCAGGCACGACACAAGGCTTCAGCAGCCTGGGAAAAA	841 TGCCTCCGGCGAGGACGAGGTGCTGCTGGGTG	886 CCGGAAGCCCTCCTTCCTGAAGGCCCTGCTGGCCACCTTCGGCTCCAGCTTCCTCATCAG	946 TGCCTGCTTCAAGCTTATCCAGGACCTGCTCTTCATCATCCACAGCTGCTCAGCT	1006 CCTGATCAGGTTTATCTCCAACCCCATGGCCCCCTCCTGGTGGGCGCTTCCTGGTGGCTGG
oy oy	9 6 Q	Oy Dp	g 4	o o	yo da	Oy Dp	Oy Db	Qy Dp	Qy Dp	Oy Dp	Qy Dp	Qy	Qy Db	Qy Db	O, Op	oy da'

٥y	106	TGTTCCTGTGCTCCATGATGCAGTCGCTGATCTTACAACACTATTACCACT
QQ	129	CTGCTGTTTGTCACTGCCTGCAGACCCTCGTGCTGCACAGTACTTCCACATCTG 135
oy S	112	GTGAAGTTTCGTACTGGGATCATGGGTGTCATCTACAGGAAGGCTCT
8 8	. II	IIICGICACIGGCAIGAGGAICAAGACCGCIGICAIIGGGGCIGICIAICGAAGGCCCT 141 GTTATCACCAACTCAGTCAAACGTGCGTCCACTGAGGGGAAATGTGAACGAAATGTC 133
q ₀	141	GGTGATCACCAATTCAGCCAGAAAATCCTCCACGGTCGGGGAATGTCAACCTCATGTC 1478
QY	1246	PGGATGCCCAGGGGTTCATGGACCTTGCCCCTTCCTCAATCTGCTGTGGGTCAGCACC 130
qq	1479	
Qγ	1306	CCTGGCGATCTACTTCCTCTGGCAAACCTAGGTCCCTCTGTCCTGGC 13
q	) 1539	CIGCAAGICAIGCTIGCICITAACICCIGGGGCGAAICIGGGCCCITCCGICGGC 159
ΟŊ	1366	STCTTGCTGATTCCACTCAACGGAGCTGTGGCCGTGAAGATGCG 142
qa	1599	GGAGTGGCGGTGATGCTCCTCATGGTGCCTGATGCTGATGGCGATGAGACCAA 16
. Оу	1426	TGAAAATTGAAGGACTCGCGCATCAAGCTGATGAGGTGAGGAT
d G	1659	GTATCAGGTGGCCCACATGAAGAGCAAAGACAATCGGATCAAGCTGATGAACGAAAT 17
Qy	1486	TGAAGCTGTACGCCTGGGAGCCCAGCTTCCTGAAGCAGGT 15
qa	1719	CAATGGGATCAAAGTTTAAAGCTTTATGCCTGGGAGCTGGCATTCAAGGAC
Qy	1546	GGGCATCAGGCAGGGTGAGCTCCAGCTGCGCACGGCGGGCCTACCTCCACACCAC 160
qa	H	
δλ	1606	CCTGGTGACCCTGATCACCCTCTGGGTGTA 1
qa	1839	CACCTICACCTGGGTCTGCACGCCCTTCTGGTGGCCTTGTGCCATTTGCCGTCTA 189
οy	, 1666	CGCCGAGAAGGCCTTTGTGTCTGTGTGCCTT 1
qq	1899	GTGACCATTGACGAGAACAACATCCTGGATGCCCAGACAGCCTTCGTGTCTTTGGCCTT 195
ογ	1	CTGCCCCAGTTAAT
qq	1959	CAACATCCTCCGGTTTCCCCTGAACATTCTCCCCATGGTCATCAGCAGCATCGTGCA 201
δλ	1	ATTCTGAGCCAAGAGGAACTTGACCCCCA 18
qa	C1 .	GGGAGTGTCTCCCTCAAACGCCTGAGGATCTTTCTCTCTC
Qy	~	AGIGIGGAAAGAAAGACCATCTCCCCAGGCTAIGCCATCACCATACACAG 189
q	2079	zarceaeceacecerercaaaeaeeeeeeeeeeacaeaacaecarceereaeaa 2
ΟŊ	, 1897	CCTTCACCTGGGCCCAGGACCTGCCCCCACTCTGCACAGCCTAGACATCCAGGT 1
q _Q	2139	GCCACATTCACCTGGGCCAGGACCACCTCCCACACTGAATGGCATCACCTTCTCCAT 2
Οy	1957	3GTGGCCGTGGGGCCTGTGGGCTGTGGGAAGTCCTCCCTGGT 2
<b>Q</b> O .	2199	CCCGAAGGTGCTTTGGTGGCCGTGGTGGCCAGGTGGGGCTGCGGGAAAGTTGTCCCTG
δλ	2017	SCTGGGAGÀATGGAGAAGCTAGAAGGCAAAGTGCACATGAAGGGCTCCGT 207
QΩ	2259	CAGCCCTCTTGGCTGAGATGGACAAAGTGGAGGGGCACGTGGCTATCAAGGGCTCCGT 23
Oy	. 2077	SCCCAGCAGCATGGATCCAGAACTGCACTCTTCAGGAAAACGTGCTT
QQ	2319	GCCTATGTGCCCACAGCCTGGATTCAGAATGATTCTCTCCGAGAAACATCCTTTT 23
Qy	2137	CGGCAAAGCCCTGAACCCCAAGCGCTACCAGCAGTCTGGAGGCCTGTGCCTTGCTAGC 2196

	197 TGACCTGGAGATGCTGCCTGGGGGATCAGACAGAGATTGGAGAGAGA	957 GTCTGGGGGCCAGCGGGTCAGTCTGGCTCGAGCTGTTTACAGTGATGCCGATAT 2316 	11 TITCITGCTGGATGACCCACTGTCCGCGGTGGACTCTCATGTGGCCAAGCACATCTTTGA 2376	177 CCACGTCATCGGGCCAAAAGGCGTGCTGGCAAGACGCGAGTGCTGGTGACGCACGG 2436 	37 CATTAGCTTCCTGCCCAGACAGACTTCATCATTGTGCTAGCTGATGGACAGGTGTCTGA 2496 	197 GATGGGCCCGTACCCAGCCTGCTGCAGCGCAACGGCTCCTTTGCCAACTTTCTCTGCAA 2556 		17 AGAGGATAAGGAGCACTGCTGATTGAAGACACACTCAGCAACCACGGATCTGACAGA 2676 	7 CAATGATCCAGTCACCTATGTGGTCCAGAAGCAGTTTATGAGACAGCTGAGTGCCTGTC 27   1   1   1   1   1   1   1   1   1	37 CTCAGATGGGGAGGGACAGGGTCGGCCTGTACCCCGGAGGCACCTGGGTCCATCAGAGAA 2796	r 4	57 TGGCACTGTGGAGCTCAGTGTTCTGGGAÝTATGCCAAGGCCGTGGGGCTCTGTACCAC 2916 	17 GCTGGCCATCTGTCTCCTGTATGTGGGTCAAAGTGCGGCTGCCATTGGAGCCAATGTGTG 2976 1	77 GCTCAGTGCCTGGACAAATGATGCCATGGCAGACAGTAGACAGAACACTTCCCTGAG 3036 	37 GCTGGGCGTCTATGCTGCTTAGGAATTCTGCAAGGGTTCTTGGTGATGCTGGCAGCCAT 3096 	97 GGCCATGGCAGCGGGGGGCTCCAGCCGGTGTTGCACCAGGACTGCTGCACAA 3156	57 CAAGATACGCTCGCCACAGTCCTTTGACACCACCACCATCAGGCCGCATCCTGAACTG 3216 1	17 CTTCTCCAAGGACATCTATGTCGTTGATGAGGTTCTGGCCCCTGTCATCCTCATGCTGCT 3276
6	7 6	6	r 6	6 0	7	r 0	6	7 6	2 2	7 6	7 4	۰ م	0 1	۷ 0	7	0 0	0 4	7
qq	Qy	Qy Dp	Oy Dp	Qy Db	Qy Db	Ογ Dp	Oy Dp	Oy Dp	Oy Dp	Qy Db	Qy Db	Qy	Qy Db	oy Db	Oy Op	Q _Y	Qy Db	ογ

3336 3396 3456 3719 3779 3636 3899 3756 3959 3816 4019 3876 4079 3936 4139 3886 4199 4056 4259 4116 4319 4176 4236 CTTCTCCAAGGAGCTGGACACAGTGGACTCCATGATCCCGGAGGTCATCAAGATGTTCAT 3479 4379 4356 4559 TTCCTCCCGGCAGCTGAAGCGCCTCGAGTCGGTCAGCCGCTCCCGGTCTATTCCCATTT CACTGTGGTCATCCTGCCCCTGGCTGTGCTCTACACCTTAGTGCAGCGCTTCTATGCAGC CACATCACGGCAACTGAAGCGGCTGGAATCAGTCAGCCGCTCACCTATCTACTCCCACTT TTCGGAGACAGTGACTGGTGCCAGTGTCATCCGGGCCTACAACCGCAGCCGGGATTTTGA i IIIII IIIIII IIIIII IIIIIII 3720 CCACCAGAGGCCAGCATGGAGGCGGGAGAACCAGAAGGCCTATTACCCCAGCATCGTGGC CAACCGGTGGCTGAGCATCGGAGTGGAGTTCGTGGGGAACTGCGTGGTGCTCTTTGCTGC ACTATITIGCCGTCATCGGGAGGAGCAGCCTGAACCCGGGGCTGGTGGGCCTTTCTGTGTC CTACTCCTTGCAGGTGACATTTGCTCTGAACTGGATGATGATGATGTCAGATTTGGA CTGGGTGGTGGAAGGCAGCCGCCCTCCCGAAGGTTGGCCCCCCACGTGGGGAGGTGGAGTT ATCTAACATCGTGGCTGTGGAGGGTCAAGGAGTACTCCAAGACAGAGACAGAGGCGCC CCTCAATGTGGCAGACATCGGCCTCCATGACCTGCGCTCTCAGCTGACCATCATCCCGCA GGACCCCATCCTGTTCTCGGGGACCCTGCGCATGAACCTGGACCCCTTCGGCAGCTACTC 4177 AGAGGAGGACATITIGGIGGCTTTGGAGCTGTCCCACCTGCACACGTTTGTGAGCTCCCA GCCGGCAGGCCTGGACTTCCAGTGCTCAGAGGGCGGGGAGAATCTCAGCGTGGGCCAGAG GCAGCTCGTGTGCCTGGCCCGAGCCCTGCTCCGCAAGAGCCGCATCCTGGTTTTAGACGA 3420 3480 3337 3540 3397 3600 3457 3277 3900 4080 4140 3997 3517 3577 3637 3697 3757 3960 3817 4020 3877 3937 4200 4057 4260 4117 4320 4380 4237 4440 4297  $\delta \lambda$ QQ qq QQ δ Ω q δ qq δ Dp Qγ g g Ω q qq . q pp ΟY δ οy δ g οy óγ g δ Q δ g ΟÝ a ò g ò 9

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LENGTH: 5011 base pairs
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                            4740 GCAGCAGAGAGGTCTTTTCTACAGCATGGCCAAAGACGCCGGCTTGGTGTGAGCCCCAGA 4799
                                                                                                                                                                                                     4537 TGCAGCTAGAGGCATCTTCTACGGGATGGCCAGAGATGCTGGACTTGCCTAAAATATAT 4596
                                                                                            4620 GTTCGAGGACTGCACCGTCCTCACCATCGCCCACCGGCTCAACACCATCATGGACTACAC
                                                                                                                                                           4357 GGCCACAGCTGCCATCGACCTGGAGACTGACAACCTCATCCAGGCTACCATCCGCACCCA
                                                                                                                                        4477 CAGGGTCCTGGTCCTGGACAAGGAGTAGTAGCTGAATTTGATTCTCCAGCCAACCTCAT
                                                                           GTTTGATACCTGCACTGTCCTGACCATCGCACACCGGCTTAACACTATCATGGACTACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS Queen's University at Kingston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,092B
FILING DATE: 05-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08463092B Patent No. 5766880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/029,340
FILING DATE: 8-MAR-1993
CLASSIFICATION: 435
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FILING DATE: 26-0CT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/407,207
FILING DATE: 20-MAR-1995
CLASSIFICATION: 435
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REGISTRATION NUMBER: 39,539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 545-2342
TELEFAX: (613) 545-6853
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Cole, Susan P.C.
APPLICANT: Deeley, Roger G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Ontario
COUNTRY: CANADA
ZIP: K7L 3N6
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
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APPLICATION NUMBER: (
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                                                                                                                                                                                                                                                                                                    4800 GCTGGCATATC 4810
                                                                                                                                                                                                                                                                    4597 CCTGAGATTTC 4607
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kingston
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US-08-463-092B-1
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1059 TTCCAAGGTGGATGCGAATGAGGAGGTGGAGGCTTTGATCGTCAAGTCCCCACAGAAGGA 1118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     625 CCCTGAGACCAGGGCTGGCTTTCTCCCGGCTGTTTTCTGGTGGTTCACAAAGATGGC 684
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                                                                                                                                                               DB 1;
                                                                                                                                                          Score 1737.8; DB 1;
Pred. No. 0;
0; Mismatches 1662;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGCCTCCGCCGAGGACGAGGTGCTGCTGGGTG----
                                                                                                                                                            34.2%;
                                                                                                                                                                          Best Local Similarity 62.2
Matches 2882; Conservative
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                     CDS
196..4788
                                                MOLECULE TYPE: CDNA FEATURE:
                                   linear
                                   TOPOLOGY:
                                                                                   ; NAME/KEY:
; LOCATION:
US-08-463-092B-1
                                                                                                                                                             Query Match
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GGCTCCAGCTTCCTCATCAG 945                            GGGCCTACTTCTCATGAG 1178	AATCCACAGCTGCTCAGCAT 1005. 	TGGGGCTTCCTGGTGGCTGG 1065 	CAACACTATTACCACTACAT 1125                      CACCAGTACTG 1358	GTCATCTACAGGAAGGCTCT 1185 	GAAATTGTCAACCTCATGTC 1245 	AATCTGCTGTGGTCAGCACC 1305                         AACATGATCTGGTCAGCCCC 1538	CTAGGTCCCTCTGTCCTGGC 1365 	GCTGTGGCCGTGAAGATGCG 1425 	ATCAAGCTGATGAGTGAGAT 1485 	CCCAGCTTCCTGAAGCAGT 1545 	SCGGCCTACCTCCACACAC 1605                 CTGCCTACCTGTCAGCCGT 1838	CTGATCACCTCTGGGTGTA 1665 	SCCITTGTGTCTGTGTCCTT 1725 	TTAATCAGCAACCTGACTCA 1785 	DAAGGAACTTGACCCCA 1845 	-TATGCCATCACCATACACAG 1896 	CACAGCCTAGACATCCAGGT 1956
CCGGAAGCCCTCCTTCCTGAAGGCCCTGCTGGCCACCTTCGGCTCCAGCTTCCTCATCAG	TGCCTGCTTCAAGCTTATCCAGGACCTGCTCCTTCATCAATCCACAGCTGCTCAGCAT	CCTGATCAGGTTTATCTCCAACCCCATGGCCCCTCCTGGTGGGGCTTCCTGGTGGCTGG	GCTGATGTTCCTGTGCTCCATGATGCAGTCGTGATCTTACAACACTATTACCACTACAT	CTTTGEGACTGGGGTGAAGTTTCGTACTGGGATCATGGGTGTCATCTACAGGAAGGCTCT	GGTFATCACCAACTCAGTCAAACGTGCGTCCACTGTGGGGGAAATTGTCAACCTCATGT/ 	AGTGGATGCCCAGCGCTTCATGGACCTTGCCCCCTTCCTCAATCTGCTGTGGTCAGCACC	CCTGCAGATCATCCTGGCGATCTACTTCCTGGCAGAACCTAGGTCCCTCTGTCCTGGC	TGGAGTCGCTTTCATGGTCTTGCTGATTCCACTCAACGGAGCTGTGGCCGTGAAGATGCG 	CGCCTTCCAGGTAAAGCAAATGAAGGACTCGCGCATCAAGCTGATGAGTGAG	CCTGAACGGCATCAAGGTGCTGAAGCTGTACGCCTGGGGAGCCCAGCTTCCTGAAGCAGGT 	GGAGGGCATCAGGCAGGGTGAGCTCCAGCTGCGCACCGCGGGCTACCTCCACACCAC 	AACCACCTICACCTGGATGTGCAGCCCCTTCCTGGTGACCTGATCACCCTCTGGGTGTA	CGTGTACGTGGACCCAAACAATGTGCTGGACGCCGAGAAGGCCTTTGTGTCTGTGTCTTTTCTTTTTTTT	GTTTAATATCTTAAGACTTCCCCTCAACATGCTGCCCCAGTTAATCAGCAACCTGACTGA	GGCCAGTGTGTCTGTGAAACGGATCCAGCAATTCCTGAGCCAAGAGGAACTTGACCCCCA 	GAGTGTGGAAAGAAGACCATCTCCCCAGGCTATGCCATCACCATACAGGG	TGGCACCTTCACCTGGGCCCAGGACCTGCCCCCCACTCTGCACAGCCTAGACATCCAGGT
886	946	1006	1066	1126	1186	1246	1306	1366	1426 1659	1486	1546	1606 1839	1666	1726	1786 2019	1846	1897
Qy Db	Qy	Qy Db	Qy Db	Qy Db	Oy Dp	Oy Dp	QQ.	OY DD	Qy Dp	Oy Dp	Qy	QY Dp	Qy Db	Qy Dp	Oy Db	Qy Dp	Qy Db

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T: Deeley, Roger G.
INVENTION: METHODS FOR IDENTIFYING
INVENTION: MULTIDRUG RESIGNANT TUMOR CELLS
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APPLICATION DATA:
ATION NUMBER: US/08/462,109A
DATE:
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APPLICATION DATA:
ICATION NUMBER: 07/966,923
NG DATE: 27-0CT-1992
ICATION NUMBER: 08/029,340
NG DATE: 8-MAR-1993
ICATION NUMBER: 06/141,893
NG DATE: 26-0CT-1993
ICATION NUMBER: 08/407,207
NG DATE: 10-MAR-1995
EX/AGGAT: 10-M
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ER: IBM PC compatible
ING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                 Length 5011;
                                                                                                                                                             Score 1737.8; DB 2; Length
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PQI-002CP4
    TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5011 base pairs
                                                                                                                                                               34.2%;
REFERENCE/DOCKET NUMBER:
                                                         TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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Matches 2882; Conservative
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COCCATTCGAGCGGGCCCGGGGGCCCCCCCCCCCCCCCCC	10.079   CAGCATCGAGCGCGCGCGCGCGCGCGCGCGCGCACCACCACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACACGACCACGACCACGACCACC
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3156 1180 GCTCAGCCTCTGGACTGATGACCCCATCGTCAACGGGACTCAGGAGCACACGAAAGTCCG 3239 3479 3516 GCTCAGTGCCTGGACAAATGATGCCATGGCAGACAGTAGACAGAACAACAACACTTCCCTGAG 3036 3779 3698 4079 3936 4139 3457 ITCGGAGACAGIGACIGGIGCCAGIGICATCCGGGCCIACAACCGCAGCCGGGAITITGA GCTGGGCGTCTATGCTGCTTTAGGAATTCTGCAAGGGTTCTTGGTGATGCTGGCAGCCAT GGCCATGGCAGGGGGGGCTGCCAGGCTGCCGGTGTTGCACCAGGCACTGCTGCACAA CAAGATACGCTCGCACAGTCCTTCTTTGACACCACCACCATCAGCCGCATCCTGAACTG CTTCTCCAAGGACATCTATGTCGTTGATGAGGTTCTGGCCCCTGTCATCCTCATGCTGCT CAATTCCTTCTTCAACGCCATCTCCACTCTTGTGGTCATCATGGCCAGCACGCCGCTCTT 3337 CACTGTGGTCATCCTGCCCTGGCTGTGCTCTACACCTTAGTGCAGCGCTTCTATGCAGC 3397 CACATCACGGCAACTGAAGCGGCTGGAATCAGTCAGCCGCTCACCTATCTACTCCCACTT 3660 CAACGAGACCTTGCTGGGGGTCAGCGTCATTCGAGCCCTTCGAGGAGCAGGAGGCCTTCAT 3720 CCACCAGAGTGACCTGAAGGTGACGAGAAGGCCTATTACCCCAGCATCGTGGC CTGGGTGGTGGAAGGCAGCCGCCCTCCCGAAGGTTGGCCCCCCACGTGGGAGGTGGAGTT CCGGAATTATTCTGTGCGCTACCGGCCGGGCCTAGACCTGGTGCTGAGAGCCTGAGTCT GCATGTGCACGGTGGCGAGAAGGTGGGGGATCGTGGGCCGCCACTGGGGCTGGCAAGTCTTC 3637 ACTATTTGCCGTCATCGGGAGGAGCAGCCTGAACCCGGGGCTGGTGGGCCTTTCTGTGTC CTACTCCTTGCAGGTGACATTTGCTCTGAACTGGATGATACGAATGATGTCAGATTTGGA ATCTAACATCGTGGCTGTGGAGAGGGTCAAGGAGTACTCCAAGACAGAGACAGAGGCGCC 2977 3217 3277 3037 3097 3157 3517 3697 3757 3960 3817 3877 4080 3937 4140 4200 4020 3997 ŏ a δ qq οy qq Óγ g Qγ Dp Qγ Ω δ Q δy qq οy qq qq Ω ద οχ Qγ οy Óγ Dp οy QQ ŏ q Dp q g οy ÓΥ ò

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                   4260 CATCAACATCGCCAAGATCGCCTGCACGACCTCCGCTTCAAGATCACCATCATCCCCCA 4319
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                                                                                           4560 GGCCACGGCAGCCGTGGACCTGGAAACGGACGACCTCATCCAGTCCACCATCCGGACACA
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Fatent No. 5891724
GENERAL INFORMATION:
APPLICANT: Deeley, Roger G.
APPLICANT: Cole, Susan P.C.
TITLE OF INVENTION: METHODS FOR CONFERRING MULTIDRUG
TITLE OF INVENTION: REISTANCE ON A CELL
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: PARTED RESEARCH & DEVELOPMENT INNOVATIONS
STREET: Queen'S University at Kingston
STATE: Ontario
COUNTRY: CANADA
21P: KTL 3N6
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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FILLING DATE: 05-JUN-1995
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/029,340
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APPLICATION NUMBER: 07/966,923
FILING DATE: 27-0CT-1992
CLASSIFTCATION: 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 5011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34.2%; Score 1737.8; DB 2; 62.2%; Pred. No. 0; tive. 0; Mismatches 1662;
                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/141,893
FILING DATE: 26-0CT-1993
CLASSIFICATION NATA:
APPLICATION NUMBER: 08/407,207
FILING DATE: 20-MAR-1995
CLASSIFICATION 1424
ATTORNEY/AGENT INFORMATION:
NAME: Steeq, Carol Migraficki
REGISTRATION NUMBER: 39,539
REFERENCE/DOCKET NUMBER: 01551
                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 545-2342
TELEFAX: (613) 545-6853
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5011 base pairs
8-MAR-1993
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                                                                                                                                                                                                                                                                                                                                             double
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196..4788
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
LOCATION:
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3180 GCTCAGCCTCTGGACTGATGACCCCATCGTCAACGGGACTCAGGAGCACACGAAAGTCCG 3239
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                                                   ----GCTGAGGCCAAGAAGGAGGAGCTGGAAGCTGAAGGCGCAGAC
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                                                                                                             CATGACCCTTTGCCTGTTCCGCATCCTGGAGGCGGCAAAGGGTGAAATCCGCATTGATGG
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Patent No. 6001563
GENERAL INFORMATION:
APPLICANT: Cole, Susan P.C.
APPLICANT: Deeley, Roger G.
TITLE OF INVENTION: METHODS FOR IDE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of COMPUTER: IBM PC com
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+ive 0; Mismatches 1662;
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                                            APPLICATION NUMBER: US/08/463,179A
                                                                                                                      FILING DATE: 27-0CT-1992
APPLICATION NUMBER: 08/029,340
FILING DATE: 8-MAR-1993
APPLICATION NUMBER: 08/141,893
FILING DATE: 26-0CT-1993
APPLICATION NUMBER: 08/407,207
FILING DATE: 20-MAR-1995
ATTORNEY/AGENT INFORMATION:
PC-DOS/MS-DOS
                                                                                                       APPLICATION NUMBER: 07/966,923 FILING DATE: 27-0CT-1992
                                                                                                                                                                                                                                                     NAME: DeConti, Giulio A. Jr. REGISTRATION NUMBER: 31,503
                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: PQ
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INPORMATION FOR SEO 1D NO: 1.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 5011 base pairs
TYPE: nucleic acid
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Matches 2882; Conservative
                           CURRENT APPLICATION DATA
                                                                                          PRIOR APPLICATION DATA:
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                                                                          CLASSIFICATION:
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US-08-463-179A-1
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1958 1785 2018 2138 2016 2258 2076 2318 2136 2196 2438 2498 2316 2496 2436 GGCCAGTGTGTCTCTGAAACGGATCCAGCAATTCCTGAGCCAAGAGGAACTTGACCCCCA **AACCACCTTCACCTGGATGTGCAGCCCCTTCCTGGTGACCCTGATCACCCTCTGGGTGTA** CGTGTACGTGGACCCAAACAATGTGCTGGACGCCGAGAAGGCCTTTGTGTCTGTGTCCTT GAGTGTGGAAAGAAAGACCATCTCCCCAGGC-----TATGCCATCACGATACACAG GTCTGCCCTGCTGGAGAGATGGAGAAGCTAGAAGGCAAAGTGCACATGAAGGGCTCCGT CTCAGCCCTCTTGGCTGAGTGGACAAAGTGGAGGGGCACGTGGCTATCAAGGGCTCCGT TGGATGTCAGCTGGAGGAACCATATACAGGTCCGTGATACAGGCCTGTGCCCTCCTCCC AAATGTGATTGGCCCCAAGGGGATGCTGAAGAAGAAGACGGGGATCTTGGTCACGCACAG TGGCACCTTCACCTGGGCCCAGGACCTGCCCCCCACTCTGCACACACCTTCCAGGT CCCGAAAGGGGCACTGGTGGTGGGGCCTGTGGGCTGTGGGAAGTCCTCCTGGT GGCCTATGTGCCCCCAGCAGGCATGGATCCAGAACTGCACTCTTCAGGAAAACGTGCTTTT TGACCTGGAGATGCTGCCTGGTGGGGATCAGACAGAGATTGGAGAAGAGAGGCATTAAACCT GATGGGCCCGTACCCAGCCCTGCAGCGCAACGGCTCCTTTGCCAACTTTCTCTGCAA CGGCAAAGCCCTGAACCCCAAGCGCTACCAGCAGACTCTGGAGGCCTGTGCCTTGCTAGC GTCTGGGGGCCAGCGGCAGCGGTCAGTCTGGCTCGAGCTGTTTACAGTGATGCCGATAT TTTCTTGCTGGATGACCCACTGTCCGCGGTGGACTCTCATGTGGCCCAAGCACATCTTTGA CCACGTCATCGGGCCAGAAGGCGTGCTGGCAGGCAAGACGCGGAGTGCTGGTGACGCACGG CATTAGCTTCCTGCCCCAGACAGACTTCATCATTGTGCTAGCTGATGGACAGGTGTCTGA AGAGGATAAGGAGGCACTGCTGATTGAAGACACCACAGCAACCACACGGATCTGACAGA 2677 CAATGATCCAGTCACCTATGTGGTCCAGAAGCAGTTTATGAGACAGCTGAGTGCCCTGTC CTATGCCCCCGATGAGGACCAAGGGCACCTGGAGGACGACGCGTTGGAAGGTGC TCCAGGGAAGGAAGCAAAGCAAATGGAGAATGGCAT 1839 1666 1899 1726 1959 1786 2019 1846 2079 23.79 1897 1957 2199 2017 2259 2077 2319 2137 2197 2439 2257 2499 2559 2377 2619 2679 2317 2497 2739 2799 2617 2437 2557 á g ŏ QQ g qq ò ò δ QQ 셤 g ò οy ò 8 οy qq δ g ò g ŏ g 9 g Óγ g ò g ò 셤 à qq ò g δ

3119 3698 3816 CTCAGATGGGGAGGGACAGGGTCGGCCTGTACCCCGGAGGCACCTGGGTCCATCAGAGAA TGGCACTGTGGAGCTCAGTGTTCTGGGATTATGCCAAGGCCGTGGGGCTCTGTACCAC CTTCCTCAGCATCTTCTTTTCATGTGAACCATGTCCGCGCTGGCTTCCAACTATTG GGTGCAGGTGACAGAGGCGAAGGCAGTGGGGCACTGACCCAGGAGGAGAAAGCAGCCAT ----GCTGAGGCCAAGAAGGAGGACCTGGAAGCTGATGGAGGCTGACAAGCCGCAGAC GCTGGCCATCTGTCTGTATGTGGGTCAAAGTGCGGCTGCCATTGGAGCCAATGTGTG GCTCAGTGCCTGGACAAATGATGCCATGGCAGACAGTAGACAGAACAACACTTCCCTGAG GCTGGGCGTCTATGCTGCTTTAGGAATTCTGCAAGGGTTCTTGGTGATGCTGGCAGCCAT GGCCATGGCAGCGGGTGGCATCCAGGCTGCCCGTGTGTTGCACCAGGCACTGCTGCACAA CTTCTCCAAGGACATCTATGTCGTTGAGGTTCTGGCCCCTGTCATCCTCATGCTGCT GATCATCAGGAGATACTAAGGTGGATGCCAACCAGAGAAGCTGCTACCCTACATCATCTC CACCAGAGTGACCTGAAGGTGGACGAGAACCAGAAGGCCTATTACCCCAGCATCGTGGC CAATTCCTTCTTCAACGCCATCTCCACTCTTGTGGTCATCATGGCCAGCACGCCGCTCTT CACTGTGGTCATCCTGCCCTGGCTGTGCTCTACACCTTAGTGCAGCGCTTCTATGCAGC CGCCATCATCATCCCCCCCTTGGCCTCATCTTCTTCTTCGTCCAGAGGTTCTACGTGGC CACATCACGGCAACTGAAGCGGCTGGAATCAGTCAGCCGCTCACCTATCTACTCCCACTT TTCGGAGACAGTGACTGGTGCCAGTGTCATCCGGGCCTACAACCGCAGCCGGGATTTTGA CAACCGGTGGCTGAGCATCGGAGTGGAGTTCGTGGGGAACTGCGTGGTGCTCTTTGCTGC ATCTAACATGGTGGTGGAGGGTCAAGGAGTACTCCAAGACAGAGACAGAGGCGCC ACTATTTGCCGTCATCGGGAGGAGCAGCCTGAACCCGGGGCTGGTGGGCCTTTCTGTGT CTACTCCTTGCAGGTGACATTTGCTCTGAACTGGATGATACGAATGATGTCAGATTTTGGA 2737 2949 3004 2857 3060 2917 2977 3180 3240 3360 2797 3120 3037 2895 3097 3300 3157 3420 3480 3600 3457 3217 3277 3337 3540 3397 3660 3517 3577 3780 3840 3900 3637 3697 3757 δ οp ΩŸ g δy CC ŏ g g Ωy Qγ g οy qq δy Op ολ g g Q δ ò ò qq Qγ Ω δ g δ οp q δy δ QQ δŽ

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3960 AACCAACATCGTGGCCGTGGAGAGCTCAAGGAGTATTCAGAGACTGAGAAGGAGGCGCC 4019
                                                                                         CCGGAATTATTCTGTGCGCTACCGGCCCGGGCCTAGACCTGGTGCTGAGAGCCTGAGTCT 3936
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                                                         4020 CTGGCAAATCCAGGAGACACGTCCGCCCAGCAGCTGGCCCCAGGTGGGCCGAGTGGAATT
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Patent No. 6025473
GENERAL INFORMATION:
APPLICANT: Cole, Susan P.C.
APPLICANT: Deeley, Roger G.
TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS
NUMBER OF SEQUENCES: 10
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ADDRESSEE: PARTEQ RE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1737.8; DB 3;
Pred. No. 0;
0; Mismatches 1662;
              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,384B
FILING DATE: 05-JUN-95
                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/966,923
FILING DATE: 27-0CT-1992
APPLICATION NUMBER: 08/029,340
FILING DATE: 8-MAR-1993
APPLICATION NUMBER: 08/141,893
FILING DATE: 26-0CT-1993
APPLICATION NUMBER: 08/407,207
FILING DATE: 20-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                              NAME: Steeg, Carol Miernicki
REGISTRATION VUMBER: 39,539
REFERENCE/DOCKET NUMBER: 01547
TELECOMMUNICATION INFORMATION:
TELEPAN: (613) 545-2342
TELEPAN: (613) 545-6853
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 62.2
Matches 2882; Conservative
COMPUTER READABLE FORM:
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STRANDEDNESS: double
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; LOCATION:
US-08-461-384B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
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QQ         50           QQ         50           QQ         56           QQ         62           QQ         62           QQ         68           QQ         74           QQ         74           QQ         74           QQ         1173           QQ         1173           QQ         1112           QQ         1128           QQ         1135           QQ         1135           QQ         124           QQ         1335           QQ         1336           QQ         134           QQ         1475           QQ         1486           QQ         1486           QQ         1486	5 CCCTTCGGCTTCACCACCTTCTACATCCACTTGCCCTGGTACTCTCTGCCCTCATCTT 564	5 GGCCTGCTTCAGGGAGAACCTCCATTTTCTCCGCAAAGATGTCGACCCTAACCCCTA 624 	5 CCCTGAGACCAGGCTTTCTCTCCCGCCTGTTTTCTGGTGGTTCACAAAGATGGC 684		5 CAGATCCCAGATGGTGGTGCAGCAGCTGCTGGAGGCATGGAGGA	9AGCAGGAAAAGCAGACGCACGACACAGAGCTTCAGCAGCACCTGGGAAAAA 840 	TGCCTCCGGCGAGGACGAGGTGCTGGGTG		5 TGCCTGCTTCAAGCTTATCCAGGACCTGCTCCTTCATCAATCCACAGCTGCTCAGCAT 1005	CCTGATCAGGTTTATCTCCAACCCCATGGCCCCCTCCTGGTGGGGGCTTCCTGGTGGCTGG 1065	GCTGATGTTCCTGTGCTCCATGATGCAGTCGCTGATCTTACAACACTATTACCACTACAT 1125	CTTTGTGACTGGGGTGAAGTTTCGTACTGGGATCATGGGTGTCATCTACAGGAAGGCTCT 1185	GGTTATCACCAACTCAGTGAACGTGCGTCCACTGTGGGGGAAATTGTCAACTCATGTC 1245 	5 AGTGGATGCCCAGCGCTTCATGGACCTTGCCCCCTTCCTCAATCTGCTGTGGTCAGCACC 1305	5 CCTGCAGATCATCCTGGCGATCTACTTCCTCGGCAGAACCTAGGTCCCTCTGTCCTGGC 1365	i tegagtegettteategtettgetgattecaeteaaggagetgtgeegtgaagatges 1425 	; CGCCTTCCAGGTAAAGCAAATTGAAGGACTCGCGCATCAAGCTGATGAGTGAG	i cetgaacgcatcaaggtgetgaagctgtacgcetgggageeccagetteetgaagcaggt 1545 
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AACCACCTTCACCTGGATGTGCAGCCCCTTCCTGGTGACCCTGATCACCCTCTGGTGTA 1665 2016 2496 2018 1845 1896 2138 2198 2076 2318 2136 2378 2196 2438 2498 2316 2558 2376 2618 2436 2676 GGAGGGCATCAGGCAGGGTAGCTCCAGCTGCGCACGCGGCCTACCTCCACACCAC 1605 1779 GCTGGCCATCAGGCAGGAGGTGCTGAAGTGCTGAAGAAGTCTGCCTACCTGTCAGCCGT 1838 2019 GGCGAGTGTCTCCCTCAAACGCCTGAGATCTTTCTCTCCCATGAGGAGCTGGAACCTGA 2078 2738 2556 CGTGTACGTGGACCCAAACAATGTGCTGGACGCCGAGAAGGCCTTTGTGTCTGTGTCCTT 1959 GTTCAACATCCTCCGGTTTCCCCTGAACATTCTCCCCATGGTCATCAGCAGCATCGTGCA GGCCAGTGTGTCTCTGAAACGGATCCAGCAATTCCTGAGCCAAGAGGAACTTGACCCCCA 1846 GAGTGTGGAAAAAAAGACCATCTCCCCAGGC-----TATGCCATCACATACACAG TGGCACCTTCACCTGGGCCCAGGACCTGCCCCCCACTCTGCACAGCCTAGACATCCAGGT CCCGAAAGGGGCACTGGTGGCCGTGGTGGGCCTGTGGGCTGTGGGAAGTCCTCCTGGT GTCTGCCCTGCTGGGAGAGATGGAGAAGCTAGAAGGCAAAAGTGCACATGAAGGGCTCCGT GTCTGGGGGCCCAGCGGCAGCGGGTCAGTCTGGCTCGAGCTGTTTACAGTGATGCCGATAT TITCITGCTGGATGACCCACTGTCCGCGGTGGACTCTCATGTGGCCCAAGCACTTTGA CATTAGCTTCCTGCCCAGACAGACTTCATCATTGTGCTAGCTGATGACAGGTGTCTGA 2617 AGAGGATAAGGAGGCACTGCTGATTGAAGACACACTCAGCAACCACCACGGATCTGACAGA GTTTAATATCTTAAGACTTCCCCTCAACATGCTGCCCCAGTTAATCAGCAACCTGACTCA CGGCAAAGCCCTGAACCCCAAGCGCTACCAGCAGACTCTGGAGGCCTGTGCCTTGCTAGC 2379 TGGATGTCAGCTGGAGGAACCATATTACAGGTCCGTGATACAGGCCTGTGCCCTCCTCCC CTATGCCCCCGATGAGGACCAAGGGCACCTGGAGGACAGCTGGACCGCGTTGGAAGGTGC 1726 1546 1839 1899 1786 1606 1666 1897 2139 2199 2017 2137 2317 2559 1957 2197 2439 2257 2499 2437 2679 2497 2739 2557 2799 Db O.Y D.b Db δ Qγ g οy ò QQ Qγ OD δy Ωp δλ qq δy qq ρp Db g δy В ōλ Db g δy ò Ω δy QQ δ οy q ŏ g ŏ

-	3900	UY 3/2/ ATCTAACATCGTGGGTGTGGAGAGGGTCAA 	Qy 3817 CTGGGTGGAAGGCAGCCGCCCTCCGAN	OY 3877 CCGGAATTATTCTGTGCGCTACCGGCCGGG	QY 3937 GCATGCACGGTGGCGAGAAGGTGGGGGATC	OY 3997 CATGACCCTTTGCCTGTTCGCATCCTGGACTGACTGACTG	QY 4057 CCTCAATGTGGCAGACATCGGCCTCCATGAC	Qy 4117 GGACCCCATCCTGTCTCGGGGACCTGCGG	Qy 4177 AGAGGAGACATTTGGTGGGCTTTGGAGCTC	Qy 4237 GCGGCAGGCCTGGACTTCCAGTGCTCAGAC 	Qy 4297 GCAGCTCGTGTGCCTGGCCCGAGCCCTGCTC	Oy 4357 GGCCACAGCTGCCATCGACCTGGAGACTGAC	Qy 4417 GTTTGATACCTGCACTGTCCTGACCATGGCP	Qy 4477 CAGGGTCCTGGTCCTGGACAAAGGAGTAGTA	OY 4537 TGCAGCTAGAGGGATCTTCTACGGGATGGCC	Qy 4597 CCTGAGATTTC 4607                   Db 4800 GCTGGCATATC 4810	RESULT 7 US-08-407-207A-1 ; Sequence 1, Application US/08407207A		; TITLE OF INVENTION: ANTIBODIES TO A ; NUMBER OF SEQUENCES: 7 ; CORRESPONDENCE ADDRESS:
	Db 2859 TCCAGGGAAGGAAGCAAAGCAAATGGAGATGGCAT	Qy 2677 CAATGATCCAGTCACCTATGTGGTCCAGAAGCAGTTTATGAGACAGCTGAGTGCCCTGTC 2736	OY 2737 CTCAGATGGGGAGGGACAGGGCTGTACCCCGGAGGCACCTGGGTCCATCAGAGAA 2796	2797 GGTGCAGGTGACAGAGGCAGATGGGGCACTGACCCAGGAGGAGAAAGCAGCAT	DD 5004GCTGAGGCCAGAC 3059  QY 2857 TGGCACTGTGGAGCTCAGTGTTCTGGGATTATGCCAAGGCCGTGGGGCTCTGTACCAC 2916  QY 1857 TGGCACTCAGGTCAGTGTTTCTGGATTATGCCAAGGCCGTGGGGCTCTGTACCAC 2916  DD 3060 AGGCAAGTCAAGTTTTCGTATATGCAAAAAAAAAAAAAA	2917 GCTGGCCATCTGTCTCTGTATGTGGGTCCAAGTGCGCTGCCATGGAGCCAATGTGTGTG	TGATGCCATGCAGACAGTAGACAGACAACACTTCCCTGAG 	Oy 3037 GCTGGGCGTCTATGCTTTAGGAATTCTGCAAGGGTTCTTGGTGATGCTGGCAGCCAT 3096	Qy 3097 GGCCATGGCAGCGGTGGCATCCAGGCTGCCGTGTTGCACCAGGCACTGCTGCACAA 3156	Qy 3157 CAAGATACGCTCGCCACAGTCCTTCTTGACACCACATCAGGCCGCATCCTGAACTG 3216	3217	y 3277 CAATTCCTTCTAACGCCATCTCCACTCTTGTGGTCATCATGGCCAGCAGGCGCTT 3336	y 3337 CACTGTGGTCATCCTGCCCTGGCTGTGCTCTACACCTTAGTGCAGCGCTTCTATGCAGC 3396	y 3397 CACATCACGGCAACTGAAGCGGCTGGAATCAGCCGCTCACCTACTACTACTCCACTT 3456	3457 TTCGGAGACAGTGGTGCCGGTGTCATCCGGGCTACCACCGCAGCCGGGATTTTGA	3517 GATCATCAGTGATACTAAGGTGGATGCCAACCAGAGAGAG	y 3577 CAACCGGTGGCTGAGCATCGGAGTTGGTGGGGAACTGCGTGGTGCTCTTTGCTGC 3636 	y 3637 ACTATTGCGTCATCGGGAGGAGCTGAACCCGGGGCTGGTGGGCCTTTCTGTGTC 3696 1	y 3697 ctactccttgcaggtgacatttgctctgaactggatgatacgaatgatgtcagatttgga 3756 
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AGGAGTACTCCAAGACAGAGACAGAGGCGCC 3816
                                                                AAGGTTGGCCCCCACGTGGGGAGGTGGAGTT 3876
                                                                           GCCTAGACCTGGTGCTGAGACCTGAGTCT 3936
                                                                                                                                                     AGGCGCAAAGGGTGAAATCCGCATTGATGG 4056
                                                                                                                                                                                                                                         ACCTGGGCTCTCAGCTGACCATCATCCCGCA 4116
                                                                                                                                                                                                                                                                                                                              TGTCCCACAGACATTTGTGAGCTCCCA 4236
                                                                                                                                                                                                                                                                                                                                                                          AGGGGGGGAGAATCTCAGCGTGGGCCAGAG 4296
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                                                                                                                                                                                                                                                                                      SCATGAACCTGGACCCCTTCGGCAGCTACTC 4176
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Page 17

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445
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RESEARCH & DEVELOPMENT INNOVATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1737.8; DB 3;
Pred. No. 0;
0; Mismatches 1662;
            Queen's University at Kingston
                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/407,207A
FILING DATE: 20-MAR-1995
CLASSIFICATION 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/966,923
FILING DATE: 27-109-1992
APPLICATION NUMBER: 08/029,340
                                                                                                                                                                                                                                                                                                     NAME: Steeg, Carol Miernicki
REGISTRATION NUMBER: 39,539
REFERENCE/DOCKET NUMBER: Q1512
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 545-2342
TELEPAX: (613) 545-6653
INFORMATION FOR SEQ ID NO: 1:
                                                                                                    COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII text
                                                                                                                                                                                                                                                FILING DATE: 8-MAR-1993
APPLICATION NUMBER: 08/141,893
EILING DATE: 26-0CT-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34.2%;
illarity 62.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 5011 base pairs
                                   ZIP: K7L 3N6
COMPUTER REDABLE FORM:
MEDIUM TYPE: Flore
                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
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196..4788
PARTEO
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Best Local Similarity
Matches 2882; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
           STREET: Queen's
CITY: Kingston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY:
; LOCATION:
US-08-407-207A-1
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GCTGCTGTTTGTCACTGCCTGCCTGCACCCTCGTGCTGCACCAGTACTTCCACATCTG 1358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1659 GACGTATCAGGTGGCCCACATGAAGAGCAAAGACAATCGGATCAAGCTGATGAACGAAAT 1718
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           939 CACGICGGAACAAGICGIGCCIGIITIIGGIAAAGAACIGGAAGAAGGAAIGCGCCAAGAC 998
     504
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                                                                                                                        GGCCTGCTTCAGGGAGAAACCTCCATTTTTCTCGGAAAGAATGTCGACCCTAACCCCTA
CGCCATCGTCCCATTCCGCTCCAAGATCCTTTTAGCCAAGGCAGAGGGTGAGATCTCAGA
                                                                                                                                                                                                                                            GTCCTGTTTCTCAGATCGCTCACCCTGTTCTCGGAAACCATCCACGACCTAATCCCTG
                                                                                                                                                                                                                                                                                                                           639 TGCCCTAGCCATCCTGAGATCCAAAATTATGACAGCCTTAAAAGAGGATGCCCAGGTGGA
                                                                                                                                                                                                                                                                                          625 CCCTGAGACCAGCGCTGGCTTTCTCCCCGCCTGTTTTTCTGGTGGTTCACAAAGATGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                745 CAGATCCCAGATGGTGGTGCAGCAGCTGGAGGCATGGAGGA-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               886 CCGGAAGCCCTCCTTCCTGAAGGCCCTGCTGGCCACCTTCGGCTCCAGCTTCCTCATCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1119 GTGGAACCCTCTCTGTTTAAGGTGTTATACAAGACCTTTGGGCCCTACTTCTCTCATGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            946 TGCCTGCTTCAAGCTTATCCAGGACCTGCTCTCCTTCATCAATCCACAGCTGCTCAGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGTGGATGCCCAGCGCTTCATGGACCTTGCCCCCTTCCTCAATCTGCTGTGGTCAGCACC
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                                                                                                                                                                                                                                                                                                                                                                                              685 CATCTATGGCTACCGGCATCCCCTGGAGGAGGACCTCTGGTCCCTAAAGGAAGAGGA
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1778	1605	1665 1898	1725	1785 2018	1845	1896	1956 2198	2016	2076	2136	2196	2256	2316	2376	2436	2496 2738	2556	2616
	6 GGAGGGCATCAGGCAGGGTGAGCTCCAGCTGCGCACGGCGGCGTTCCTCCACACCAC	6 AACCACCTTCACCTGGATGTGCAGCCCCTTCCTGGTGACCCTGATCACCCTCTGGGTGTA	6 CGTGTACGTGGACCCAAACAATGTGCTGGACGCCGAGAAGGCCTTTGTGTCTGTGTCTCTTT	6 GTTTAATATCTTAAGACTTCCCCTCAACATGCTGCCCCAGTTAATCAGCAACCTGACTCA	6 GGCCAGTGTGTCTCTGAAACGGATCCAGCAATTCCTGAGCCAAGAGGAACTTGACCCCCA	6 GAGTGTGGAAAGAAAGACCATCTCCCCAGGCTATGCCATCACCATACAGG	7 TGGCACCTTCACCTGGGCCCAGGACCTGCCCCCACTCTGCAGCAGCCTAGACATCCAGGT	7 CCCGAAAGGGGCACTGGTGGCCGTGGTGGGCCTGTGGGCTGTGGGAAGTCCTCCCTGGT 	7 GTCTGCCCTGCTGGGAGAGAGTGGAGAAGCTAGAAGGCAAAGTGCACATGAAGGCTCCGT	7 GGCCTAIGTGCCCCAGCAGCATGGATCCAGAACTGCACTCTTCAGGAAAAGGTGCTTTT	7 CGCCAAAGCCCTGAACCCCAAGCGCTACCAGACTCTGGAGGCCTGTGCCTTGCTAGC	7 TGACCTGGAGATGCTGCCTGGTGGGGATCAGACAGAGATTGGAGAGAGGGCATTAACCT	7 GTCTGGGGGCGAGCGGCAGCGGGTCAGTCTGGCTCGAGCTGTTACAGTGATGCCGATAT	7 TTTCTIGCTGGATGACCACTGTCCGCGGTGGACTCTCATGTGGCCAAGCACATCTTTGA	7 CCACGTCATCGGCCAGAAGGCGTGCTGGCAGCAGAGACGCGAGTGCTGGTGACGCACGG	7 CATTAGCTTCCTGCCCCAGACGAGCTTCATCATTGTGCTAGCTGATGGACAGGTGTCTGA	7 GATGGGCCCGTACCCAGCCCTGCAGCGCAACGGCTCCTTTGCCAACTTTCTCTGCAA	7 CTATGCCCCCGATGAGGACCAGGACAGCTGGACGGCGTTGGAAGGTGC
171	154	160	1666	172	178(	1846	1897	195	201	207	2137	2197	2257	2317	2377	2437	2497	2557
අ	Oy Dp	g G	Oy Op	a G	0 <u>y</u>	Qy Db	Qy Db	QY Db	Qy Db	Qy Bb	QY Db	Q D	Oy Db	Oy Dp	0.y 0.b	Qy Db	Qy Db	δ٥,

2916 3119 3179 3036 3156 3479 3576 3839 2799 CTATGCCAGCACAGAGCAGGAGCAGGATGCAGAGGAGAACGGGGTCACGGGCGTCAGCGG 2858 CAATTCCTTCTTCAACGCCATCTCCACTCTTGTGGTCATCATGGCCAGCACGCCGCTCTT 3336 TTCGGAGACAGTGACTGGTGCCAGTGTCATCCGGGCCTACAACCGCAGCCGGGATTTTGA 3516 AGAGGATAAGGAGGCACTGCTGATTGAAGACACACTCAGCAACCACGGGATCTGACAGA GCTGGCCATCTGTCTCCTGTATGTGGGGTCAAAGTGCGGCTGCCATTGGAGCCAATGTGTG CTTCCTCAGCATCTTCCTTTTCATGTGTAACCATGTCTCGCGCTGGCTTCCAACTATTG GCTCAGTGCCTGGACAAATGATGCCATGGCAGACAGTAGACAGAACACACTTCCCTGAG GCTGGGCGTCTATGCTGCTTTAGGAATTCTGCAAGGGTTCTTGGTGATGCTGGCAGCCAT GGCCATGGCAGCGGGTGGCATCCAGGCTGCCCGTGTGTTGCACCAGGCACTGCTGCACAA CAATGATCCAGTCACCTATGTGGTCCAGAAGCAGTTTATGAGACAGCTGAGTGCCCTGTC -----GCTGGTGACGGACAGTGCAGGAACCAGCAGAGACAGCTCAGCAGCTCCTC AGGCCAGGTCAAGCTTTCCGTGTACTGGGACTACATGAAGGCCATCGGACTCTTCATCTC CACATCACGGCAACTGAAGCGGCTGGAATCAGTCAGCCGCTCACCTATCTACTCCCACTT CTCAGATGGGGACAGGGTCGGCCTGTACCCCGGAGGCACCTGGGTCCATCAGAGAA TGGCACTGTGGAGCTCAGTGTTCTGGGATTATGCCAAGGCCGTGGGGGCTCTGTACCAC CAAGATACGCTCGCCACAGTCCTTTGACACCACCATCAGGCCGCATCCTGAACTG CACTGTGGTCATCCTGCCCCTGGCTGTGCTCTACACCTTAGTGCAGCGCTTCTATGCAGC 3600 TICCTCCCGGCAGCTGAAGGCCCTCGAGTCGGTCAGCCGCTCCCCGGTCTATTCCCATTT GGTGCAGGTGACAGAGGCGAAGGCAGATGGGGCCACTGACCCAGGAGGAGGAAGCCAT GATCATCAGTGATACTAAGGTGGATGCCAACCAGGAAGCTGCTACCCCTACATCTC CTTCTCCAAGGACATCTATGTCGTTGATGAGGTTCTGGCCCCTGTCATCCTCATGCTGCT CAACCGGTGGCTGAGCATCGGAGTGGAGTTCGTGGGGAACTGCGTGCTGCTTTTGCTGC ACTATITICCCGTCATCGGGAGGAGCAGCCTGAACCCGGGGCTGGTGGGCCTTTCTGTGTC TCCAGGGAAGGAAGCAAATGGAGAATGGCAT 2949 2617 2859 2895 2737 2857 3060 2917 3120 3180 3240 3300 3157 3360 3420 3277 3480 3337 3457 3660 3780 2677 2797 3004 2977 3037 3097 3217 3540 3397 3577 3637 3517 g δλ qq Ω Db Ω Q ŏ Ω ΟŻ qq g q Op οy δŽ ò ŏ qq qq Db Qy g ò δ Qy Db οy qq Qγ d δ g Qγ qq δλ Db

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ISOLATED NUCLEIC ACID MOLECULES ENCODING MULTIDRUG RESISTANCE PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 5011 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 2881; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
196..4788
                         NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: CDNA
             INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 8-
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 26 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION:
US-08-463-092B-3
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                        3900 TTACTCATTGCAGGTCACCTACTTGAACTGGCTGGTTCGGATGTCATCTGAAATGGA 3959
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         CTACTCCTTGCAGGTGACATTTGCTCTGAACTGGATGATACGAATGATGTCAGATTTGGA
                                                                                                                       CTGGGTGGTGGAAGGCAGCCGCCTCCCGAAGGTTGGCCCCCCACGTGGGAGGTGGAGTT
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Patent No. 5766880
GENERAL INFORMATION:
APPLICANT: Cole, Susan P.C.
APPLICANT: Deeley, Roger G.
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ADDRESSEE: PARTED RESEARCH & DEVELOPMENT INNOVATIONS STREET: Queen's University at Kingston CITY: Kingston STATE: Ontario STATE: Ontario ZIVIRK: CANADA ZIP: K7L 3N6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches 1663;
                                                                                                                                                                                                                                      SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,092B
FILING DATE: 05-JUN-1995
                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 07/966,923
FILING DATE: 27-0CT-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/029,340
FILING DATE: 8-MAR-1993
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APPLICATION NUMBER: 08/141,893
FILING DATE: 26-0CT-1993
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APPLICATION NUMBER: 08/407,207
FILING DATE: 20-MAR-1995
CLASSIFICATION: 435
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NAME: Steeg, Carol Miernicki
REGISTRATION NUMBER: 39,539
REFERENCE/DOCKET NUMBER: 01546
TELECOMMUNICATION INFORMATION:
TELEPAX: (613) 545-6853
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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1485 1539 CCTGCAAGTCATCCTTGCTCTCTACCTCTGTGGCTGAATCTGGGCCCTTCCGTCCTGGC 1598 1958 2136 2378 2196 2438 2256 2498 2316 2376 GGAGGGCATCAGGAGGTGAGCTCCAGCTGCGGCGACGGGGGCCTACCTCCACACCAC 1605 GAGTGTGGAAAGAAAGACCATCTCCCCAGGC-----TATGCCATCACCATACACAG 1896 TGGCACCTTCACCTGGGCCCAGGACCTGCCCCCCACTCTGCACAGCCTAGACATCCAGGT 1956 1366 TGGAGTCGCTTTCATGGTCTTGCTGATTCCACTCAACGGAGCTGTGGCCGTGAAGATGCG 1426 CGCCTTCCAGGTAAAGCAAATGAAATTGAAGGACTCGCGCATCAAGCTGATGAGTAAGT GTTTAATATCTTAAGACTTCCCCTCAACATGCTGCCCCAGTTAATCAGCAACCTGACTCA GCCCAGTGTGTCTCTGAAACGGATCCAGCAATTCCTGAGCCAAGAGGAACTTGACCCCCA 2319 GGCCTATGTGCCACAGCAGGCCTGGATCAGAATGATTCTCTCCGAGAAAACATCCTTT CCTGCAGATCATCCTGGCGATCTACTTCCTCTGGCAGAACCTAGGTCCCTCTGTCCTGGC CGTGTACGTGCACCCAAACAATGTGCTGGACGCCGAGAAGGCCTTTGTGTGTCTGTGTCCTT GTCTGCCCTGCTGGGAGAGATGGAGAAGCTAGAAGGCAAAGTGCACATGAAGGGCTCCGT GGCCTATGTGCCCCCAGCAGGCATGCAGAACTGCACTCTTCAGGAAAACGTGCTTTT CGGCAAAGCCCTGAACCCCAAGCGCTACCAGCAGACTCTGGAGGCCTGTGCCTTGCTAGC TGACCTGGAGATGCTGCCTGGTGGGGATCAGACAGAGATTGGAGAGAAGGGCATTAACCT GTCTGGGGGCCAGCGGCAGCGGGTCAGTCTGGCTCGAGCTGTTTACAGTGATGCCGATAT 1306 1599 1659 1546 1779 1666 1899 1959 1786 2019 2139 2199 2197 1726 1846 1897 1957 2017 2077 2137 2439 2257 2499 2317 2559 ŏ g δλ Q Óχ g 셤 q g g g Ôγ Qγ Qγ òγ οy Qγ Dp oγ Db δý g QY Db 90 90 90 oy ag οy g Óγ qq δŻ qq

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GATIGGGCCCGTAACCAGCCCTGCAGCGACGGCTCTTTGCCAACTTTCTTCTGCAA GATIGGTCCCCTAACACCCTGCTGCAGCGCCCTCCAACTTCTTCTTCTCTCA GATIGGGCCCCTAACACCAGGCCCTCGCAACTTCTCTGCAACTTCTTCTCTCTC	N N	CATTAGCTTCCTGCCCCAGACACTTCATCATTGTGCTAGCTGATGGACAGGTGTCTGA 249	*
CTATGCCCCGATGAGGACCAAGGGCACCTGGAGGACAGGCTGGACCGCTTGGAAGGTGC CTATGCCCCCGATGAGGAGGAGGAGGAGGACACGGACTGGAGGAAGGA	2 2	97 GATGGGCCCGTACCCAGCCCTGCTGCACGCGCACGGCTCCTTTGCCAACTTTCTCTGCAA 255	
AGAGGATAAGGAGGACTGCTGATTGAAGACACACTCAGCAACCACGGATCTGACAGA  TCCAGGGAAGGAAGCAAATGGAATGG	7 7	57 CTATGCCCCGGATGAGGACCAAGGCACCTGGAGGACAGCTGGACCGCGTTGGAAGGTGC 261	
CANTGATCCAGTCACCTATGTGGTCCAGAAGCAGTTTATGAGACAGTGAGTG	8 8	AGAGGATAAGGAGGCACTGGTTGAAGACACACTCAGCAACCACGGATCTGACAGA 267	
CTCAGATGGGAGGACAGGGTCGGCTGTACCCCGGAGGCACCTGGGTCCATCAGAGAA-  GGTGCAGAGGCAAGCACCACACACCACACCACACACACAC	5 5	CAATGATCCAGTCACCTATGTGGTCCAGAAGCAGTTTATGAGACAGCTGAGTGCCCTGTCGCTGGTGACGGACAGTGCAGGGAAGCAACTGCAGAGAACAGCTCATCCTC	
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CTTCTCCAAGGACATCTATGTGGTTGATGAGGTTCTGGCCCCTGTCATCCTCATGGTGCTGCTGTCTCTCCAAGGACATCTGTGGTGCTGCTCTCTCAAGGACGTCCATGGTGGAGGTCTCTCAAGGAGGTCATCCAAGGAGGTCATCAAGGTGTTCATCTCTCTC	Э. Э.	CAAGATACGCTCGCCACAGTCCTTTGACACCACCACCATCAGGCCGCATCCTGAACTG	
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CACTGTGGTCATCCTGCCCCTGGCTGTACTACACCTTAGTGCAGCGCTTCTATGCAGC 33	, w	CAATICCITCITCAACGCCAICICCACICITGIGGICAICAIGGCCAGCACGCGCTCIT 3   1   1   1   1   1   1   1   1   1	
397 CACATCACGGCAACTGAAGCGGCTGGAATCAGTCAGCCGCTCACCTATCTACTCCCACTT 34	m m	CACTGTGGTCATCCTGCCCTGGCTGTGCTCTACACCTTAGTGCAGCGCTTCTATGCAGC 33	
457 TTCGGAGACAGTGACTGCTGCTGTCATCCGGGCCTACAACCGCAGCGGGATTTTGA 351	36	CACATCACGCAACTGAAGCGGCTGGAATCAGTCAGCCGCTCACCTATCTACTCCCACTT 34	
	36	57 TTCGGAGACAGTGACTGGTGCCAGTGTCAGGGGCCTACAACCGCAGCCGGGATTTTGA 351	

3779 3756 3876 3668 3816 4019 4079 4199 4056 4259 4236 4439 4559 4416 CAACGAGACCTTGCTGGGGGTCAGCGTCATTCGAGCCTTCGAGGAGCAGGAGCGCTTCAT 3719 4139 4116 4319 4176 4379 4619 4476 4679 4536 GCAGCAGAGAGGTCTTTTCTACAGCATGGCCAAAGACGCCGGCTTGGTGTGAGCCCCAGA 4799 4537 IGCAGCTAGAGGCATCTTCTACGGGATGGCCAGAGATGCTGGACTTGCCTAAAATATATT 4596 CCTCAATGTGGCAGACATCGGCCTCCATGACCTGCGCTCTCAGCTGACCATCATCCGCAAAACATCGCCAAGATCGCCTGCACGACCTCCGCTTCAAGATCACCATGAACATCGCCACGACGTGCACGACCTCCGCTTCAAGATCACCATCATCACCCCA CAGGGTCCTGGTCCTGGACAAAGGAGTAGTAGCTGAATTTGATTCTCCAGCCAACCTCAT CAACCGGTGGCTGAGCATCGGAGTTCGTGGGGAACTGCGTGGTGCTCTTTGCTGC ACTATTTGCCGTCATCGGGAGGAGCAGCCTGAACCCGGGGGCTGGTGGGCCTTTCTGTGTC CTACTCCTTGCAGGTGACATTTGCTCTGAACTGGATGATACGAATGATGTCAGATTTTGGA CTGGGTGGTGGAAGGCAGCCGCCCTCCCGAAGGTTGGCCCCCCACGTGGGGAGGTT CCGGAATTATTCTGTGCGCTACCGGCCCGGGCCTAGACCTGGTGCTGAGAGACCTGAGTCT GCATGTGCACGGTGGCGAGAAGGTGGGGATCGTGGGCCGCACTGGGGCTGGCAAGTCTTC CATGACCCTTTGCCTGTTCCGCATCCTGGAGGCGGCAAAGGGTGAAATCCGCATTGATGG AGAGGAGGACATTTGGTGGGCTTTTGGAGCTGTCCCACCTGCACACGTTTGTGAGCTCCCA 4237 GCCGGCAGGCCTGGACTTCCAGTGCTCAGAGGCGGGGGAGAATCTCAGCGTGGGCCAGAG 4297 GCAGCTCGTGTGCCTGGCCCGAGCCCTGCTCCGCAAGAGCCGCATCCTGGTTTTAGACGA GCCCACAGCTGCCATCGACCTGGAGACTGACATCCAGGCTACCATCCGCACCCA GTTTGATACCTGCACTGTCCTGACCATCGCACACCGGCTTAACACTATCATGGACTACAC 3780 3840 3900 3960 3660 3517 3720 3577 3637 3697 3757 3817 4020 3877 4080 3937 4140 3997 4200 4057 4260 4320 4177 4357 4560 4417 4620 4477 4680 4740 4117 Óγ a Qγ Dp ò g Ω Dp δý g δŻ Op g δy g δ g g 용 qq ò à òγ g ò οy qq ρý ò g δy g g ŏλ g ò

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999 TAGGAAGCAGCCGGTGAAGGTTGTGTACTCCTCCAAGGATCCTGCCCAGCCGAAAGAGAG 1058
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                 CTGTTTCCCCTTCTACTTCTCTATCTCCCGACATGACCGAGGCTACATTCAGATGAC 398
                                                                                       399 ACCTCTCAACAAAACCAAAACTGCCTTGGGATTTTTGCTGTGGATCGTCTGCTGGGCAGA 458
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                                                                                                                                               CACCCCCTTGGTGGTGGGGGTCACCATGCTGGCGGCCACCCTGCTGATACAGTATGAGCG
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                                                                                                                            CCTTTTTTACTCCTTCCATGGCCTGGTCCATGGCCGGGCCCCTGCCCTGTTTTCTTTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                         APPLICANT: Cole, Susan P.C.
APPLICANT: Deeley, Roger G.
TITLE OF INVENTION: METHODS FOR IDENTIFYING
TITLE OF INVENTION: MULTIDRUG RESISTANT TUMOR CELLS
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
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0; Mismatches 1663;
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Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: DeConti, Giulio A. Jr.
REGISTRATION NUMBER: 31,503
REFERNCE/DOCKET NUMBER: PQI-002CP4
TELECOMUNICATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/462,109A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/966,923
FILING DATE: 27-0CT-1992
APPLICATION NUMBER: 08/029,340
FILING DATE: 8-MAR-1993
APPLICATION NUMBER: 08/141,893
FILING DATE: 26-0CT-1993
APPLICATION NUMBER: 08/407,207
FILING DATE: 20-MAR-1995
ATTONREY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                       E: LAHIVE & COCKFIELD 60 State Street, suite
                                                                                                                                        Sequence 3, Application US/08462109A
Patent No. 5882875
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62.2%;
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MEDIUM TYPE: Floppy disk
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5011 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                              STATE: Massachusetts
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196..4788
                                               4800 GCTGGCATATC 4810
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                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
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             4597 CCTGAGATTTC
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STREET: bv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY:
; LOCATION:
US-08-462-109A-3
                                                                                                                         US-08-462-109A-3
                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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Best Local S
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q	1419 GGTGATCACCAATTCAGCCAGAAAT	CCTCCACGGTCGGGGAGATTGTCAACCTCATGTC	1478
6 G	y 1246 AGTGGATGCCCAGCGCTTCATGGACCTTGCCCCCTTCCTCAATCTGCTGTGGTCAGCACC	CCTCAATCTGCTGTGGTCAGCACC	1305
3 8	1306		2 1
<u>8</u>	153	MAACCTAGGTCCTCTGTCCTGGC	
Qy Dp	y 1366 TGGAGTCGCTTTCATGGTCTTGCTGATTCCACTCAACGGAGCTGTGGCCGTGAAGATGCG	CGGAGCTGTGGCCGTGAAGATGCG	1425 1658
Qy Db	y         1426         CGCCTTCCAGGTAAAGCAAATTGAAGGACTCGCGCATCAAGCTGATGAGGAGATCAAGTGAAGTGAAATTGAAGTGACAATGAAGAGAAATGAAGATCAAGCTGATCAACGAAATGAAGAAATGAAGAAATGAAGATGAAGAAATGAAGATGAAGAA	GCGCATCAAGCTGATGAGTGAGAT 	1485 1718
Οy	1486	GGAGCCCAGCTTCCTGAAGCAGGT	
qq	1719	GGAGCTGGCATTCAAGGACAAGGT	1778
Oy Db	y 1546 GGAGGCATCAGGCAGGGTGAGCTCCAGCTGCGCACGGGGGGCCTACCTCCACACCACACACA	CCACGCCGCCTACCTCCACACCAC	1605 1838
Oy Dp	y 1606 AACCACCTTCACCTGGATGTGCAGCCCCTTCCTGGTGACCCTGATCACCCTCTGGGGTGTA	GACCCTGATCACCCTCTGGGTGTA	1665 1898
οy	y 1666 CGTGTACGTGGACCCAAACAATGTGCTGGACGCCGAGAAGGCCTTTGTGTCTGTGTCTTT	GAAGGCCTTTGTGTCTGTGTCCTT	1725
qq	1899	GACAGCCTTCGTGTCTTTGGCCTT	1958
Q D	y 1726 GTTTAATATCTTAAGACTTCCCCTCAACATGCTGCCCCAGTTAATCAGCAACCTGACTCA	CCCAGTTAATCAGCAACCTGACTCA 	1785 2018
Oy Dp	y 1786 GGCCAGTGTCTCTGAAACGGATCCAGCAATTCCTGAGCCAAGAGGAACTTGACCCCCA	GAGCCAAGAGGAACTTGACCCCCA                    CTCCCATGAGGAGCTGA	1845 2078
οy	1846	TATGCCATCACCATACACAG	1896
QQ	2079	cacgaacagcarcaccgrgaggaa	2138
Qy Dp	1897 TGGCACCTTCACCTGGGCCCAGGACCTGCCCCCCACTGTGCAGCCTAGACATCCAGGT	TCTGCACAGCCTAGACATCCAGGT	1956 2198
Qy Db	1957 CCCGAAAGGGCACTGGTGGCGGGGCCTGTGGGCTGTGGGAAGTCCTCCCTGGT	GGGCTGTGGGAAGTCCTCCCTGGT 	2016 2258
O.Y	2017 GTCTGCCTGCTGGAGAGAGGGAGAGCTAGAAGGCAAAGTGCACATGAAGGCTCCGT	CAAAGTGCACATGAAGGGCTCCGT 	2076 2318
Oy Dp	2077	CACTCTTCAGGAAAACGTGCTTTT 	2136 2378
Qy	7 2137 CGGCAAAGCCCTGAACCCCAAGCGCTACCAGCAGACTCTGGAGGCCTGTGCCTTGCTAGC	TCTGGAGGCCTGTGCCTAGC	2196
Op	2379	GATACAGGCCTGTGCCTCCTCCC	2438
0y Db	7 2197 TGACCTGGAGATGCTGCCTGGTGGGGATCAGACAGAGATTGGAGAGAGA	GATTGGAGAGAAGGGCATTAACCT 	2256 2498 ·
O.Y Db	2257 GTCTGGGGGCCAGCGGCAGGGGTCAGTCTGGCTCGAGCTGTTTACAGTGATGCCGATAT	AGCTGTTTACAGTGATGCCGATAT	2316 2558
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2376 2678 2496 2736 2796 2556 2798 2616 2676 2856 3059 2916 2976 3179 3156 3216 3239 3096 3359 2617 AGAGGATAAGGAGGCACTGCTGATTGAAGACACACTCAGCAACCACGGATCTGACAGA CCACGTCATCGGGCCAGAAGGCGTGCTGGCAGGCAAGACGCGAGTGCTGGTGACGCACGG GATGGGCCCCGTACCCAGCCCTGCTGCAGCGCAACGGCTCCTTTGCCAACTTTCTCTGCAA CTATGCCCCCGATGAGGACCAAGGCCACCTGGACAGCTGGACCGCGTTGGAAGGTGC CAATGATCCAGTCACCTATGTGGTCCAGAAGCAGTTTATGAGACAGCTGAGTGCCCTGTC CTCAGATGGGGAGGGACAGGGTCGGCCTGTACCCCGGAGGCACCTGGGTCCATCAGAGAA GGTGCAGGTGACAGAGGCGAAGGCAGATGGGGCCACTGACCCAGGAGGAGAAAGCAGCCAT ----GCTGAGGCCAAGAAGGAGGAGCTGGAAGCTGATGGAGGCTGACAAGGCGCAGAC CTTCCTCAGCATCTTCCTTTTCATGTGTAACCATGTGTCCGCGCTGGCTTCCAACTATTG GCTCAGTGCCTGGACAAATGATGCCATGGCAGACAGTAGACAGAACAACACTTCCCTGAG GCTGGGCGTCTATGCTGCTTTAGGAATTCTGCAAGGGTTCTTGGTGATGCTGGCAGCCAT GCCCATGCCAGCGGTGCCATCCAGGCTGCCGTGTGTTGCACCAGGCACTGCTGCACAA CAAGATACGCTCGCCACAGTCCTTCTTTGACACCACCATCAGGCCGCATCCTGAACTG CATTAGCTTCCTGCCCCAGACAGACTTCATTGTGCTAGCTGATGGACAGGTGTCTGA GCTGGCCATCTGTCTCCTGTATGTGGGGTCAAAGTGCGGCTGCCATTGGAGCCAATGTGTG CATCCTGCGGTCACCCATGAGCTTCTTTGAGCGGACCCCCAGTGGGAACCTGGTGAACCG 3480 GGGCTCCCTGTTCAACGTCATTGGTGCCTGCATCGTTATCCTGCTGGCCACGCCCATCGC TGGCACTGTGGAGCTCAGTGTGTTTGGGATTATGCCAAGGCCGTGGGGCTCTGTACCAC 3217 CTTCTCCAAGGACATCTATGTCGTTGATGAGGTTCTGGCCCCTGTCATCCTCATGCTGCT 3277 CAATTCCTTCTTCAACGCCATCTCCACTCTTGTGGTCATCATGGCCAGCACGCCGCTCTT 3337 CACTGTGGTCATCCTGCCCCTGGCTGTGCTCTACACCTTAGTGCAGCGCTTCTATGCAGC 2677 2949 2377 2437 2679 2497 2739 2557 2799 2859 2895 2737 2797 3004 2857 2917 3120 2977 3180 3240 3300 3157 3360 3420 3037 3097 ò Ω qq Qγ qq δŽ QΩ δ QQ ò qq ď g δ QQ ö qq οy q δ q a οy g Q οy οy q δ q δ g ò g δy

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SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,907B
FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: 08/029,340
FILING DATE: 8-MAR-1993
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FILING DATE: 26-0CT-1993
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APPLICATION NUMBER: 08/407,207
FILING DATE: 20-MAR-1995
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APPLICATION NUMBER: 07/966,923
FILING DATE: 27-0CT-1992
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ATTORNEY/AGENT INFORMATION:
NAME: Steed, Carol Miernicki
REGISTRATION NUMBER: 39,539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39,539
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TELEFAX: (613) 545-6853
INFORMATION FOR SEQ ID NO: 3:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 5011 base pairs
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
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STRANDEDNESS: double
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196..4788
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                                                                                                            4597 CCTGAGATTTC 4607
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ZIP: K7L 3N6
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY:
; LOCATION:
US-08-460-907B-3
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CACATCACGGCAACTGAAGCGGCTGGAATCAGTCAGCCGCTCACCTATCTACTCCACTT 3456
                                                          3457 TTCGGAGACAGTGACTGGTGCCAGTGTCATCCGGGCCTACAACCGCAGCCGGGATTTTGA 3516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGACCCCATCCTGTTCTCGGGGACCCTGCGCATGAACCTGGACCCCTTCGGCAGCTACTC 4176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCAGCTCGTGTGCCTGGCCCGAGCCCTGCTCCGCAAGAGCCGCATCCTGGTTTTAGACGA 4356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGAGGAGGACATTTGGTGGGCTTTGGAGCTGTCCCACCTGCACACGTTTGTGAGCTCCCA 4236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCCGGCAGGCCTGGACTTCCAGTGCTCAGAGGGCGGGGAGAATCTCAGCGTGGGCCAGAG 4296
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                                                                                                                                                                                                                                                                                                                       CCGGAATTATTCTGTGCGCTACCGGCCGGGCCTAGACTGGTGCTGAGAGACCTGAGTCT
              3600 TICCTCCCGGCAGCTGAAGCGCCTCGAGTCGGTCAGCCGCTCCCCGGTCTATTCCCATTT
                                                                         GATCATCAGGAGGATGCTAACCAGCAACCAGAAGATGCTGCTACCATCATCTC
                                                                                                                                                  3720 CCACCAGAGTGACCTGAAGGTGGACGAGAACCAGAAGGCCTATTACCCCAGCATCGTGGC
                                                                                                                                                                                                                                             ACTATITGCCGTCATCGGGAGGAGCAGCCTGAACCCGGGGCTGGTGGGCCTTTCTGTGTC
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4740 GCAGCAGAGGTCTTTCTACAGCATGGCCAAAGACGCCGGCTTGGTGTGAGCCCCAGA 4799
4537 TGCAGCTAGAGGCATCTTCTACGGGATGGCCAGAGATGCTGGACTTGCCTAAAATATAT 4596
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                                                                                                                                                                                                                                                            RESULT 10

US-08-460-907B-3

Sequence 3, Application US/08460907B

Patent No. 5891724

GENERAL INFORMATION:
APPLICANT: Deeley, Roger G.
APPLICANT: Cole, Susan P.C.
TILLE OF INVENTION: METHODS FOR CONFERRING MULTIDRUG
TITLE OF SEQUENCES: 9

NUMBER OF SEQUENCES: 9
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1485 1478 1425 1305 1365 1605 2018 1898 1896 2138 2198 2016 2136 GCTGATGTTCCTGTGCTCCATGATGCAGTCGCTGATCTTACAACACTATTACCACTACAT GAGTGTGGAAAGAAAGACCATCTCCCCAGGC-----TATGCCATCACCATACACAG CTTTGTGACTGGGGTGAAGTTTCGTACTGGGATCATGGGTGTCATCTACAGGAAGGCTCT GGTTATCACCAACTCAGTCAAACGTGCGTCCACTGTGGGGGAAATTGTCAACCTCATGTC AGTGGATGCCCAGCGCTTCATGGACCTTGCCCCCTTCCTCAATCTGCTGTGGTCACC TGGAGTCGCTTTCATGGTCTTGCTGATTCCACTCAACGGAGCTGTGGCCGTGAAGATGCG CCTGAACGCCATCAAGGTGCTGAAGCTGTACGCCTGGGAGCCCAGCTTCCTGAAGCAGGT GTTTAATATCTTAAGACTTCCCCTCAACATGCTGCCCCAGTTAATCAGCAACCTGACTCA GGCCTATGTGCCCCAGCAGGCATGGATCCAGAACTGCACTCTTCAGGAAAACGTGCTTTT GGCCAGTGTGTCTCTGAAACGGATCCAGCAATTCCTGAGCCAAGAGGAACTTGACCCCCA TGGCACCTTCACCTGGGCCCAGGACCTGCCCCCCACTCTGCACAGCCTAGACATCCAGGT CCCGAAAGGGGCACTGGTGGCCGTGGGGGCCTGTGGGCTGTGGGAAGTCCTCCCTGGT GTCTGCCCTGCTGGAGAGATGGAGAAGCTAGAAGGCAAAGTGCACATGAAGGGCTCCGT

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yo g	2137	CGGCAAAGCCCTGAACCCCAAGGGGCTACCAGCAGTCTCTGGAGGCCTGTGCTTGCT	
3 6	2197		
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ος Op	2257	GTCTGGGGGCCAGCGGCAGCGGGTCAGTCTGGCTCGTTTACAGTGATGCCGATAT 2316	
Q Q	2317	TITCITGCIGGAIGACCCACTGTCCGCGGIGGACTCTCAIGTGGCCAAGCACATCTTTGA 2376	
δ d	2377	CCACGTCATCGGGCCAGAAGGCGTGCTGGCAGGCGAAGACGCGAGGTGCTGGTGACGCACGG 243	
3 2 2	2437		
Oy Dp	2497		
Qy Db	2557 2799	CTATGCCCCGATGAGGACCAAGGGCACCTGGAGGACGGCGTTGGAAGGTGC 2616	
Qy Dp	2617	AGAGGATAAGGAGGCACTGCTGAFTGAAGACACACTCAGCAACCACGGATCTGACAGA 2676	
a S	2677	CAATGATCCAGTCACCTATGTGGTCCAGAAGCAGTTTATGAGACAGCTGAGTGCCTGTC	
oy Ob	2737		
Oy Db	3004	GGTGCAGGTGACAGAGGCAGATGGGGCACTGACCAGGAGAAAGCAGCCAT 2856	
Qy Db	2857 3060	TGGCACTGTGGAGCTCAGTGTGTTCTGGGATTATGCCAAGGCCGTGGGGCTCTGTACCAC 2916	
Oy Dp	2917 3120	GCTGGCCATCTGTCTCTGTATGTGGGTCAAAGTGCGGCTGCCATTGGAGCCAATGTGTG 2976	
Ωγ Dp	2977 3180	GCTCAGTGCCTGGACAATGATGCCATGGCAGACAGTAGACAACAACAACTTCCCTGAG 3036	
Oy Db	3037	GCTGGGCGTCTATGCTGCTTTAGGAATTCTGCAAGGGTTCTTGGTGATGCTGGCAGCCAT 3096	
9	3097	GGCCATGGCAGCGGGTGGCATCCAGGCTGCCGGTGTTGCACCAGGCACTGCTGCTGCACAA 3156	
Oy Db	3157	CAAGATACGCTCGCCACAGTCCTTGTGACACCACCATCAGGCCGCATCCTGAACTG 3216	

3839 3456 4079 4139 4056 4116 4176 GCCGCCAGGCCTGGACTTCCAGTGCTCAGAGGCGGGGGAGAATCTCAGCGTGGGCCAGAG 4296 CTTCTCCAAGGACATCTATGTCGTTGATGAGGTTCTGGCCCCTGTCATCCTCATGCTGCT CAATTCCTTCTACACGCCATCTCCACTCTTGTGGTCATCATGGCCAGCACGCCGCTCTT CACATCACGCCAACTGAAGCGGCTGGAATCAGTCAGCCGCTCACCTATCTACTCCCACTT 3600 TICCTCCCGGCAGCTGAAGCCCTCGAGTCGGTCAGCCGCTCCCCGGTCTATTCCCATTT 3457 ITCGGAGACAGTGACTGGTGCCAGTGTCATCCGGGCCTACAACCGCAGCCGGGATTTTGA GATCATCAGTGATACTAAGGTGGATGCCAACCAGAGAAGCTGCTACCCCTACATCATCTC ACTATTTGCCGTCATCGGGAGGAGCAGCCTGAACCCGGGGCTGGTGGCCTTTCTGTGTC 3720 CCACCAGAGTGACCTGAAGGTGGACGAGAACCAGAAGGCCTATTACCCCCAGCATCGTGGC CAACCGGTGGCTGAGCATCGGAGTTCGTGGGGAACTGCGTGGTGGTCTTTGCTGC CTACTCCTTGCAGGTGACATTTGCTCTGAACTGGATGATACGAATGATGATGTTTGGA CTGGGTGGTGGAAGGCAGCCGCCCTCCCGAAGGTTGGCCCCCCACGTGGGGAGGTGGAGTT CCTCAATGTGGCAGACATCGGCCTCCATGACCTGCGCTCTCAGCTGACCATCATCCCGCA CACTGTGGTCATCCTGCCCCTGGCTGTGCTCTACACCTTAGTGCAGCGCTTCTATGCAGC ATCTAACATCGTGGCTGTGGAGGGGTCAAGGAGTACTCCAAGACAGAGACAGAGGCGCC CCGGAATTATTCTGTGCGCTACCGGCCCGGGCCTAGACCTGGTGCTGAGAGACCTGAGTCT CATGACCCTTTGCCTGTTCCGCATCCTGGAGGCGGCAAAGGGTGAAATCCGCATTGATGG AGAGGAGGACATTTGGTGGGCTTTGGAGCTGTCCCACCTGCACGTTTGTGAGCTCCCA GGACCCCATCCTGTTCTCGGGGACCCTGCGATGAACCTGGACCCTTCGGCAGCTACTC 3217 3277 3397 3337 3517 3577 3637 3697 3757 3960 3817 4020 3877 4200 4380 3997 4057 4260 4117 4320 4177 4237 ò g Óχ g δ q ŏ g ò Ω δy qq Óγ qq δ g g οχ qq g q g g Ω δ ò οy δy ò q ŏ q g δ qq ŏ

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4620 GTTCGAGGACTGCACCGTCCTCACCATCGCCCACCGGCTCAACACCATCATGGACTACAC 4679
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4297 GCAGCTCGTGTGCCTGGCCCGAGCCCTGCTCCGCAAGAGCCGCATCCTGGTTTTAGACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Cole, Susan P.C.
APPLICANT: Deeley, Roger G.
TITLE OF INVENTION: METHODS FOR IDENTIFYING CHEMOSENSITIZERS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: POI-002CPB TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 227-7400 TELEPHONE: (617) 227-5941 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3: LAHIVE & COCKFIELD
60 State Street, suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/463,179P
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APPLICATION NUMBER: 07/966,923
FILING DATE: 27-0CT-1992
APPLICATION NUMBER: 08/029,340
FILING DATE: 8-MAR-1993
APPLICATION NUMBER: 08/141,893
FILING DATE: 26-0CT-1993
APPLICATION NUMBER: 08/407,207
FILING DATE: 20-MAR-1995
ATORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: DeConti, Giulio A. Jr. REGISTRATION NUMBER: 31,503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CITY: Boston
STATE: Massachusetts
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EDNESS: double
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                                                        Length 5011;
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                                                           DB 3;
                                                        Score 1736.2;
Pred. No. 0;
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62.2%;
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NAME/KEY:
            . LOCATION:
US-08-463-179A-3
                                                          Query Match
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                                                                                     GCAGCTCGTGTGCCTGGCCCGAGCCCTGCTCCGCAAGAGCCGCATCCTGGTTTTAGACGA
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APPLICANT: Deeley, Roger G.
TITLE OF INVENTION: MUTIDRUG RESISTANCE PROTEINS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
STREET: Queen's University at Kingston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
FILING DATE: 05-JUN-95
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 07/966,923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/08461384B Patent No. 6025473 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08/141,893
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APPLICATION NUMBER: 08/407,207
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REGISTRATION NUMBER: 39,539
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (613) 545-2342
TELEFAX: (613) 545-6853
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 27-0CT-1992
APPLICATION NUMBER: 08/0
FILING DATE: 8-MAR-1993
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TTCCAAGGTGGATGCGAATGAGGAGGTGGAGGCTTTGATCGTCAAGTCCCCACACAAGGA 1118 458 518 444 638 698 758 818 204 264 324 384 504 564 624 Gaps 84 219 cecceareceacceercreeacresaarercaceacaecae CCCTGAGACCAGCGCTGCTTTCTCTCCCCCCTGTTTTTCTGGTGGTTCACAAAGATGGC CCTCACTCCCTGCTTCCAGAACTCCCTGCTGGCCTGGGTGCCCTGCATCTACCTGTGGGT CGCCCTGCCCTGCTACTTGCTCTACCTGCGCACCATTGTCGTGGCTACATCATCCTCTC CACCCCCTTGGTGGTGGGGGTCACCATGCTGGTGGCCACCCTGCTGATACAGTATGAGCG GGCCTGCTTCAGGGAGAAACCTCCATTTTTCTCCGCAAAGAATGTCGACCCTAACCCCTA CATCTATGGCTACCGGCATCCCCTGGAGGAGGACCTCTGGTCCCTAAAGGAAGAGGA -----AGCAGGAAAAGCAGACGGCACGACACAAGGCTTCAGCAGCACCTGGGAAAAA 999 TAGGAAGCAGCCGGTGAAGGTTGTGTACTCCTCCAAGGATCCTGCCCCAGCCGAAAGAGG CCACCTGTCCAAGCTCAAGATGGTCCTGGGTGTCCTGCTGTGGTGCGTCTCCTGGGCGGA CCTCTTCTACTCTTTCTGGGAAAGAAGTCGGGGCATATTCCTGGCCCCAGTGTTTCTGGT CGCCATCGTCCCATTCCGCTCCAAGATCCTTTTAGCCAAGGCAGAGGGTGAGATCTCAGA CCCCTTCCGCTTCACCACCTTCTACATCCACTTTGCCCTGGTACTCTCTGCCCTCATCTT CACGTCGGAACAAGTCGTGCCTGTTTTGGTAAAGAACTGGAAGAAGGAATGCGCCAAGAC 5011; 87; Length Indels CAGATCCCAGATGGTGGTGCAGCAGCTGCTGGAGGCATGGAGGA-Score 1736.2; DB 3; Pred. No. 0; 0; Mismatches 1663; recercescassacsassrscrscrsssrs-Query Match 34.2%; Best Local Similarity 62.2%; Matches 2881; Conservative TYPE: nucleic acid STRANDEDNESS: double CDS 196..4788 TOPOLOGY: linear MOLECULE TYPE: CDNA NAME/KEY: COCATION: US-08-461-384B-3 519 639 939 85 145 205 399 445 1059 265 459 325 579 505 669 565 759 625 819 685 745 789 385 841 g g à ò ô g ò g ò g ò g ò g ò g ò g οχ g ò οq ò g οy g οy g ò qq

1425 945 1119 GIGGAACCCCTCTCTTTAAGGIGTTTATACAAGACCTTTGGGCCCTACTTCCTCATGAG TGCCTGCTTCAAGCTTATCCAGGACCTGCTCTTCCATCAATCCACAGCTGCTCAGCAT CCTGATCAGGTTTATCTCCAACCCCATGGCCCCTCCTGGTGGGGCTTCCTGGTGGCTGG 1239 GCTCATCAAGTICGTGAATGACACGAAGGCCCCAGACTGGCAGGGCTACTICTACACCGT 1186.GGTTATCACCAACTCAGTCAAACGTGCGTCCACTGTGGGGGAAATTGTCAACCTCATGTC TGGAGTCGCTTTCATGGTCTTGCTGATTCCACTCAACGGAGCTGTGGCCGTGAAGATGCG regaerescerearescerearescereces GGAGGGCATCAGGCAGGGTGCTCCAGCTGCTGCGCGCGGCGGCCTACCTCCACACCAC 886 CCGGAAGCCCTCCTTCCTGAAGGCCCTGCTGGCCACCTTCGGCTCCAGCTTCCTCATCAG GCTGATGTTCCTGTGCTCCATGATGCAGTCGCTGATCTTACAACACTATTACCACTACAT AGTGGATGCCCAGCGCTTCATGGACCTTGCCCCTTCCTCAATCTGCTGTGGTCAGCACC CCTGCAGATCATCCTGGCGATCTACTTCCTCTGGCAGAACCTAGGTCCCTCTGTCCTGGC CGTGTACGTGGACCCAAACAATGTGCTGGACGCCCGAGAAGGCCTTTGTGTCTGTGTCCTT GTTTAATATCTTAAGACTTCCCCTCAACATGCTGCCCCAGTTAATCAGCAACCTGACTCA GGCCAGTGTGTCTCTGAAACGGATCCAGCAATTCCTGAGCCAAGAGGAACTTGACCCCCA GAGTGTGGAAAGAAAGACCATCTCCCCAGGC-----TATGCCATCACATACACAG CTTTGTGACTGGGGTGAAGTTTCGTACTGGGATCATGGGTGTCATCTACAGGAAGGCTCT CCTGAACGCCATCAAGGTGCTGAAGCTGTACGCCTGGGAGCCCAGCTTCCTGAAGCAGGT TGGCACCTTCACCTGGGCCCCAGGACCTGCCCCCCACTCTGCACAGCCTAGACATCCAGGT TGCCACATTCACCTGGGCCAGGAGCGACCTCCCACACTGAATGGCATCACCTTCTCCAT 946 1066 1359 1246 1599 1006 1126 1419 1306 1539 1659 1546 1779 1606 1839 1899 1959 1366 1486 1666 1726 1786 2019 1846 2079 1897 2139 ρp ò G Óγ g δy pp à q g q g οp qq δý ò δ Ω Q δ g δ g qq g Ωp ò à QΥ δ οy ò g ò g

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2199	2017	2077	2137 2379	2197	2257	2317	2377	2437	2497	2557 2799	2617 2859	2677	2737	2797	2857 3060	2917 3120	2977 3180	3037
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3419 3479 3336 3516 3719 3456 3576 3636 3839 3696 3756 3816 4019 3876 4079 GCTGAGCGTCTATGGAGCCCTGGGCATTTCACAAGGGATCGCCGTGTTTGGCTACTCCAT 3299 4259 4116 4176 4139 4056 4379 4319 CAATTCCTTCTTCAACGCCATCTCCACTCTTGTGGTCATCATGGCCAGCACGCCGCTCTT CAAGATACGCTCGCCACAGTCCTTCTTTGACACCACCATCAGGCCGCATCCTGAACTG 3457 TTCGGAGACAGTGACTGGTGCCAGTGTCATCCGGGCCTACAACCGCAGCCGGGATTTTGA 3720 CCACCAGAGTGACCTGAAGGTGGACGAGAACCAGAAGGCCTATTACCCCAGCATCGTGGC GGCCATGGCAGCGGTGGCATCCAGGCTGCCCGTGTGTTGCACCAGGCACTGCTGCACAA CTICICCAAGGACATCTATGICGTIGAIGAGGTICIGGCCCCTGICATCCICATGCTGCT 3480 GGGCTCCCTGTTCAACGTCATTGGTGCCTGCATCGTTATCCTGCTGGCCACGCCCATCGC CGCCATCATCATCCCGCCCCTTGGCCTCATCTACTTCTTCGTCCAGAGGTTCTACGTGGC CTGGGTGGTGGAAGGCAGCCGCCCTCCCGAAGGTTGGCCCCCCACGTGGGGAGGTGGAAGTT 4020 CIGGCAAATCCAGGAGAACAGCTCGCCCAGGCGGCCCAGGTGGAATT 4080 CGGGAACTACTGCCTGCGCTACCGAGAGGACCTGGACTTCGTTCTCAGGCACATCAATGT CACTGTGGTCATCCTGCCCCTGGCTGTGCTCTACACCTTAGTGCAGCGCTTCTATGCAGC CAACCGGTGGCTGAGCATCGGAGTTGGTGGGGAACTGCGTGGTGCTCTTTGCTGC ACTATITICCCGTCATCGGGAGGAGCAGCCTGAACCCGGGGCTGGTGGGCCTTTCTGTGTC CCGGAATTATTCTGTGCGCTACCGGCCCGGGCCTAGACCTGGTGCTGAGAGCCTGAGTCT GCATGTGCACGTGGCGAGAAGGTGGGGATCGTGGGCCCCCACTGGGGCTGGCCAAGTCTTC CCTCAATGTGGCAGACATCGGCCTCCATGACCTGCGCTCTCAGCTGACCATCATCCCGCA GGACCCCATCCTGTTCTCGGGGACCCTGCGCATGAACCTGGACCCCTTCGGCAGCTACTC CATGACCCTTTGCCTGTTCCGCATCCTGGAGGCGGCAAAGGGTGAAATCCGCATTGATGG 3240 3097 3300 3157 3360 3217 3420 3277 3337 3540 3517 3577 3780 3697 3757 3960 3637 3817 3877 3937 3997 4200 4057 4260 4117 4320 a qq Qγ òγ δ g á qq δ qq δ g Ωp δ g δ g ò g g Dp ò à δý Qy g õ a à ò qq ŏ g δ 9

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4177 AGAGGAGGACATTTGGTGGGCTTTGGAGCTGTCCCACCTGCACGTTTGTGAGCTCCCA 4236
                                                                                                                                 4297 GCAGCTCGTGTGCCTGGCCCGAGCCCTGCTCCGCAAGAGCCGCATCCTGGTTTTAGACGA 4356
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                                                                   GCCGGCAGGCCTGGACTTCCAGTGCTCAGAGGGCGGGGAGAATCTCAGCGTGGGCCAGAG
                                                                                                                                                                                                 4357 GGCCACAGCTGCCATCGACCTGGAGACTGACAACCTCATCCAGGCTACCATCCGCACCCA
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APPLICANT: Deeley, Roger G.
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING
TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
Queen's University at Kingston
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APPLICATION NUMBER: US/08/463,092B
FILING DATE: 05-JUN-1995
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21P: K7L 3NG
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC. Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/08463092B Patent No. 5766880 GENERAL INFORMATION:
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APPLICATION NUMBER: 08/029,340
FILING DATE: 8-MAR-1993
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FILING DATE: 26-0CT-1993
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APPLICATION NUMBER: 07/966,923
FILING DATE: 27-0CT-1992
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CORRESPONDENCE ADDRESS
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STATE: Ontario
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 5889;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 0;
0; Mismatches 1699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31.8%; Score 1612.6; 60.8%; Pred. No. 0;
                                                         ATTORNEY/AGENT INFORMATION:
NAME: Steeg, Carol Miernicki
REGISTRATION NUMBER: 39,539
REFERENCE/DOCKET NUMBER: 01546
TELEPHONE: (613) 545-2342
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 5889 base pairs
08/407,207
                       20-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 31.8 Best Local Similarity 60.8 Matches 2794; Conservative
                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
APPLICATION NUMBER:
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                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
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US-08-463-092B-5
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765	AGCAGCTGGAGGCATGGAGGAGGAGGAAAGCAGAC	0 7
805	GGCACGACACAGGCTTCAGCAGCACTGGGAAAAATGCCTCCGGCGAGGACGGGCACGACAGGAGGACGAGGACGAGGACGAGGACGAGGACGAGGAG	857 888
858 889	AGGIGCIGCIGGGTGCCCGGCCCAGGCCCCGGAAGCCCTTCC	902 948
903 949	TGAAGGCCCTGCTGGCCACCTTCGGCTCCAGCTTCCTCATCAGTGCCTGCTTCAAGCTTA	962 1008
963 1009	TCCAGGACCTGCTCTTCATCATCCACAGCTGCTCAGCTCCTGATCAGTTTATCT	1022 1068
1023 1069	CCAACCCCATGGCCCCCTCTGGTGGGGCTTCCTGGTGGCTGGGCTGATGTTCCTGTGCT	1082 1128
1083 1129	CCATGATGCAGTCGCTGATCTTACAACACTATTACCACTACATCTTTGTGACTGGGTGA 1	1142 1188
1143	AGTITCGIACTGGGAICATGGGTGTCAACAGGAAGGCTCTGGTTATCACCAACTCAG 1	1202 1248
1203 1249	TCAAACGIGCGTCCACTGIGGGGAAATTGICAACCTCATGICAGTGGATGCCCAGGGCT	1262 1308
1263 1309	TCATGGACCTTGCCCCTTCCTCAATCTGCTGTGGTCAGCACCCCTGCAGATCATCCTGG	1322
1323 1369	CGATCTACTTCCTCTGGCAGAACCTAGGTCCCTCTGCTCGCTGGGTGGCTTTCATGG	1382
1383 1429	TCTTGCTGATTCCACTCAACGGAGCTGTGGCCGTGAAGATGCGCGCCTTCCAGGTAAAGC	1442 1488
1443 1489	AAATGAAATTGAAGGACTCGCGCATCAAGCTGATGAGTGAG	1502 1548
1503 1549	TGCTGAAGCTGTACGCCTGGGAGCCCAGCTTCCTGAAGCAGGTGGAGGCATCAGGCAGG	1562 · 1608
1563 1609	GIGAGCICCAGCIGCAGCACCACACCTCCACACACACACCACCTCACCT	1622 1668
1623 1669	TGTGCAGCCCCTTCCTGGTGACCTGATCACCCTCTGGGTGTACGTGTACGTGGACCCGAT	1682 1728
1683 1729	ACAATGTGCTGGACGCCGAGAGGCCTTTGTGTCTGTGTGTG	1742 1788
1743	TTCCCCTCAACATGCTGCCCCAGTTAATCAGCAACCTGACTCAGGCCAGTGTGTCTCTGA	1802 1848

2268 2276 2388 2036 2088 2096 2148 2336 2396 2576 2682 AGCGTCTCAGGATTTTTCTGTCTCATGAGGAGCTGGAGCCAGACAGCATTGAGCGGAGGT 1908 2156 2448 2456 2508 2516 2636 2696 2756 2757 2817 2876 2877 2209 ATTACTACAAGGCAGTTATGGAAGCCTGTGCCCTTCTTCCAGATTTGGAAATCCTGCCCA TGCTGCAGCGCAACGGCTCCTTTGCCAACTTTCTCTGCAACTATGCCCCCGATGAGGACC 2710 CCGTAGGAAAGCACCTGCAGGATCTCAGCAACTCGTCTTC--------CCACA 1917 AGGACCTGCCCCCCACTCTGCACAGCCTAGACATCCAGGTCCCGAAAGGGGGCACTGGTGG CCGTGGTGGGCCTGTGGGGAAGTCCTCCCTGGTGTCTGCCCTGCTGGGAGAGA CATGGATCCAGAACTGCACTCTTCAGGAAAACGTGCTTTTCGGCAAAAGCCCTGAACCCCA CCTGGATTCAGAATGACTCTCTCCGAGAACATACTGTTTGGGCACCCCCTGCAGAAA AGCGCTACCAGCAGACTCTGGAGGCCTGTGCCTTGCTAGCTGACCTGGAGATGCTGCCTG GCGTGCTGGCAGGCAAGACGCGAGTGCTGGTGACGCACGGCATTAGCTTCCTGCCCCAGA TGGATGTCATCATGATGAGTGGCGGCAAGATCTCAGAGATGGGTTCTTATCAGGAGC CCATC-----TCCCCAGGCTATGCCATCACCATACACAGTGGCACCTTCACCTGGGCCC TGTCCGCGGTGGACTCTCATGTGGCCAAGCACATCTTTGACCACGTCATCGGGCCAGAAG AAGGCCACCTGGAGGACAGCTGGACCGCGTTGGAAGGTGCAGAGGATAAGGAGGCACTGC ACCTGGCCTCGGAGGATGACAGTGTCAGTGCTTCAGGGAAGGAGTCAAAGCCGG-----CAGACTTCATCATTGTGCTAGCTGATGGACAGGTGTCTGAGATGGGCCCGTACCCAGCCC GTCGGCCTGTACCCCGGAGGCACCTGGGTCCATCAGAGAAGGTGCAGGTGACAGAGGCGA AGGCAGATGGGGCACTGACCCAGGAGGAGAAAGCAGCCATTGGCACTGTGGAGCTCAGTG 1849 2457 1803 1863 1909 1969 1977 2029 2037 2089 2097 2149 2157 2277 2329 2337 2389 2397 2449 2509 2517 2569 2577 2629 2637 2683 2757 2758 2817 2818 QQ ò qq Q Ω οχ qq οy QQ ογ qq οχ q Q g Oy Db δy g Οy a ο̈́λ q QY QQ QΛ qq οy qq qq qq Qγ ŏ g ò

2877 TGTTCTGGGATTATGCCAAGGCCGTGGGGCTCTGTACCACGCTGGCCATCTGTCTCTGT

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AAAAGGTGGGTATTGTAGGTCGTACGGGAGCTGGGAAATCATCTCTCACCCTGGGTTTGT 4017
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MEDIUM TYPE: Floppy
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                                     2937 ATGTGGGTCAAAGTGCGGCTGCCATTGGAGCCAATGTGGTGGCTCAGTGCCTGGACAAATG
                                                                                        ATGCCATGGCAGACA - - - GTAGACAGAACAACACTTCCCTGAGGCTGGGCGTCTATGCTG
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                                TCCGCATCCTGGAGGCGCCAAAGGGTGAAATCCGCATTGATGGCCTCAATGTGGCAGACA
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APPLICANT: Cole, Susan P.C.
APPLICANT: Deeley, Roger G.
TITLE OF INVENTION: METHODS FOR IDENTIFYING
TITLE OF INVENTION: MULTIDRUG RESISTANT TUMOR CELLS
NUMBER OF SEQUENCES:
CORRESPONDENCES:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
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APPLICATION NUMBER: US/08/462,109A
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/966,923
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Patent No. 5882875
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                                                                                                                                                                                                                                                                                                                               Score 1612.6; DB 2; Length 5889;
Pred. No. 0;
0; Mismatches 1699; Indels 102;
                                   APPLICATION NUMBER: 08/407,207
FILING DATE: 20-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: DECONTI, GIULIO A. Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PQI-002CP4
TELECOMMUNICATION INFORMATION:
FILING DATE: 8-MAR-1993
APPLICATION NUMBER: 08/141,893
FILING DATE: 26-0CT-1993
APPLICATION NUMBER: 08/407,207
                                                                                                                                  TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
LENGTH: 5889 base pairs
                                                                                                                                                                                                                                                                                                                               31.8%;
60.8%;
                                                                                                                                                                                                                                                                                                                                                         Matches 2794; Conservative
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STRANDEDNESS: double
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; LOCATION: 6 4
US-08-462-109A-5
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903 TGAAGGCCCTGCTGGCCACCTTCGGCTCCTCCTCATCAGTGCCTGCTTCAAGCTTA
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ATCCAGCAATTCCTGAGGCAAGAGGAGGCAAGCCCAGAGGCAAGGCAATTTTCTCTCTC	
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CTCAACATCCTGCCA  ATCCAGGATTTTTCTGT TCCCCAGGCT  AAGAGTGAAGGGA  CTGCCCCCACTTGC  GAACCTCCCACTTGC  GAACCTCCCACTGA	
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3053 TGTTCTGGGATTATGCCAAGGCCGTGGGGCTCTGTACCACGCTGGCCATCTGTCTCTGT 2936 CTTTAGGAATTCTGCAAGGGTTCTTGGTGATGCTGGCCATGGCCATGGCAGCGGGTG 3113 GCATCCAGGCTGCCCGTGTTGCACCAGGCACTGCTGCACAACAAGATACGCTCGCCAC 3173 ACACAGTGGACTCCATGATCCCGCAGGTCATCAAGATGTTCATGGTTCACTCTTCAGTG 3297 3413 3473 3477 3654 GGAGGAGCAGCCTGAACCCGGGGCTGGTGGCCTTTCTGTGTCCTACTCCTTGCAGGTGA 3713 3777 3178 TGAGTTTCTTCGAGCGTACACCCAGTGGGAACCTAGTGAACCGATTCTCCAAGGAGCTGG 3237 3534 AGGTGGATGCCAACCAGAGAAGCTGCTACCTACATCATCTCCAACCGGTGGCTGAGCA 3593 3714 CATTIGCICIGAACIGGAIGAIACGAAIGAIGICAGAITIGGAAICIAACAICGIGGCIG 3773 AGCGGCTGGAATCAGTCAGCCGCTCACCTATCTACTCCCACTTTTCGGAGACAGTGACTG ATGTGGGTCAAAGTGCGGCTGCCATTGGAGCCAATGTGTGGCTCAGTGCCTGGACAAATG 2938 TCCTGTGCAACCATGTATCTGCACTGGCCTCTAACTATTGGCTGAGCCTCTGGACAGATG ATGCCATGGCAGACA---GTAGACAGAACAACATTCCCTGAGGCTGGGCGTCTATGCTG AGTCCTTCTTTGACACCACACCACCACCATCCTGAACTGCTTCTCCCAAGGACATCT ATGTCGTTGATGAGGTTCTGGCCCCTGTCATGCTGCTGCTCATTCCTTCTTCAACG CCATCTCCACTCTTGTGGTCATCATGGCCAGCACGCCGCTCTTCACTGTGGTCATCCTGC CCCTGGCTGTGCTCTACACCTTAGTGCAGCGCTTCTATGCAGCACATCACGGCAACTGA GTGCCAGTGTCATCCGGGCCTACAACCGCAGCCGGGATTTTGAGATCATCAGTGATACTA CCCGGCACAGCCTCAGTGCTGGTGGGGCCTCTCTGTGTCTTACTCACTGCAGATAA 3834 GCCGCCTCCCGAAGGTTGGCCCCCACGTGGGGAGGTGGAGTTCCGGAATTATTCTGTGC 2998 2877 2937 2997 3054 3058 3114 3174 3234 3238 3294 3298 3354 3358 3414 3418 3474 3478 3538 3594 3598 3658 3718 3898 δ g δ <u>6</u> δ g ōγ Dp Qγ qq Οy qq òγ QQ g b g oy O oy Oy Q Db Qy qq Qγ qq QQ Qy Db QΫ́ Qγ Op οy g

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45 TCTGGGACTCCAACCTGTCTGTGCACACAGAAAACCCGGACCTCACTCCCTGCTTCCAGA 104
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AGAAGGTGGGGATCGTGGCCCGCACTGGCGAAGTCTTCCATGACCCTTTGCCTGT
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/08460907B
Patent No. 5891724
GENERAL INFORMATION:
APPLICANT: Deeley, Roger G.
APPLICANT: Cole, Susan P.C.
TITLE OF INVENTION: METHODS FOR CONFERRING MULTIDRUG
TITLE OF INVENTION: RESISTANCE ON A CELL
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATION
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,907B
FILING DATE: 05-UUN-1995
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: 07/966,923
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CCAAGATCCTTTTAGCCAAGGCAGAGGGTGAGATCTCAGACCCCTTCCGCTTCACCACCT

CGGGGGTCCTCATTATCTTGTGTTCCTGTGTGTGTGTGCGCCATCGTCCCATTCCGCT

TCTACATCCACTTTGCCCTGGTACTCTCTGCCCTCATCTTGGCCTGCTTCAGGGAGAAAC 584

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Score 1612.6; DB 2; Length 5889;
Pred. No. 0;
0; Mismatches 1699; Indels 102;
                                                   APPLICATION DATE: 8-MAK-12).
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/141,893
                                                                                                                                                                                        APPLICATION NUMBER: 08/407,207
FILING DATE: 20-MAR-1995
CLASSIFICATION: 424
ATTORNEY AGENT INFORMATION:
NAME: Steeg, Carol Miernicki
REGISTRATION NUMBER: 39,539
REFERENCE/DOCKET NUMBER: 0151
TELEPHONE: (613) 545-2342
TELEPHONE: (613) 545-6853
INFORMATION FOR SED ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 5889 base pairs
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60.8%;
27-0CT-1992
: 424
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Best Local Similarity 60.89
Matches 2794; Conservative
                                                                                                                                                      CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0
                                 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 4589
FILING DATE: 27 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY:
; LOCATION:
US-08-460-907B-5
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Qy Dp	585	CTCCATTITCTCCCCAAAGAAGGACTCGACCCTAACCCTGAGACCAGGGCTGGCT	
Qy Dp	645	TTCTCTCCCGCCTGTTTTTCTGGTGGTTCACAAAGATGGCCATCTATGGCTACCGGCATC 704	
Qy Db	705	CCCTGGAGGAGAGCTCTGGTCCTAAAGGAAGAGAGACAGATCCCAGATGGTGCTGC 764 	
VO 4	765	80	
oy Oy	05	CIGIOCIOGRISMAITMALIGOMAGENOSMAIGIGAIAMOILCANGGANGCAGCCIGIACGGA 828 GGCACGACACAAGGCTTCAGCAGCACCTGGGAAAAATGCCTCCGGCGAGGAGG 857	
QQ	829		
Oy Dp	858	AGGIGCIGCIGCGCGGG	
ογ	903	TGAAGGCCCTGCTGGCCACCTTCGGCTTCCTCATCAGTGCCTTGAAGCTTA 962	
Q D	949	TCAAGGTGTTATACAAGACTTTTGGTCCCTACTTCCTCATGAGCTTCCTGTACAAGGCCC 1008	
Oy Dp	963	TCCAGGACCTGCTCCTTCATCAATCCACAGCTGCTCAGCATCCTGATCAGGTTTATCT 1022 	
B 5	1023	CCAACCCCATGGCCCCTCCTGGTGGGCTTCCTGGTGGCTGGGTGATGTTCCTGTGCT 1082	
oy d	1083	CCATGATGCAGTCGCTGATCTTACAACACTATTACCACTACATTGTGACTGGGGTGA 1142 	
λō	143	120	
qq	1189		
Qy Dp	1203	TCAAACGTGCGTCCACTGTGGGGGAAATTGTCAACCTCATGTCAGTGGATGCCCAGGGT 1262 	
′γ do	1263	TCATGGACCTTGCCCCTTCCTCAATCTGCTGTGGTCAGCACCCCTGCAGTCATCTGG 1322 	
δy	1323	138	
qq	1369	CCTCTACTTCCTGTGGCTGAGCTGGGCCCTTCTGTGTGTG	
oy Og	1383	TCTTGCTGATTCCACTCAACGGAGCTGTGGCCGTGAAGATGCGCGCCTTCCAGGTAAAGC 1442 	
Q P	1443	AAATGAAATTGAAGGACTGGGCATCAAGCTGAGGGGATCCTGAACGGCATCAGG 1502 	
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οy	1563	GTGAGCTCCAGCTGCGCGCGGCCTACCTCCACACACCACCTTCACCTGGA 1622	
QQ		aggagereaaggreergaagaarergeeraeerggeagergraggeagererggg	
λy	1623	TGTGCAGCCCCTTCCTGGTGACCCTGATCACCCTCTGGGTGTACGTGTACGTGGACCCAA 1682	

2036 1976 2276 TGGAGAAGCTAGAAGGCAAAAGTGCACATGAAGGGCTCCGTGGCCCTATGTGCCCCCAGCAGG 2096 AGCGCTACCAGCAGACTCTGGAGGCCTGTGCTTGCTAGCTGACCTGGAGATGCTGCCTG 2216 2209 ATTACTACAAGGCAGTTATGGAAGCCTGTGCCCTTCTTCCAGATTTGGAAATCCTGCCCA 2268 GCGTGCTGGCAGGCAAGACGCGAGTGCTGGTGACGCACGGCATTAGCTTCCTGCCCCAGA 2456 -------TGGAAATGGGATGCTGGTGACAGACA 2709 TICCCCTCAACATGCTGCCCCAGTTAATCAGCAACCTGACTCAGGCCAGTGTGTCTCTGA CCATC-----TCCCCAGGCTATGCCATCACCATACAGTGGCACCTTCACCTGGGCCC AGGACCTGCCCCCCACTCTGCACAGCCTAGACATCCAGGTCCCGAAAGGGGGCACTGGTGG GGGTCAGTCTGGCTCGAGCTGTTTACAGTGATGCCGATATTTTCTTGCTGGATGACCCAC CAGACITCAICAITGTGCTAGCIGATGGACAGGIGTCTGAGATGGGCCCGTACCCAGCCC TGGATGTCATCATTGTCATGAGTGGCGGCAAGATCTCAGAGATGGGTTCTTATCAGGAGC AAGGGCACCTGGAGGACAGCTGGACCGCGTTGGAAGGTGCAGAGATAAGGAGGCACTGC 2697 IGGICCAGAAGCAGITIAIGAGACAGCIGAGTGCCCTGICCTCAGAIGGGGAGGGACAGG GTGGGGATCAGACAGTGGAGAGAGAGGGCATTAACCTGTCTGGGGGCCCAGCGGCAGC ACCTGGCCTCGGAGGATGACAGTGTCAGTGGTTCAGGGAAGGAGTCAAAGCCGG-----= = = <u>=</u> 1669 1743 1803 1863 1909 1917 1969 2089 2389 1977 2029 2037 2157 2217 2269 2277 2329 2337 2449 2509 2569 2629 2397 2457 2517 2577 2637 2683 qq Q g ογ ΩŽ g à Q οy g ò q οy g οy οq óλ Dp οy q δy g δŽ Dp δλ q δ a qq QQ qq ŏ ò δ δ

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                                          GTCGGCCTGTACCCCGGAGGCACCTGGGTCCATCAGAGAAGGTGCAGGTGACAGAGGCGA
                                                                          AGGCAGATGGGGCACTGACCCAGGAGAGAAAGCAGCCATTGGCACTGTGGAGCTCAGTG
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- nucleic search, using sw model OM nucleic

December 18, 2002, 07:00:25; Search time 635.101 Seconds Run on:

(without alignments)
18009.573 Million cell updates/sec

US-09-647-140A-5 5079

Perfect score: Sequence:

1 ccccatggacgccctgtgcg......tgatgaaataaaactacag 5079

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

2185239 seqs, 1125999159 residues Searched:

4370478 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

N_Geneseq_101002:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	cDNA encoding a hu	Human cDNA encodin	Human multidrug re	Gene #3408 used to	Lung cancer relate	Ovary cancer relat	Multidruq resistan	cDNA encoding mult	Human multidrug re
ID		ABK61466	AAT94052	ABN96910	ABL65494	ABL67998	AAQ65377	AAT17173	AAV31497
DB	20	24	18	24	24	24	15	17	19
Length	5079	5193	4762	1977	1977	1977	5011	5011	5011
% Query re Match Length DB I	100.0	6.66	90.3	34.4	34.4	34.4	34.2	34.2	34.2
Score	5079	5071.6	4586.8	1749.4	1749.4	1749.4	1737.8	1737.8	1737.8
Result No.	1	2	m	4	S	9	7	8	6

Human multidrug re Human multidrug re	rug resista	Human ATP binding	Human multidrug re		•	Human MRP variant	Human multidrug re	MDR variant	Multidrug resistan	Human MRP variant	Murine multidrug r	Mouse multidrug re		Murine multidrug r		cDNA encoding mult		cDNA encoding mult		colon ca	cDNA encoding mult	Human ATP binding	Human canalicular	Gene #3374 used to	ä	cDNA encoding a hu	Human ATP-binding							
AAX19817 AAX21976	AAA60522	AAZ94741	AAZ90192	AAZ39555	ABK92125	AAV31498	AAX19818	AAX21977	AA290193	AAZ39556	AAV31499	AAX19819	AAX21978	AA290194	AAZ39557	AAT14910	AAT14911	AAT14912	AAT14914	AAC98147	AAT14913	AA294737	AAV26068	ABN96876	AAT94023	AAZ30081	AAD16231	AAD16258	AAD16256	AAD16257	AAD16260	AAD16261	AAD16262	AAD16263
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## ALIGNMENTS

CDNA encoding a human MPR-related ABC transporter designated MOAT-D. Human; MPR-related ABC transporter; MOAT protein; MOAT-D; MOAT mediated transport; anticancer drug sensitivity; transporter mediated cellular efflux; anticancer; ss. AAZ30080 standard; cDNA; 5079 BP. 26-JAN-2000 (first entry) AAZ30080; RESULT 1

Homo sapiens.

/*tag= a /*tag= a /*product= "MOAT-D" //transl_except= (pos: 638..640, aa: Val) //tote= "MPR-related ABC transporter" Location/Qualifiers 5..4588 W09949735-A1. Key

07-0CT-1999

99WO-US06644. 26-MAR-1999;

98US-0079759 98US-0095153 27-MAR-1998; 03-AUG-1998;

Bain Lee K, Belinsky M, CANCER WPI; 1999-610812/52 FOX CHASE P-PSDB; AAY43543 õ 

anti-cancer drugs for New transporter gene useful for screening Claim 23; Page 138-140; 153pp; English The present sequence encodes a human MPR-related ABC transporter (MOAT) protein, designated MOAT-D. The protein comprises a multi-domain structure including a tandem repeat of nucleotide binding folds appended C-terminal to a hydrophobic domain, having Walker A and B ATP binding sites and several potential membrane spanning domains. The MOAT nucleic acids are useful for screening a test compound for inhibition of MOAT mediated transport, indicated by restoration of anticancer drug sensitivity, which in turn causes a reduction of transporter mediated cellular efflux of anticancer agents. MOAT DNA or RNA may be used as probes to detect the presence or expression of genes encoding MOAT proteins. Anti-MOAT antibodies are useful for detecting and quantitating proteins MOAT

0 other; Sequence 5079 BP; 1040 A; 1476 C; 1388 G; 1175 T;

ö 180 GTCTGTGCACACAGAAAACCCGGACCTCACTCCCTGCTTCCAGAACTCCCTGCTGGCCTG 120 9 1 CCCCATGGACGCCCTGTGCGGTTCCGGGAGCTCGGCTCCAAGTTCTGGGACTCCAACCT GGTGCCCTGCATCTACCTGTGGGTCGCCCTGCCTGCTACTTGCTCTACCTGCGGCACCA 1 CCCCATGGACGCCCTGTGCGGTTCCGGGGACTCGGGTTCTGGGACTCCAACCT Length 5079; 0; Indels 20; ; 0 DB Score 5079; Pred. No. 0; ); Mismatches ó 100.0%; Best Local Similarity 100 Matches 5079; Conservative Match 61 61 121 g ö g õ

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                             CCATGACCTGCGCTCTCAGCTGACCATCATCCGGCAGGACCCCATCCTGTTCTCGGGGAC
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activity, e.g. cancers (e.g. adenocarcinoma, lymphona, prostate cancer or uterus cancer), immune response, graft-versus-host disease, acquired immunodeficiency syndrome (AIDS), asthma, Crohn's disease, hypertension, congenital heart defects, multiple sclerosis, inflammation or Albright hereditary osteodystrophy and many other diseases listed in the specification. The DNA encoding the protein is useful in gene therapy for treating the conditions. This is also useful in detection assays, chromosome mapping, tissue typing, diagnostic or prognostic assays, or

for developing a powerful assay system for functional analysis of various human disorders, as well as in diagnostic applications. I

The invention relates to an isolated polypeptide (NOVX) a mature form of NOVX, a NOVX variant (differing by no more than 15%), the nucleotide encoding NOVX (or its complement, fragment or variant). NOVX is NOVI-14, 15%, 15%, 16%, and 16%. The NOVX polypeptide, nucleic acid encoding it and antibody against it, are useful for treating or preventing (e.g. by gene therapy) a NOVX-associated disorder in humans, e.g. cardiomyopathy, atherosolerosis, a disorder related to cell signal processing and metabolic pathway modulation, diabetes or cancers. The NOVX polypeptide and nucleic acids are also useful for determining the presence of predisposition to the diseases. The NOVX nucleic acid and polypeptide are especially useful in therapeutic or prophylactic

with

disorder associated

polypeptides for treating or preventing a disorder associate 1, in humans, e.g. cardiomyopathy, atherosclerosis or cancers

P-PSDB; AAU91309

them,

Claim 1; Page 104-105; 263pp; English.

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Human; gene; ss; NOVX; gene therapy; cardiomyopathy; atherosclerosis; cell signal processing disorder; metabolic pathway modulation disorder; diabetes; cancer; adenocarcionam; lymphoma; prostate cancer; uterus cancer; immune response; graft-versus-host disease; acquired immunodeficiency syndrome; AIDS; asthma; Crohn's disease; hypertension; congenital heart defects; multiple sclerosis; inflammation; Albright hereditary osteodystrophy.
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Tomlinson JE, Topper JN,
Human cDNA encoding protein NOV14.
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2001US-267300P.
2001US-269961P.
2001US-277337P.
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                                                                                                                                                                                                                                                  27-AUG-2001; 2001WO-US26510.
                                                                                              (first entry)
                                                           ABK61466 standard; cDNA;
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Szekeres ES,
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20-MAR-2001;
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08-FEB-2001;
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1200 1266 1260 1380 1440 1500 1566 1740 1806 1866 1860 1320 1560 1686 1680 1926 2046 2040 2100 AAGTTTCGTACTGGGATCATGGGTGTCATCTACAGGAAGGCTCTGGTTATCACCAACTC VIGTGCAGCCCCTTCCTGGTGACCCTGATCACCCTCTGGGTGTACGTGTACGTGGACCC AGCTAGAAGGCAAAGTGCACATGAAGGCTCCGTGGCCTATGTGCCCCAGCAGCATG PCCAACCCCATGGCCCCCTCCTGGTGGGGCTTCCTGGTGGCTGGGCTGATGTTCCTGTG ACAATGTGCTGGACGCCGAGAAGGCCTTTGTGTCTGTGTCCTTGTTTAATATCTTAAG TTCCCCTCAACATGCTGCCCCAGTTAATCAGCAACCTGACTCAGGCCAGTGTGTCTCT "TCATGGACCTTGCCCCCTTCCTCAATCTGCTGGTCAGCACCCCTGCAGATCATCCT FICTTGCTGATTCCACTCAACGGAGCTGTGGCCGTGAAGATGCGCGCCTTCCAGGTAAA CCATCTCCCCAGGCTATGCCATCACCATACACAGTGGCACCTTCACCTGGGCCCAGGA TGCCCCCCACTCTGCACAGCCTAGACATCCAGGTCCCGAAAGGGGCACTGGTGGCCGT

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Qy	3181	CTTTGACACCACCATCAGGCCGCATCCTGAACTGCTTCTCCAAGGACATCTATGTCGT 3240 
QY	3241	ATTCCTTCTTCAACGCCATCTC 330 
Qy	3301	TCATCCTGCCCCTGGC 33 
Qy	3361	CCACATCACGGCAACTGAAGCGGCT 34
Qy	3421	SCTCACCTATCTACTCCCACTTTTCGGAGACAGTGACTGGTGCCGG 348
Qy Db		ACCGCAGCCGGGATTTTGAGATCATCAGTGATACTAAGGTGGA 35 
Qy	3541	CAACCAGAGAAGCTGCTACCCCTACATCTCCAACCGGTGGCTGAGCATCGGAGT 36 
Qy	3601	IGCGIGGIGCICITIGCIGCACIAITIGCCGICATCGGGAGGAG 36
Qy	3661	CTTGCAGGTGACATTTGC 37 
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Qy Db	3781	CAAGGAGTACTCCAAGACAGAGACACAGAGCGCCCTGGGTGGTGGTGGAGGCAGCCGCCC 38
Oy Db	3841	CCCACGIGGGGAGGIGGAGITCCGGAATTATTCIGIGCGCTACCG 39
Qy Db	3901	GCCGGCCTAGACCTGGTGCTGAGAGCCTGAGTCTGCATGTGCACGGTGGCGAGAAGGT 3960 
Qy	3961	3TCTTCCAFGACCCTTFGCCTGTTCCGCAT
QY	4021	GAAATCCGCATTGATGGCCTCAATGTGGCAGACATCGGCCT ( 
oy Db	4081	CAGCTGACCATCCCGGGGGGCCCGA 
Oy Db	4141	CCTGCGCATGAACCTGGACCCCTTCGGCAGCTACTCAGAGGAGACATTTGGTGGGCTTT 4200 
Qy	4201	AGCCGCAGGCCTGGACTTCCAGTG 4

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Homo sapiens

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Canalicular multispecific organic anion transporter protein; cCMAT protein; ATP-binding cassette transporter family; ABC transporter; hepatobiliary excretion; multidrug resistance-associated protein; MRP3; cMOAT protein activity; multidrug resistance-related protein; MDR-1; Dubin-Johnson disease; Rotor disease; Ss.
                                                                                                                                              Human multidrug resistance-associated protein 3 (hMRP3) cDNA sequence
                                   AAT94052 standard; cDNA; 4762
                                                                                                            (first entry)
                                                                                                          01-APR-1998
                                                                       AAT94052;
                AAT94052
RESULT
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240 306

247

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The present cDNA sequence encodes a human multidrug resistance-associated protein 3 (MRP3). The MRP3 gene has been localised to chromosome 17. The MRP3 protein is a member of the ATP-binding cassette (ABC) transporter family of anorganic anion transporters. MRP3 is a 4 domain protein, with 2 ATP-binding domains, and 2 domains with transmembrane regions. The correction is a homologue of MRP1, which is involved in ATP-dependent transport of glutathione conjugates such as dimitrophenyl glutathione. These substrates are also transported by a novel canalicular multispecific organic anion transported by a novel canalicular dependent cMOAT transporter system mediates hepatobiliary excretion in the liver. CMOAT may be a liver-specific homologue of multidrug collis with cMOAT protein activity. CMOAT protein activity in cells calls with cMOAT protein activity. CMOAT protein activity in cells collisense constructs, especially derived from another multidrug callstance (AMDR)-related protein, e.g. MMP-1, to the nucleic acids and vectors can be used to decrease the level of cMOAT in a cell. The nucleic acids and vectors can be used as an be used especially in diagnosis of public-Johnson acids and proteins and protein, e.g. MMP-1, it or the nucleic acids and acids and proteins and protein, allesses involving man and protein protein acids and a proteins and proteins acids and proteins and proteins and proteins of manner and acids and acids and proteins and proteins acids and proteins and proteins acids and acids and acids a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding human and rat canalicular multispecific organic transporter proteins – useful for diagnosis and treatment of Dubin-Johnson disease and Rotor disease
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                                               Cocation/Qualifiers
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Matches 4645; Conservative
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P-PSDB; AAW33363.
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Qy.	241	GCTGTGTGCGTCCTGGGCGGACCTTTTTTACTCCTTCCATGGCTGGTCCATGGC 298	
Qy Db	367	CGGGCCCCTGCTTTTCTTTGTCACCCCCTTGGTGGGGGGTCACCCATGCTGCTG 358	
Qy	359	GCCACCCTGCTGATACAGTATGAGCGGCTGCAGGGCGTACAGTCTTCGGGGGTCCTCATT 418 	
Qy Dp	419	ATCTICTGGTTCCTGTGTGGTCTGCGCCATCGTCCCATTCCGCTCCAAGATCCTTTA 478	
Qy Dp	479	GCCAAGGCAGAGGGTGAGATCTCAGCCCTTCCGCTTCACCACCTTCTACATCCACTTT 538	
Oy Dp	539	GCCCIGGTACTCTCTGCCCTCATCTTGGCCTGCTTCAGGGAGAAACCTCCATTTTTCTCC 598 	
Oy Dp	599	GCAAAGAATGTCGACCTAACCCCTACCCTGAGACCAGCGCTGGCTTTCTCTCCCGCCTG 658 	
Qy Dp	659	TTTTCTGGTGGTTCACAAAGATGGCCATCTATGGCTACCGGCATCCCCTGGAGGAGAG 718 	
Qy Db	719	GACCTCTGGTCCCTAAAGGAAGAGGACAGATCCCAGATGGTGCTGCAGCAGCTGCTGGAG 778 	
Oy Dp	779	GCATGGAGGAAGCAGAAAAGCAGACACGACACAAGGCTTCAGCAGCACCCTGGGAAA 838 	
Qy Db	839	AATGCCTCCGGCGAGGAGGTGCTGCTGGTGCCCGGCCCAGGCCCCGGAAGCCCTCC 898	
Qy Dp	899		
S G	959	CTTATCCAGGACCTGCTCCTTCATCAATCCACAGCTGCTCAGCATCCTGATCAGGTT 1018 	
Oy Dp	1019	ATCTCCAACCCCATGGCCCCCTCCTGGTGGGGCTTCCTGGTGGCTGGGC-TGATGTTCCT 1077 [	
Q Dp	1078	GTGCTCCATGATGCAGTCGCTGATCTTACAACACTATTACCACTACATCTTTGTGACT 1135 	
Qy Db	1136	PATGGGTGTCATCTACAGGAAGGCTCTGGTTATCACC 119	
Qy Dp	1196	AACTCAGTCAAACGTGCGTCCACTGTGGGGGAAATTGTCAACCTCATGTCAGTGGATGCC 1255 	
ço d	1256	CAGCGCTTCATGGACCTTGCCCCTTCCTCAATCTGCTGTGGTCAGGACCCCTGCAGATC 1315 	
	31	CUTGGCGATCTACCTCTGGCAGAACCTAGGTCCCTCTGTCCTGGCTGG	

65 56	GCAGGCAAGACGCGAGTGCTGACGCACGGCATTAGCTTCCTGCCCCA ATCATTGTGCTAGCTGATGGACAGGTGTCTGAGATGGGCCCGTACCCAGC	Qy	3536 GTGGATC
ACAGACTTC	ATCATTGTGCTAGCTGATGGACAGGTGTCTGAGATGGGCCCGTACCCAGCC 258	qa ,	S I
CTGCTG         CTGCTG	CTGCTGCAGCGCAACGGCTCCTTTGCCAACTTTCTGCAACTATGCCCCGATGAGGAC 2575 	aa aa	3596 GGAGTGG 
CAAGG	Ø 9	Qy	3656 AGGAGCA          3725 AGGAGCA
2636 CTGAT        2705 CTGAT	CTGATTGAAGACACACTCAGCAACCACGGATCTGACAGACA	Qy Dp	3716 TTTGCTC 
GTGG1       GTGG1	27	Qy Dp	3776 GAGAGGG          3845 GAGAGGG
GGTC(  - - -  - - -	GGTCGGCCTGTACCCCGGAGGCACCTGGGTCCATCAGAGAAGGTGCAGGTGACAGAGGCG 2815 	Qy Dp	3836 CGCCCTC         3905 CGCCCTC
AAGG             AAGG	AAGGCAGATGGGGCACTGACCAGGAGGAGAAGCAGCCATTGGCACTGTGGAGCTCAGT 2875 	Oy Op	3896 TACCGGC         3965 TACCGGC
GTGT       GTGT	GTGTTCTGGGATTATGCCAAGGCCGTGGGGCTCTGTACCACGCTGGCCATCTGTCCTG 2935 	Oy Op	3956 AAGGTGG         4025 AAGGTGG
TATG      TATG	TATGTGGGTCAAAGTGCGGCTGCCATTGGAGCCAATGTGTGGCTCAGTGCCTGGACAAAT 2995 	Qy Qū	2 0
GATG        GATG	GATGCCATGGCAGACAGTAGACAGACACACTTCCCTGAGGCTGGGCGTCTATGCTGCT 3055 	Oy Dp	9 LO
TTAG      TTAG	TIAGGAATTCTGCAAGGGTTCTTGGTGATGCTGGCCATGGCCATGGCGGGGGGGG	Oy Dp	36 0
ATCC ATCC	ATCCAGGCTGCCCGTGTTGCACCAGGCACTGCTGCACAACAAGATACGCTCGCCACAG 3175 	Qy	4196 GCTTTGG          4265 GCTTTGG
1001 101	TCCTTCTTTGACACCACCACCATCAGCCGCATCCTGAACTGCTTCTCCAAGGACATCTAT 3235 	Qy	4256 CAGIGCT         4325 CAGIGCT
GTCG	GTCGTTGATGAGGTTCTGGCCCCTGTCATCCTCATGCTGCTCAATTCCTTCAACGCC 3295 	Qy	4316 CGAGCCC          4385 CGAGCCC
ATCT 	33	Qy	4376 CTGGAGA                 4445 CTGGAGA
CTGG 	34	ολ	36
	CGGCTGGAATCAGTCAGCCGCTCACCTATCTACTCCCACTTTTCGGAGACAGTGACTGGT 3475 	Oy Dp	496 565
GCCAG         GCCAG	GCCAGTGTCATCCGGGCCTACAACCGCGGCGGGATTTTGAGATCATCATCATCATAGTGATACTAAG 3535 	Oy Dp	4556 TACGGGA:         4625 TACGGGA:

GCCAACCAGAGAAGCTGCTACCCCTACATCTCCCAACCGGTGGCTGAGCATC GGGATCGTGGGCCGCACTGGGCTGGCAAGTCTTCCATGACCCTTTGCTGTTC CCCGAAGGTTGGCCCCCACGTGGGGAGGTGGAGTTCCGGAATTATTCTGTGCGC CCGGCCCTAGACCTGGTGCTGAGACCTGAGTCTGCATGTGCACGGTGGCGAG CTGAACTGGATGATACGAATGATGTCAGATTTGGAATCTAACATCGTGGCTGTG CTGCTCCGCAAGAGCCGCATCCTGGTTTTAGACGAGGCCACAGCTGCCATCGAC GTCAAGGAGTACTCCAAGACAGAGACAGGGGGCGCCCTGGGTGGTGGAAGGCAGC GAGCTGTCCCACCTGCACACGTTTGTGAGCTCCCAGCCGGCAGGCCTGGACTTC CATGACCTGCGCTCTCAGCTGACCATCATCCCGCAGGACCCCATCCTGTTCTCG CTGCGCATGAACCTGGACCCCTTCGGCAGCTACTCAGAGGAGGACATTTGGTGG **ACTGACAACCTCATCCAGGCTACCATCCGCACCCAGTTTGATACCTGCACTGTC** ATCGCACACCGGCTTAACACTATCATGGACTACACCAGGGTCCTGGTCCTGGAC STAGTAGCTGAATTTGATTCTCCAGCCAACCTCATTGCAGCTAGAGGCATCTTC **ATGGCCAGAGATGCTGGACTTGCCTAAAATATATTCCTGAGATTTCCTCCTGGC** 

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The invention relates to a novel method for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumour in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, involving detecting the level of expression of two or more genes represented in ABN93503-ABN97455 in a tissue sample. The method of the invention has hepatotropic, and cytostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression,
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                                                                                                                                                                                                                                                                     Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic; metastatic liver tumour; cytostatic; expression profile; disease state; disease progression; drug toxicity; drug efficacy; drug metabolism.
                in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a patient, involves detecting the level of expression of two or more genes
CTTTCCTGGTTTTCATCAGGAAGGAAATGACACCAAATATGTCCGCAGAATGGACTTG
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Note: The sequence data for this patent did not form specification, but was obtained in electronic format
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                                                                                                                                                                                                                                   Gene #3408 used to diagnose liver cancer.
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                                                                                                                           DNA; 1977
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                                                                                             AGTCAGCCGCTCACCTATCTACTCCCACTTTTCGGAGACAGTGACTGGTGCCAGTGTCAT
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                   AGCTGAATTTGATTCTCCAGCCAACCTCATTGCAGCTAGAGGCATCTTCTACGGGATGGC
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Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                                                          Lung cancer related gene sequence SEQ ID NO:3831
                    ABL65494 standard; DNA; 1977 BP
                                                                 15-MAY-2002 (first entry)
                                           ABL65494;
                                                                                                                                                      gene;
        ABL65494
RESULT
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30-MAY-2001; 2001WO-US10838

WO200194629-A2. Homo sapiens

13-DEC-2001

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03-0CT-2000; 2000US-22, 2
03-0CT-2000; 2000US-237604P.
03-0CT-2000; 2000US-237606P.
                         2000US-233617P.
2000US-234009P.
2000US-234034P.
2000US-234052P.
2000US-234509P.
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2000US-235134P.
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02-0CT-2000;
02-0CT-2000;
02-0CT-2000;
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## (AVAL-) AVALON PHARM.

s; Horrigan Ebner R, Endress G, Carter KC, Augustus M, Weaver 2; Young PE, *H* Soppet DR,

## WPI; 2002-188264/24.

Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set

## Claim 1; SEQ ID 3831; 44pp; English.

The present invention describes a method (MI) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a respect to the anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the structure and/or properties of the agent. MI can be used in the creatment of cancer such as colon, breast, stomach, lung, thyroid, cesophageal, ovarian, kidney, prostate or pancreatic cancer.

Cadenocarcinoma, carcinoma, clear cell carcinoma, neuroendocrine infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine

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                       Length 1977
                                  15;
                                  Indels
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                      24;
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                      DB
                     Score 1749.4;
Pred. No. 0;
0; Mismatches
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           513.
and
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carcinoma
           450 A; 537
                      34.4%;
Similarity 96.7%;
39; Conservative
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Matches 1889;
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DNA;

BP

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(AVAL-) AVALON PHARM
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                                          WO200194629-A2
                                                                                          22-SEP-2000;
25-SEP-2000;
25-SEP-2000;
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25-SEP-2000;
                                   Homo sapiens
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Soppet DR,
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The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 comprises a sequence (S) selected from 8447 sequences (given in ABL61664 comprises) is indicative of anti-neoplastic activity. (I) has cytostatic expression is indicative of anti-neoplastic activity, and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, escophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lung, incompared to the concer, infiltrating ductal cancer, and infiltrating lung, according a colon, pression of the concertion and colon and c
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0; Mismatches
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Best Local Similarity 96.7
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                                                                                                              Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
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                                                                 cancer related gene sequence SEQ ID NO:6335
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Gaps

λο δ	3847	' AGGTYGGCCCCACGYGGGGAGGTGCAGTTCCGGAATTATTCTGTGCGCTACCGGCCGG	Db 17
3 8			Qy 49
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δ	9 (	CGTGGGCCGCACTGGGGCTGGCAAGTCTTCCATGACCCTTTGCCTGTTCCGCATCCTGGA 40	Qy 50, Db 19:
QQ	836	-	
Qy Db	4027	GGCGGCAAAGGGTGAAATCCGCATTGATGGCCTCAATGTGGCAGACATCGGCCTCCATGA 4086 	RESULT AAQ65377 ID AA(
Qy Dp	4087	CCTGCGCTCTCAGCTGACCATCATCCCGCAGGACCCATCCTGTTCTCGGGGACCCTGCG 4146	XX AC AA( XX DT 14
Qy Dp	4147	CATGAACCTGGACCCCTTCGGCAGCTACTCAGAGGAGACATTTGGTGGCTTTGGAGCT 420	ΣΣ
Oy Dp	4207	GTCCCACCTGCACACTTTGTGAGCTCCCAGCCGGCAGGCCTGGACTTCCAGTGCTCAGA 426	
oy Ob	4267	GGGCGGGGAGAATCTCAGCGTGGGCCAGAGCAGCTCGTGTGCCTGGCCCGAGCCCTGCT 4326	FH Key FT CDS FT XX
oy Oy	4327	CCGCAAGAGCCGCATCCTGGTTTTAGACGAGGCCACAGCTGCCATCGACCTGGAGACTGA 4386 	
Oy Dp	4387	0-0	PF 27 XX PR 27 PR 08
O.Y D.D	4447	ACACCGGCTTAACACTATCATGGACTACACCAGGGTCCTGGTCCTGGACAAAGGAGTAGT 4506 	XX PA (TC
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QY Dp	4567 1436	CAGAGATGCTGGACTTGCCTAAAATATACTCCTGAGATTTCCTCCTGGCCTTTCCTGGTT 462)	PT Mul PT COU PT and XX
Oy Dp	4627	TTCATCAGGAAGGAAATGACACCAAATATGTCCGCAGAATGGACTTGATAGCAAACACTG 46	PS Dis XX CC The CC use
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Qy	4746	TTAGATGAGGAAATGATCCCCAAGTGGTGAATGACACGCCTAAGGTCACAGCTAGTTTGA 4805 	SQ Sec Query Best
oy Oy	4806 1674	GCCAGTTAGACTAGTCCCGGTCTCCCGATTCCCAACTGAGTGTTATTTGCACACTGCAC 4865 	Matc
Oy Db	4866	TGTTTTCAAATAACGATTTTATGAAATGACCTCTGTCCTCCTGATTTTTCATATTTT 4925 	0b 21 QY 8
٥ý,	7	CTAAAGTTTCGTTTCTGTTTTTAATAAAAAGCTTTTTCCTCCTGGAACAGAAGACAGCT 498:	Db 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34.2%; Score 1737.8; DB 15; Length 5011; llarity 62.2%; Pred. No. 0; Conservative 0; Mismatches 1662; Indels 87; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ulti-drug resistance gene - encodes protein capable of onferring multi-drug resistance on cells, useful in diagnostic of treatment methods
                                                                                                                                                                                                                                                                                                                                                                                                                  ultidrug resistance protein; MRP; H69AR; cancer cell line;
tem cell; cardiac muscle; transgenic animal; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           quence 5011 BP; 1064 A; 1497 C; 1394 G; 1056 T; 0 other;
                                                                                                                                                   346 TAAAAATGGGAGTACTGATGAAATAAAACTACA 5078
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196..4791
/*tag= a
                                                                                                                                                                                                                                                              AQ65377 standard; cDNA; 5011 BP.
                                                                                                                                                                                                                                                                                                                                                                             ultidrug resistance protein.
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93US-0029340.
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nes 2882; Conserv
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<b>~</b> 0	339	CGCCCTGCCTACTTGCTCTACCTGCGGCACCATTGTCGTGGCTACATCATCATCTTC	
~ 0	399	CCACCTGTCCAAGCTCAAGATGGTCCTGGGTGTCCTGTGGTGCGTCTCCTGGGCGGA 264	
	265	CCITITIACTCCTTCCATGGCCTGGTCCATGGCCGGGCCCCTGCCCCTGTTTTTTTT	
	325	CACCCCTIGGIGGIGGIGGICACCAIGCTGCTGGCCACCCTGCTGATACAGIATGAGCG 384	
	385	GCIGCAGGCGTACAGTCTTCGGGGGTCCTCATTATCTTCTGGTTCCTGTGTGGCTTG 444	
	445	CGCCATGTCCCATTCGCTCCAAGATCCTTTTAGCCAAGGCAGAGGTGAGATCTCAGA 504	
,	505	CCCCTTCGGCTTCACCACCTTCTACATCCACTTTGCCCTGGTACTCTTGCCCCTCATCTT 564	
	565 759	GGCCTGCTTCAGGAGAAACCTCCATTTTTCTCCGCAAAGAATGTCGACCCTAACCCCTA 624 	•
	625 819	CCCTGAGACCAGGGCTGGCTTTCTCTCGCCTGTTTTCTGGTGGTGGTTGAGAGGTGGC 684	
_	685	CATCTATGGCTACGGGGATCCCCTGGAGGAGGACCTCTGGTCCCTAAAGGAAGAGGA 744 	
	745 939	CAGATCCCAGATGGTGGTGCAGCAGCTGCTGGAGGA	
	789	AGCAGGAAAAGCAGACGCACGACAAAGGCTTCAGCAGCACCTGGGAAAAA 840 	
	841	TGCCTCCGGCGAGGACGAGGTGCTGGGTGCCCGGCCCAGGCC 885	
	886 1119	CCGGAAGCCCTCCTTCCTGAAGGCCCTGCTGGCCTCCAGCTTCCTCATCAG 945	
	946 1179	TGCCTGCTTCAAGCTTATCCAGGACCTGCTCCTCATCAATCCACAGCTGCTCAGCAT 1005	
	1006 1239	CCTGAICAGGTITAICTCCAACCCCATGGCCCCTCCTGGTGGGGCTTCCTGGTGGCTGG 1065	
	1066 1299	GCTGATGTTCCTGTGCTCCATGATGCAGTCGTACAACACTATTACCACTACAT 1125 	
	1126 1359	CTTTGTGACTGGGGTGAAGTTTCGTACTGGGATCATGGGTGATCATCTACAGGAAGGCTCT 1185 	
	1186	GGTTATCACCAACTCAGTCAAACGTGCGTCCACTGTGGGGGAAATTGTCAACCTCATGTC 1245	

Q D Oy Oy Ob φo.

1665 1845 1785 2078 2198 2076 2318 2136 2378 2196 2316 1599 TGGAGTGGCGGTGATGGTCCTCATGGTGCTCGTCAATGCTGTGATGGCGATGAGAGCCAA TGGAGTCGCTTTCATGGTCTTGCTGATTCCACTCAACGGAGCTGTGGCCGTGAAGATGCG GACGTATCAGGTGGCCCACATGAAGACAAAGACAATCGGATCAAGCTGATGAACGAAAT 1546 GGAGGGCATCAGGCAGGGTGAGCTCCAGCTGCGCACGGGGGGCGTACCTCCACACCAC 1486 CCTGAACGCCATCAAGGTGCTGAAGCTGTACGCCTGGGAGCCCAGCTTCCTGAAGCAGGT 1606 AACCACCTTCACCTGGATGTGCAGCCCCTTCCTGGTGACCCTGATCACCCTCTGGGTGTA CGTGTACGTGGACCCAAACAATGTGCTGGACGCCGAGAAGGCCTTTGTGTCTGTGTCCTT GGCCAGTGTGTCTCTGAAACGGATCCAGCAATTCCTGAGCCAAGAGGAACTTGACCCCCA CAGCATCGAGCGACGCCTGTCAAAGACGGGGGGGCACGAACAGCATCACCGTGAGGAA GAGTGTGGAAAGAAAGACCATCTCCCCAGGC-----TATGCCATCACATACACAG GTCTGCCCTGCTGGGAGAGATGGAAGCTAGAAGGCAAAGTGCACATGAAGGGCTCCGT GGCCTATGTGCCCCAGCAGGCATGGATCCAGAACTGCACTCTTCAGGAAAACGTGCTTTT TGACCTGGAGATGCTGCTGGTGGGGATCAGACAGAGATTGGAGAAGAGCCATTAACCT GTCTGGGGGCCAGCGGCAGCGGGTCAGCTGTTACAGTGATGCCGATAT TGGCACCTTCACCTGGGCCCAGGACCTGCCCCCCACTCTGCACAGCCTAGACATCCAGGT CCCGAAAGGGGCACTGGTGGCCGTGGGGCCTGTGGGCTGTGGGAAGTCCTCCCTGGT CGGCAAAGCCCTGAACCCCAAGCGCTACCAGCAGACTCTGGAGGCCTGTGCCTTGCTAGC 1366 1419 1306 1539 1779 1839 1666 1899 1726 1786 2019 1846 2079 1897 2139 1957 2199 2017 2259 2319 1959 2077 2137 2257 2197 δ Ωp δy qq ò pp g q Óγ g Qγ QΥ Ω Op qq δ ò g ò QQ Ω ΩQ Óχ Q ò qq ò g qq g Q ò à

qq	2499	GTCTGGGGGACAGAAGCAGCGGGGGGGGGGGGGGGGGGG	1	
Οÿ		TITCITGCTGGATGACCCACTGTCCGGGTGGACTCTCATGTGGCCAAGCACATCTTTGA 2376	oy S	3397 CACA   
<u>අ</u>		TTACCTCTTCGATGATCCCCTCTCAGCAGTGGATGCCCATGTGGGAAAACACATCTTTGA	· vo	3457 TTCG
O D D	2619	CCACGTCATCGGGCCAGAAGGCGTGCTGGCAGGCAAGACGCGAGGTGCTGGTGACGCACGG 2436	Dp	3660 CAAC
ŏ		249	QY	3517 GATC
og q			q	3720 CCAC
\$ 6	2497	GATGGGCCCGTACCCGGCCTGCTGCAGCGCAACGGCTCCTTTGCCAACTTTCTCTGCAA 2556	Qy Dp	3577 CAAC
ò		261	Qγ	3637 ACTA
qq			qa	
δ		AGAGGATAAGGAGGCACTGCTGATTGAAGACACACCACACGCATCTGACAGA 2676	Qy	3697 CTAC       3900 TTAC
g		TCCAGGGAAGGAAGCAAAGGAAATGGAGATT	ò	3757 ATCT
ç d	2895	CAATGAICCAGTCACTATGTGGTCCAGAAGCAGTTTATGAGACAGCTGAGTGCCTGTC 2736	qq	3960 AACC
ò			Qy	3817 CTGG
. a			QQ	4020 CTGG
ογ	2797 (		οy	3877 CCGG
g	3004	GCTGAGGCCAAGAAGGAGGAGCTGGAAGCTGATGAGGCTGACAAGCGCGAGAC 3059	q	4080 CCGG
δý	2857	TGGCACTGTGGAGCTCAGTGTTTTGGGGATTATGCCAAGGCCGTGGGGCTCTGTACCAC 2916	δΣ	
qq	3060	AGGCCAGGTCAAGCTTTCCGTGTACTGGGACTACATGAAGGCCATCGGACTCTTCATCTC 3119	අු ,	
οy	2917 (	GCTGGCCATCTGTTGTTGTGGGTCAAAGTGCGGCTGCCATTGGAGCCAATGTGTG 2976	δ d	3997 CATG
qq	3120 (	CTTCCTCAGCATCTTCCTTTTCATGTGTACCATGTGTCCCGCTGGCTTCCAACTATTG 3179	3 8	
ΟŸ		GCTCAGTGCCTGGACAATGATGCCATGGCAGACAGAACAACACTTCCCTGAG 3036	r S	405/ CCTC
qq		GCTCAGCCTCTGGACTGATGACCCCATCGTCAACGGGACTCAGGAGCACACGAAAGTCCG 3239	Ã	
oy D	3037 ( 3240 (	GCTGGGCGTCTATGCGATTAGGAATTCTGCAAGGGTTCTTGGTGATGCTGGCGGCCAT 3096	qq	
0y	3097		Qy	4177 AGAGG
QQ	3300		Dp	
ογ	3157	CAAGATACGCTCGCCACAGTCCTTCTTGACACCACCATCAGGCCGCATCCTGAACTG 3216	y g	
op	3360	CATCCTGCGGTCACCCATGAGCTTCTTTGAGCGGACCCCCAGTGGGGAACCTGGTGAACCG 3419	g (	
Qy	3217	CTTCTCCAAGGACATCTATGTCGTTGATGAGGTTCTGGCCCTGTCATCCTCATGCTGCT	ò f	4297 GCAGO
QQ	3420	CTTCTCCAAGGAGCTGGACACAGTGGACTCCATGATCCCGGAGGTCATCAAGATGTTCAT 3479	2 2	
yo 4	3277 (	CAATICCTTCTTCAACGCCATCTCCACTCTTGTGGTCATCATGGCCAGCCA	S q	4337 GGCCP 11111 4560 GGCCP
3 8		505	Qy	4417 GTTTG
ζ, Op.	3540 (	333/ CACIGIGATALCTICCCCTGGCTGTGCTCTACACCTTAGTGCAGCGCTTCTATGCAGC 3396	qa	4620 GTTCG
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3816 4019 3756 3876 4079 3936 4139 3996 4199 4176 4379 4236 4439 4056 4319 4356 4416 4476 STCCTTGCAGGTGACATTTGCTCTGAACTGGATGATACGAATGATGTCAGATTTGGA 3GAGACAGTGACTGGTGCCAGTGTCATCCGGGCCTACAACCGCAGCCGGGATTTTGA CCAGAGTGACCTGAAGGTGACGAGAACCAGAAGGCTATTACCCCAGCATCGTGGC GGTGGTGGAAGGCAGCCGCCCTCCCGAAGGTTGGCCCCCCACGTGGGGAGGTGGAGTT GAAGAAGTCTGGACCTCGGAGCTGGCCCACCTGAAGGACTTCGTGTCAGCCT :ATCAGTGATACTAAGGTGGATGCCAAACCAGAGAAGCTGCTACCCTACATCATCTC CGGTGGCTGAGCATCGGAGTTGGTGGGGGAACTGCGTGGTGCTCTTTGCTGC ATTTGCCGTCATCGGGAGGAGCAGCCTGAACCCGGGGCTGGTGGGCCTTTCTGTGT JAATTATTCTGTGCGCTACCGGCCGGGCCTAGACCTGGTGCTGAGACACCTGAGTCT GTGCACGTGGCGAGAAGGTGGGGATCGTGGGCCGCACTGGGGCTGGCAAGTCTTC SGAGGACATTTGGGGCTTTGGAGCTGTCCCACCTGCACGTTTGTGAGCTCCCA GCAGGCCTGGACTTCCAGTGCTCAGAGGGCGGGGAGAATCTCAGCGTGGGCCAGAG GATACCTGCACTGTCCTGACCATCGCACACCGGCTTAACACTATCATGGACTACAC SCTCGTGTCCTGCCCCGAGCCCTGCTCCGCAAGAGCCGCATCCTGGTTTTAGACGA ACAGCTGCCATCGACCTGGAGACTGACAACCTCATCCAGGCTACCATCCGCACCCA

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The present sequence encodes a multi-drug resistance protein (MRP), isolated from H69AR, a small cell lung cancer cell line, which is about 50-did resistant to doxorubicin as compared to the parental H69 cell line. The human MRP gene has been mapped to 16p13.1, and is not linked to either CFTR or MDR genes. The MRP protein is overapressed in multi drug resistant cellsindependently of overexpression of P-glycoprotein camember of a superfamily of membrane proteins, across cell membranes, and associated with a variety of tumours). Antisense nucleic acids can be used to protect a drug sensitive cell from cytotoxicity due to exposure to a drug, or to develop improved forms of therapy, particularly for small cell lung cancers which exhibit a high initial response to chemotherapy which is almost always followed by a
              4477 CAGGGTCCTGGTCCTGGACAAAGGAGTAGTAGCTGAATTTGATTCTCCAGCCAACCTCAT
                                                      4537 TGCAGCTAGAGGCATCTTCTACGGGATGGCCAGAGATGCTGGACTTGCCTAAAATATATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - for
                                                                                                                                                                                                                                                                                                                     MRP; multi-drug resistance protein; small cell lung cancer; protect; cytotoxicity; therapy; P-glycoprotein; ss.
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/product= multi-drug_resistance_protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Column 41-52; 50pp; English.
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P-PSDB; AAR93153.
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08-MAR-1993;
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999 TAGGAAGCAGCCGGTGAAGGTTGTGTACTCCTCCAAGGATCCTGCCCAGCCGAAAGAGA 1058
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                                                                                                     85 CCTCACTCCCTGCTTCCAGAACTCCCTGCTGGCCTGGGTGCCCTGCATCTACCTGTGGGT
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                                                     DB 17; Length 5011;
                          Sequence 5011 BP; 1064 A; 1497 C; 1394 G; 1056 T; 0 other;
                                                                   Pred. No. 0;
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                                                     Score 1737.8;
multi-drug resistance form of the disease.
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                                                Query Match
Best Local Similarity 62,28
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DNA encoding protein associated with multi-drug resistance - useful

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                                            The human and murine MRP nucleic acid molecules can be used as probes fidentlfying multidary resistant tumour cells by hybridisation to mRNA from tumour cells. The antisense nucleic acid can be used to reverse multidary resistance (MDR). A recombinant expression vector containing the MRP nucleic acid molecules operatively linked to at least one regulatory sequence can be used to transform a host cell to produce a recombinant MDR-associated protein.
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                                                                                                                                                                          Score 1737.8; DB 19; Length 5011; Pred. No. 0; 0; Mismatches 1662; Indels 87;
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                                                        GCCGGCAGGCCTGGACTTCCAGTGCTCAGAGGGCGGGGAGAATCTCAGCGTGGGCCAGAG
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                     GGACCCCATCCTGTTCTCGGGGACCCTGCGATGAACCTGGACCCTTCGGCAGCTACTC
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                                                                                                                                                               4417 GTTTGATACCTGCACTGTCCTGACCATCGCACACCGGCTTAACCACTATCATGGACTACAC
                                                                                                                                                                                                                                                                                                                                                         Human; multidrug resistance-associated protein; MRP; cytotoxic cancer; chemotherapy; ds.
                                                                                                                                                                                                                                                                                                                                            Human multidrug resistance-associated protein encoding cDNA
                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                  AAX19817 standard; cDNA; 5011 BP
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93US-0029340.
93US-0141893.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                    cells against cytotoxic drugs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 20;
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Matches 2882; Conservative
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Deeley RG;
                                          WPI; 1999-253868/21.
P-PSDB; AAW99893.
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CATCTATGGCTACGGCATCCCTGGAGGAGGAGGACCTCTGGTCCCTAAAGGAAGAAGA	CAGATCCCAGATGGTGGTGCAGCTGCTGGTGGAGGA			TAGGAAGCAGCCGGTGAAGGTTGTACTCCTCCAAGGATCCTGCCCAGCCGAAAAGACAG	TGCCTCCGGCGAGGACGAGGTGCTGCTGGGTG		CCGGAAGGCCCTCCTTGAAGGCCCTGCTGGCCACCTTCGGCTCCAGCTTCCTCAG	GTGGAACCCCTCTGTTTAAGGTGTTATACAAGACCTTTGGGCCCTACTTCCTCATGAG	TGCCTGCTTCAAGCTTATCCAGGACCTGCTCTTCATCAATCCACAGCTGCTCAGCAT		CCTGATCAGGTTTATCTCCAACCCCATGGCCCCCTCCTGGTGGGGCTTCCTGGTGGTGG	GCTCATCAAGTTCGTGAATGACACGAAGGCCCCAGACTGCGAGGGCTACTTCTACACGT	GCTGATGTTCCTGTGCTCCATGATGCAGTCGCTGATCTTACAACACTATTACCACTACAA		CTTTGTGACTGGGGTGAAGTTTCGTACTGGGATCATGGGTGTCATCTACAGGAAGGCTCT		GGTTATCACCAACTCAGTCAAACGTGGGGTGGTGGGGGGAAATTGTCAACCTCATGTC		TGGATC		TGCAG	CCTGCAAGTCATCCTTGCTCTCTACCTCCTGTGGCTGAATCTGGGCCCTTCCGTCCTGGC	GAGTCG		CCTTCC	GACGTATCAGGTGGCCCACATGAAGAGAAATGGGATCAAGCTGATGAACGAAAT	TGAACC		AGGGCA		CCACCI		CGTGTACGTGGACCCAAACAATGTGCTGGACGCCGAGAAGGCCTTTGTGTGTG	CGTGACCATTGACGAGAACAACATCCTGGATGCCCAGACAGCCTTCGTGTCTTTGGCCTT	GTTTAATATCTTAAGACTTCCCCTCAACATGCTGCCCCAGTTAATCAGCAACCTGACTCA
685 C. 879 Te	745 C		789	. 999 TA	841 TC		986 CC		946 TC	1179 CI	1006 CC	1239 GC	1066 GC	1299 GC	1126 CT	           	1186 GG		1246 AG	1479 TC	1306 CC	1539 CC	1366 TG		1426 CG	1659 GA	1486 CC	1719 TC	1546 GG	1 1779 GC	1606 AA	1839 GG	1666 CG	1899 CG	1726 GT
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GGCCAGTGTGTCTCTGAAACGGATCCAGCAATTCCTGAGCCAAGAGGAACTTGACCCCCA 1845 GAGTGTGGAAAGAAAGACCATCTCCCCAGGC-----TATGCCATCACCATACACAG 1896 2136 2196 2438 2498 2316 2376 2436 2496 2738 2618 GGTGCAGGTGACAGAGGCGAAGGCAGATGGGGCACTGACCCAGGAGGAGAAAGCAGCCAT 2856 TGGATGTCAGCTGGAGGAACCATATACAGGTCCGTGATACAGGCCTGTGCCCTCCTCCC GGCCTATGTGCCCCCAGCAGGCATGGATCCAGAACTGCACTCTTCAGGAAAACGTGCTTTT CCACGTCATCGGGCCAGAAGGCGTGCTGGCAGGCAAGACGCGAGTGCTGGTGACGCACGG TGGCACCTTCACCTGGGCCCAGGACCTGCCCCCACTCTGCACAGCCTAGACATCCAGGT GTCTGCCCTGCTGGGAGAGGTGGAGAAGCTAGAAGGCAAAGTGCACATGAAGGGCTCCGT CGGCAAAGCCCTGAACCCCAAGCGCTACCAGCAGACTCTGGAGGCCTGTGCCTTGCTAGC GTCTGGGGGCCAGCGGCAGCGGGTCAGTTGGCTCGAGCTGTTTACAGTGATGCCGATAT GATGGCCCCGTACCCAGCCCTGCTGCAGCGCAACGGCTCCTTTGCCAACTTTCTCTGCAA CATTAGCTTCCTGCCCCAGACAGACTTCATCATTGTGCTAGCTGATGGACAGGTGTCTGA CTATGCCCCCGATGAGGACCAAGGGCACCTGGAGGACAGCTGGACCGCGTTGGAAGGTGC AGAGGATAAGGAGGCACTGCTGATTGAAGACACCACTCAGCAACCACACGGATCTGACAGA CTCAGATGGGGAGGGACAGGGTCGGCCTGTACCCCGGAGGCACCTGGGTCCATCAGAGAA CAATGATCCAGTCACCTATGTGGTCCAGAAGCAGTTTATGAGACAGCTGAGTGCCCTGTC

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                                                                                       4177 AGAGGAGACATTTGGTGGGCTTTGGAGCTGTCCCACCTGCACACGTTTGTGAGCTCCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human multidrug resistance-associated protein coding sequence
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This sequence encodes the human multidrug resistance-associated (MDR)
protein. The invention relates to a method for identifying a multidrug
resistant (WDR) tumour cell. Compositions and methods utilising the MDR
proteins can be used to treat patients with tumours displaying multidrug
resistance, particularly those displaying resistance to anthracyclines,
epipodophyllotoxins, vinca alkaloids, and hydrophobic drugs. The methods
for inhibiting/killing a MDR tumour cell can be useful for treating
breast cancer, leukaemias, fibrosarcomas, cervical cancer, gliomas,
thyomas, neuroblastomas and lung cancer. The MDR DNA sequences when
labeled are useful as molecular probes for diagnosing multidrug
resistance of a tumour (using cells from a tumour biopsy) and for
designing ribozymes which are capable of cleaving a single-stranded
nucleic acid encoding a protein having MRP activity. Recombinant
expression vectors containing human MDR coding sequences can be
transfected into a drug sensitive cell line to produce a protein in the
cell which confers MDR, protecting non-resistant non-tumour cells from
the effects of chemotherapeutics has major clinical importance. Cells
transformed with the MDR coding sequences are useful for testing
potential therapeutic agents for their effectiveness against MDR cells
and for identifying chemosensitisers of a therapeutic agent. with an antibody/antigen-binding fragment - which binds to an expressed protein encoded by multidrug resistance-associated protein (MRP) nucleic acid Claim 1; Column 51-62; 80pp; English. (TOOH ) UNIV QUEENS KINGSTON 93US-0141893. 95US-0407207. 93US-0029340 Deeley RG; WPI; 1999-214061/18. P-PSDB; AAW74470. 08-MAR-1993; 26-OCT-1993; 20-MAR-1995; Cole SPC, 

Length 5011; Sequence 5011 BP; 1064 A; 1497 C; 1394 G; 1056 T; 0 other; Score 1737.8; DB 20; Lengt Pred. No. 0; Mismatches 1662; Indels 0; 34.2%; ilarity 62.2%; Conservative ( Similarity Query Match

9 CCTCACTCCCTGCTTCCAGAACTCCCTGCTGGCCTGGGTGCCCTGCATCTACCTGTGGGT 144 GGCCCTGCCCTGCTACTTGCTCTACCTGCGGCACCATTGTCGTGGCTACATCATCCTCTC 204 Gaps CTGTTTCCCCTTCTACTTCTTCTCTCCCGACATGACCGAGGCTACATTCAGATGAC CCACCTGTCCAAGCTCCAAGATGGTCCTGGTGCTGCTGGTGCGTCTCCTGGGCGGA CCTTTTTTACTCCTTCCATGGCCTGGTCCATGGCCGGGCCCCTGCTGTTTCTTTGT CACCCCTTGGTGGTGGGGGTCACCATGCTGCTGGCCACCCTGCTGATACAGTATGAGCG Matches 2882; Best Local 25 219 82 279 145 339 205 399 592 459 325 519 385 g ò 음 ò 9 ò q ò g ò q ð 5 ò

1418 TAGGAAGCAGCCGGTGAAGGTTGTGTACTCCTCCAAGGATCCTGCCCAGCCGAAAGAGAG 1058 639 TGCCCTAGCCATCCTGAGATCCAAAATTATGACAGCCTTAAAAGAGGATGCCCAGGTGGA 1119 GTGGAACCCCTCTCTGTTAAGGTGTTATACAAGACCTTTGGGCCCTACTTCCTCATGAG GGCCTGCTTCAGGGAGAAACCTCCATTTTTCTCCGCAAAGAATGTCGACCCTAACCCCTA CACGTCGGAACAAGTCGTGCTGTTTTGGTAAAGAACTGGAAGAAGGAATGCGCCAAGAC GGTTATCACCAACTCAGTCAAACGTGCGTCCACTGTGGGGGAAATTGTCAACCTCATGTC CGCCATCGTCCCATTCCGCTCCAAGATCCTTTTAGCCAAGGCAGAGGGTGAGATCTCAGA CCCTGAGACCAGCGCTGCTTCTCTCCCCGCCTGTTTTTCTGGTGGTTCACAAAGATGGC -----AGCAGGAAAAGCAGGCACGACACAAAAAAA TGCCTGCTTCAAGCTTATCCAGGACCTGCTCTTCATCAATCCACAGCTGCTCAGCAT AGTGGATGCCCAGGGTTCATGGACCTTGCCCCTTCGTCATCTGCTGGTCAGCACC CCCCTTCCGCTTCACCTCCTACATCCACTTTGCCCTGGTACTCTGCCCTCATCTT 886 CCGGAAGCCCTCCTTCCTGAAGGCCCTGCTGGCCACCTTCGGCTCCAGCTTCCTCATCAG CATCTATGGCTACCGGCATCCCCTGGAGGAGGACCTCTGGTCCCTAAAGGAAGAGGA 1179 CTTCTTCTTCAAGGCCATCCACGACCTGATGATGTTTTCCGGGCCGCAGATCTTAAAGTT 1006 CCTGATCAGGTTTATCTCCAACCCCATGGCCCCCTCCTGGTGGGGGCTTCCTGGTGGCTGG GCTGATGTTCCTGTGCTCCATGATGCAGTCGCTGATCTTACAACACTATTACCACTACAT CTTTGTGACTGGGGTGAAGTTTCGTACTGGGATCATGGGTGTCATCTACAGGAAGGCTCT CTTCGTCAGTGGCATGAGGATCAAGACCGCTGTCATTGGGGCCTGTCTATCGGAAGGCCCT CGCCTTCCAGGTAAAGCAAATGAAATTGAAGGACTCGCGCATCAAGCTGATGAGTCAGAT GACGTATCAGGTGGCCCACATGAAGACAAAGACAATCGGATCAAGCTGATGAACGAAAT CCTGAACGGCATCAAGGTGCTGAAGCTGTACGCCTGGGAGCCCCAGCTTCCTGAAGCAGGT CAGATCCCAGATGGTGGTGCAGCAGCTGCTGGAGGCATGGAGGA-------CCTGCAGATCATCCTGGCGATCTACTTCCTCGCAGAACCTAGGTCCCTCTGTCCTGGC TGGAGTCGCTTTCATGGTCTTGCTGATTCCACTCAACGGAGCTGTGGCCGTGAAGATGCG TGGAGTGGCGGTGATGGTCCTCATGGTGCCCGTCAATGCTGTGATGGCGATGAAGACCAA 445 669 265 759 819 685 879 745 939 666 1066 1299 1126 1186 ( 1246 505 625 789 1419 1359 1539 1599 1486 g Dp Qγ g g δý q g q g δ ò QΩ ò g ŏ δ ò ŏ q δ g g ð 셤

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Qy Db	1546 GGAGGGCATCAGGCAGGGTGAGCTCCAGCTGCGCCACGGCGGCCTACCTCCACACACA	1605 1838
Oy Dp	1606 AACCACCTTCACCTGGATGTGCAGCCCCTTCCTGGTGACCCTGATCACCCTCGGGTGTA	1665 1898
Oy Dp	1666 CGTGTACGTGGACCCAAACAGCTGGACGCCGAGAAGGCCTTTGTGTGTG	1725 1958
Oy Db	1726 GTTTAATATCTTAAGACTTCCCCTCAACATGCTGCCCCAGTTAATCAGCAACCTGACTCA	1785 2018
Q _Y	1786 GGCCAGTGTCTCTGAAACGGATCCAGCAATTCCTGAGCCAAGAGGAACTTGACCCCCA	1845 2078
Qy Dp	y 1846 GAGTGTGGAAAGAAGACCATCTCCCCAGGCTATGCCATCACCATACACA 1	896 138
Qy Dp	y 1897 TGGCACCTTCACCTGGGCCCAGGACCTGCCCCCACTCTGCAGGCTAGACATCCAGGT 1	956 198
6 Q	y 1957 CCCGAAAGGGGCACTGGTGGCCGTGGGGCCTGTGGGCTGTGGGAAGTCCTCCCTGGT 2	016 258
Qy Dp	y 2017 GTCTGCCCTGCTGGGAGAGGTGGGGTAGGCTAGAAGGGAAAGTGCACATGAAGGGCTCCGT 2	076 318
Qy Dp	y 2077 GGCCTATGTGCCCCAGCAGGCATGGATCCAGAACTGCACTCTTCAGGAAAACGTGCTTTT 2	136 378
Oy Db	2 2137 CGGCAAAGCCCTGAACCCCAAGCGCTACCAGCAGACTCTGGAGGCCTGTGCCTTGCTAGC 2 11	196 438
Qy Db	7 2197 TGACCTGGAGATGCTGCCTGGGGATCAGACAGAGATTGGAGAGAGA	256 498
Qy Db	7 2257 GTCTGGGGGCCAGCGGCAGCGGGTCAGTCTGGCTCGAGCTGTTACAGTGATGCCGATAT 2	316 558
Qy Dp	y 2317 TITCTIGCIGGATGACCCACIGICCGGGTGGACTCTCATGTGGCCAAGCACATCTTGA 2	376 618
Oy Op	7 2377 CCACGTCATCGGCCAGAAGCGTGCTGGCAGCCAAGACGCGAGTGCTGGTGACGCACGG 2 1	436
Oy Db	7 2437 CATTAGCTTĊCTGCCCAGACAGACTTCATCATGTTGTGCTAGCTGATGGACAGGTGTCTGA 2 III	496 738
Oy Dp	7 2497 GATGGGCCCGTACCCAGCCCTGCTGCAGCGCAACGGCTCCTTTGCCAACTTTCTCTGCAA 2	556
ζō	2557 CTATGCCCCCGATGAGGACCAAGGGCACCTGGAGGACGCTGGAAGGTGC :	`

2736 2948 3239 2796 2976 3036 3096 3300 GGCCGTGTCCATCGGGGGGATCTTGGCTTCCCGCTGTCTGCACGTGGACCTGCTGCACGAG 3359 CAAGATACGCTCGCCACAGTCCTTCTTTGACACCACCACCATCAGGCCGCATCCTGAACTG 3216 CAATTCCTTCTTCAACGCCATCTCCACTCTTGTGGTCATCATGGCCAGCACGCCGCTCTT 3336 140 GGGCTCCCTGTTCAACGTCATTGGTGCCTGCATCGTTATCCTGCTGGCCCATCGC 3539 CTATGCCAGCACAGCAGCAGCAGCATGCAGAGGAGAACGGGGTCACGGGCGTCAGCGG 2858 AGAGGATAAGGAGGCACTGCTGATTGAAGACACCTCAGCAACCACACGGATCTGACAGA 2676 GGCCATGGCAGCGGGTGGCATCCAGGCTGCCCGTGTTGCACCAGGCACTGCTGCACAA 3156 3457 ITCGGAGACAGTGACTGGTGCCAGTGTCATCGGGCCTACAACCGCAGCCGGGATTTTGA 3516 CTGTTTGCGGTGATCTCCAGGCACAGCCTCAGTGCTGGCTTGGTGGGCCTCTCAGTGTC 3899 GCTGGGCGTCTATGCTTTAGGAATTCTGCAAGGGTTCTTGGTGATGCTGGCAGCCAT CTCAGATGGGGAGGGACAGGGTCGGCCTGTACCCCGGAGGCACCTGGGTCCATCAGAGAA GCTCAGTGCCTGGACAAATGATGCCATGGCAGACAGTAGACAGAACAACACTTCCCTGAG CAATGATCCAGTCACCTATGTGGTCCAGAAGCAGTTTATGAGACAGCTGAGTGCCCTGTC GGTGCAGGTGACAGGCGAAGGCAGATGGGGCACTGACCCAGGAGGAGAAAGCAGCAT TGGCACTGTGGAGCTCAGTGTTTCTGGGATTATGCCAAGGCCGTGGGGCTCTGTACCAC GCTGGCCATCTGTCTCCTGTATGTGGGGTCAAAGTGCGGCTGCCATTGGAGCCAATGTGT CTTCTCCAAGGACATCTATGTCGTTGATGAGGTTCTGGCCCCTGTCATCCTCATGCTGCT CACTGTGGTCATCCTGCCCCTGGCTGTGCTCTACACCTTAGTGCAGCGCTTCTATGCAGC CCACCAGAGTGACCTGAAGGTGGACGAGACCAGAAGGCCTATTACCCCCAGCATGGTGGC ACTATTTGCCGTCATCGGGAGGAGCAGCCTGAACCCGGGGCTGGTGGGCCTTTCTGTGTC GATCATCAGTGATACTAAGGTGGATGCCAACCAGAGAAGCTGCTACCCTACATCTC CAACCGGTGGCTGAGCATCGAGTTCGTGGGGAACTGCGTGGTGCTCTTTGCTGC 2799 2617 2677 2949 2797 2895 2737 3060 2917 2859 3004 2857 2977 3037 3277 3097 3157 3217 3337 3517 3637 3840 3660 3720 3577 3780 q Dβ δ ò q δy δ qq δý q Op QQ PP Οý Οy ò ŏ q οy qq Qγ qq Οy g QΛ QQ  $^{\circ}$ Op QY g g g ò Ω Qγ

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The present invention describes an antibody or antigen-binding fragment, which binds to a multidrug resistance-associated protein (MMP). The antibody or antigen-binding fragment does not bind only to a nucleotide antibody or antigen-binding fragment does not bind only to a nucleotide binding fold of the protein corresponding to the amino acid residues of 61-810 or the amino acid residues 1310-1469 of the amino acid sequence of given in AAB03582. The MMP is encoded by a fully defined 5011 bp sequence (the present sequence) or its allelic variant. The protein confers multidrug resistance to a drug-sensitive mammalian cell in which confers multidrug resistance is not substantially reversed by chemosensitisers, which reverse P-19roprotein-mediated multidrug resistance. The antibodies and bispecific and terameric antibody resistance. The antibodies and bispecific and treating multidrug resistant tumours, for inhibiting multidrug resistance of a cell by blocking the activity of an MMP, and for killing a multidrug resistance conferes and quantify the amount of MMP in a sample in order to diagnose multidrug resistance and determined the role of MMP in a particular cellular or pathological state. The new antibodies may be used in treating cancers and tumours, however the antibodies may be used in treating cancers and tumours, however the antibodies may be used in treating cancers and tumours, however the antibodies may be used in treating calculate to
                                                                                              Multidrug resistance protein; MRP; cytostatic; gene therapy; diagnosis; tumour; cancer; antibody; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New anti-multidrug resistance-associated protein antibodies useful identifying and treating multidrug resistant tumors and inhibiting
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                                                                                                                                                                                                                                                                                                                                            /*tag= a
/product= "multidrug resistance protein"
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                                      П
                               Multidrug resistance protein nucleotide sequence SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 5; Column 47-58; 58pp; English.
                                                                                                                                                                                                                                                                   Location/Qualifiers
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93US-0141893.
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Matches 2882; Conservative
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AAA60522 standard; cDNA; 5011 BP.

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17-OCT-2000 (first entry)

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CTGTTTCCCCTTCTACTTCCTCTTCTCCCGACATGACCGAGGTACATTCAGATGAC	CCACCTGTCCAAGCTCAAGATGGTCCTGGGTGCTGTGTGGTGCGTCTCCTGGGCGGAAIIIIIIIIII	CCTTTTTACTCCTTCCATGGCCTGGTCCATGGCCGGGCCCCTGCCCTGTTTTCTTTGT	CACCCCTIGGIGGIGGIGGICACCAIGCTIGCTGCCACCTIGCIGAIACAGIAIGAGGGIIIII	GCTGCAGGGCGTACAGTCTTCGGGGGTCCTCATTATCTTCTGGTTCCTGTGTGTG	CGCCATCGTCCCATTCCGCTCCAAGATCCTTTTAGCCAAGGCAAGGGGTGAGATCTCAGA		GGCCTGCTTCAGGAGAAACCTCCATTTTCTCCGCAAAGAATGTCGACCCTAACCCCTA	CCCTGAGACCAGGGCTGGCTTTCTCCCCGCCTGTTTTCTGGTGGTGTTCACAAAGATGGC	CATCTATGGCTACGGGCATCCCCTGGAGGAGGACCTCTGGTCCCTAAAGGAAGAGGA 	CAGATCCCAGATGGTGGTGCAGCAGCTGCAGGAGGA	AGCAGGAAAAGCAGGCACGACACAAAGGCTTCAGCAGCCTGGGAAAAA	TGCCTCCGGCGAGGACGAGGTGCTGGGTGCCCGGCCCAGGCC	CCGGAAGCCCTCCTTCCTGAAGGCCCTGCTGGCCACCTTCGGCTCCAGCTTCCTCATCAG	TOCCTGCTTCAAGCTFATCCAGACCTGCTCTTCATCAATCCACAGCTGCTCAGCTTCATCATCATCAAGCGCTCAGCTTAAGTTTTCCGGGCCGCAGATCTTAAAGTT	CCTGATCAGGTTTATCTCCAACCCCATGGCCCCTCCTGGTGGGGCTTCCTGGTGGCTGG	GCTGATGTTCCTGTGCTCCATGATGCAGTCGCTGATCTTACAACACTATTACCACTACAT	CTTTGTGACTGGGGTGAAGTTTCGTACTGGGATCATGGGTGTCATCTACAGGAAGGCTCT	GGTTATCACCAACTCAAACGTGCGTCCACTGTGGGGGAAATTGTCAACCTCATGTC
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1365 1425 1485 1665 1898 2018 2136 GGAGGGCATCAGGCAGGGTGAGCTCCAGCTGCCACACGCGGCCTACCTCCACACCAC 1605 GGCCAGTGTGTCTCTGAAACGGATCCAGCAATTCCTGAGCCAAGAGGAACTTGACCCCCA 1845 2019 GGCGAGTGTCTCCCTCAAACGCCTGAGGATCTTTCTCTCCCATGAGGAGCTGGAACCTGA 2078 2198 2318 2378 1846 GAGTGTGGAAAGAAAGACCATCTCCCCAGGC-----TATGCCATCACCATACACAG 1896 2196 2438 2498 CCTGAACGGCATCAAGGTGCTGAAGCTGTACGCCTGGGAGCCCAGCTTCCTGAAGCAGGT 1839 GGGCACCTTCACCTGGGTCTGCACGCCCTTTTCTGGTGGCCTTGTGCCACATTTGCCGTCTA CCTGCAGATCATCCTGGCGATCTACCTCCTGGCAGAACCTAGGTCCCTCTGTCCTGGC TGGAGTCGCTTTCATGGTCTTGCTGATTCCACTCAACGGAGCTGTGGCCGTGAAGATGCG AACCACCTTCACCTGGATGTGCAGCCCCTTCCTGGTGACCCTGATCACCCTCTGGGTGTA GTTTAATATCTTAAGACTTCCCCTCAACATGCTGCCCCCAGTTAATCAGCAACCTGACTCA TGGCACCTTCACCTGGGCCCAGGACCTGCCCCCCCACTCTGCACGCCTAGACATCCAGGT CCCGAAAGGGGCACTGGTGGCCGTGGGGCCTGTGGGCTGTGGGAAGTCCTCCCTGGT 2017 GTCTGCCCTGCTGGGAGAGATGGAGAAGCTAGAAGGCAAAGTGCACATGAAGGGCTCCGT GGCCTATGTGCCCCAGCAGGCATGGATCCAGAACTGCACTCTTCAGGAAAACGTGCTTTT CGGCAAAGCCCTGAACCCCAAGCGCTACCAGCAGACTCTGGAGGCCTGTGCCTTGCTAGC TGACCTGGAGATGCTGCCTGGTGGGGATCAGACAGAGATTGGAGAGAAGGGCATTAACCT GTCTGGGGGCCAGCGGCAGCGGGTCAGTCTGGCTCGAGCTGTTTACAGTGATGCCGATAT 1306 1539 1366 1426 1719 1546 1606 1899 1726 1959 1786 1599 1659 1486 1666 2379 1897 1957 2077 2319 2137 2197 2439 2257 2499 qq ò Вb Dp ŏ g οy οy QQ ōλ Q ΟY Db ΩŸ qq Qy Db δy qq  $^{\circ}$ ρp δy δy ρp QY Db Óλ Dp δy g ŏ Pρ  $^{\circ}$ g ÓΣ

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CAAGCAC	GCTGGTG	CTTGGTC	TGGACAG	II II	CAACTTT	I II	CGCGTTGC	SACGGGCC	CACGGATO		SCTGAGTO	III II	GGTCCAI	I I	GAGAAAG	GACAAGG	SGGCTCI	I I I I I	GGAGGG	- III	AACACTT			TTTGGCT	GCACTGC	GACCTGG	CGCATCC	AACCTGG	ATCCTCA	GTCATCAAGA	AGCACGC	GCCACGC	CGCTTCT	AGGTTCT	ATCTACT
ATGTGGC	CGCGAGT	CGCGGAT	TAGCTGA	- TGAGTGG	CCTTTGC	CCTTCGC	GCTGGAC	ACGGGGT	GCAACCA		TGAGACA	GCTGGTGACGGACAGTGCAGCAACTGCAGAGACAGCTCAGCAGCTCCTC	GGCACCTO	11111 AGCACCG	CCCAGGA	 TGGAGGC	AGGCCGT	AAGGCCATCGGACTCT	CTGCCAT	1 - 1 - 1	GACAGAAC	LIII I	Julio Julio Li	11 11	TGCACCAC	IIIII FGCACGTG	CATCAGGC	CCAGTGG	CCCTGTC	GGAGGTC	rcatggc	II II rccigcig	PAGTGCAG	rcgrccad	SCTCACCI
SGACTCTC	AGGCAAGA	IIIII BAACAAGA	ATTGTGC	II II SATCGICA	PACGGCT	11111 GACGGCG	GAGGACA	IIIII I I GAGGAGAACG	ACACTCA	GGCAT	CAGTTTA		CCCCGGA	GGCACCACAAC	GCACTGA	IIII	TATGCCA	TACATGA	AGTGCGG	CATGTGT	GACAGTA	AACGGGA	ייייייייייייייייייייייייייייייייייייייי	CAAGGGA	CGTGTGT	11 CGCTGTC	ACCACAC	CGGACCC	GTTCTGG	ATGATCC	GTGGTCA	ATCGTTA	TACACCT	TACTTOT	GTCAGCC
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2317 TT    2559 TT	2377 CC.		2437 CA	11 2679 CA	2497 GA	11 2739 GAS	2557 CT	11 2799 CT	2617 AG	2859 TC	2677 CA	2895	2737 CTC	11   2949 CTC	2797 GG1		2857 TGC				2977 GCI				3097 GGC	3300 GGC	3157 CAA		3217 CTT		3277 CAP	3480 GG	3337 CAC	3540 CGC	3397 CACATCACGGCAACTGAAGCGGCTGGAATCAGTCAGCCGCTCACCTATCTACTCCCACTT
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3659 3516 3576 3636 3816 3876 4079 3698 3899 3756 3959 3936 3668 4056 4259 4176 4416 4356 4536 TICTCCGGCAGCTGAAGGCCTGGAGTCGGTCAGCCGCTCCCGGGTCTATTCCCATTT TTCGGAGACAGTGACTGGTGCCAGTGTCATCCGGGCCTACAACCGCAGCCGGGATTTTGA CCACCAGAGTGACCTGAAGGTGGAGACCAGAACGCCTATTACCCCAGCATCGTGGC CAACCGGTGGCTGACATCGGAGTGGAGTTCGTGGGGAACTGCGTGGTGCTCTTTGCTGC CTACTCCTTGCAGGTGACATTTGCTCTGAACTGGATGATACGAATGATGTCAGATTTGGA CTGGGTGGTGGAAGGCAGCCGCCCTCCCGAAGGTTGGCCCCCCACGTGGGGAGGTGGAGTT CCGGAATTATTCTGTGCGCTACCGGCCGGGCCTAGACCTGGTGCTGAGAGACCTGAGTCT GCATGTGCACGGTGGCGAGAGGTGGGGATCGTGGGCCGCCACTGGGGCTGGCAAGTCTTC AGAGGAGGACATTTGGTGGCTTTTGGAGCTGTCCCACCTGCACGTTTGTGAGCTCCCA CAGGGTCCTGGTCCTGGACAAAGGAGTAGTAGTGAATTTGATTCTCCAGCCAACCTCAT CATGACCCTTTGCCTGTTCCGCATCCTGGAGGCGGCAAAGGGTGAAATCCGCATTGATGG GGACCCCATCCTGTTCTCGGGGACCCTGCGCATGAACCTGGACCCTTCGGCAGCTACTC GCCGGCAGGCCTGGACTTCCAGTGCTCAGAGGGCGGGGAGAATCTCAGCGTGGGCCAGAG GCAGCTCGTGTGCCTGGCCCGAGCCCTGCTCCGCAAGAGCCGCATCCTGGTTTTAGACGA GGCCACAGCTGCCATCGACCTGACTGACAACCTCATCCAGGCTACCATCCGCACCCA

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4680 AAGGGTGATCGTCTTGGACAAAGGAGAAATCCAGGAGTACGGCGCCCCCATCGGACCTCCT 4739
                                                                   TGCAGCTAGAGGCATCTTCTACGGGATGGCCAGAGATGCTGGACTTGCCTAAAATATATT 4596
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                                                                                                                                          4740 GCAGCAGAGAGGTCTTTTCTACAGCATGGCCAAAGACGCCCGGCTTGGTGTGTGAGCCCCAGA 4799
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lupus erythematosus; diagnosis; gene therapy; MRP1;
multidrug resistance associated protein; chromosome 16q13.12;
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for treating atherosclerosis and
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Gaps 84

87;

Score 1737:8; DB 21; Length 5011;

Pred. No. 0; 0; Mismatches 1662; Indels

34.28;

Best Local Similarity 62.2 Matches 2882; Conservative

25

Pp à

Query Match

	147	AGTGGATGCCCAGCGCTTCATGGACCTTGCCCCTTCCTCAATCTGCTGTGAGCACC 1305	CCTGCAGATCATCCTGGCGATCTACTTCCTCTGGCAGAACCTAGGTCCCTCTGTCCTGGC 1365	TGGAGTCGCTTTCATGGTCTTGCTGATTCCACTCAACGGAGCTGTGGCCGTGAAGATGCG 1425	CGCCTTCCAGGTAAAGCAAATGAAAGGACTCGCGCATCAAGCTGATGAGTGAG	CCTGAACGGCATCAAGGTGCTGAAGGTGTACGCCTGGGAGCCCAGCTTCCTGAAGCAGGT 1545 	GGAGGGCATCAGGCAGGGTGAGCTCCAGCTGCGCACCGCGCCTACCTCCACACCC 1605	AACCACCTTCACCTGGATGTGCAGCCCCTTCCTGGTGACCCTGATCACCCTCTGGGTGTA 1665	CGTGTACGTGGACCCAAACAACTGCTGGACGCCGAGAAGGCCTTTGTGTCTGTGTCCTT 1725 	GTTTAATATCTTAAGACTTCCCCTCAACATGCTGCCCCAGTTAATCAGCAACCTGACTGA	GGCCAGTGTGTCTCTGAAACGGATCCAGCAATTCCTGAGCCAAGAGGAACTTGACCCCCA 1845 	GAGTGTGGAAAGAACATCTCCCCAGGCTATGCCATCACCATACAGAG 1896	TGGCACCTTCACCTGGGCCCAGGACCTGCCCCCCACTCTGCAGACATCCAGGT 1956	CCCGAAAGGGCACTGGTGGCCGTGGGGCCTGTGGGAAGTCCTCCTGGT 2016	GTCTGCCCTGCTGGAGAGATGGAGAAAGCTAGAAGTGCACATGAAGGGCTCCGT 2076	GGCCTATGTGCCCCAGCAGGCATGGATCCAGAACTGCACTCTTCAGGAAAACGTGCTTTT 2136  [	CGGCAAAGCCCTGAACCCCAAGCGCTACCAGCAGACTCTGGAGGCCTGTGCTAGC 2196	TGACCTGGAGATGCTGCTGGTGGGGATCAGACAGAGATTGGAGAGGGCATTAACCT 2256
	0	1246 AGTGGATGCCCAGCGCTTCATGGACCTTGC 	1306 CCTGCAGATCATCCTGGCGATCTACTTCCT 	1366 TGGAGTCGCTTTCATGGTCTTGCTGATTCC 	1426 CGCCTTCCAGGTAAAGCAAATGAAATTGAA 	1486 CCTGAACGCATCAAGGTGCTGAAGCTGTA 	1546 GGAGGGCATCAGGCAGGTGAGCTCCAGCT 	1606 AACCACCTTCACCTGGATGTGCAGCCCCTT	1666 CGTGTACGTGGACCCAAACAATGTGCTGGA 1111	1726 GTTTAATATCTTAAGACTTCCCCTCAACAT 	1786 GGCCAGTGTGTCTCTGAAACGGATCCAGCA 	846 080	897 140	957	017	077 320	2137 CGGCAAAGCCCTGAACCCCAAGCGCTACCA 	2197 TGACCTGGAGATGCTGCCTGGTGGGGATCA
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2440 AGACCTGGAAATCCTGCCCAGTGGGGATCGGACAGAGTTGGCGAGAAGGGCGTGAACCT 2499 2496 2739 2617 AGAGGATAAGGAGGCACTGCTGATTGAAGACACACTCAGCAACCACGGATCTGACAGA 2676 2949 2916 2976 3156 3216 GGGCTCCCTGTTCAACGTCATTGGTGCCTGCATCGTTATCCTGCTGGCCCACGC 3540 TITCITGCTGGATGACCCACTGTCGGGGGGGACTCTCATGTGGCCAAGCCACTTTTGA 2560 TTACCTCTTCGATGATCCCCTCTCGGGAAGCACACATGTTGG CATTAGCTTCCTGCCCCAGACAGACTTCATCATTGTGCTAGCTGATGGACAGGTGTCTGA CTTCCTCAGCATCTTCCTTTTCATGTGAACCATGTGTCCGCGCTGCCTCCAACTATTG CCACGTCATCGGGCCAGAAGGCGTGCTGGCAGGCAAGACGCGAGTGCTGGTGACGCACGG GATGGGCCCGTACCCAGCCCTGCTGCAGCGCAACGGCTCCTTTGCCAACTTTCTCTGCAA CTATGCCCCCGATGAGGACCAAGGGCACCTGGAGGACAGCTGGACGCTTGGAAGGTGC CTATGCCAGCAGAGCAGGAGCAGGATGCAGAGGAGAACGGGGTCACGGGGGTCAGGGGGGTCAGGGG TCCAGGAAGGAAAGGAAATGAAATGCCAT------CTCAGATGGGGAGGACAGGGTCGGCCTGTACCCCGGAGGCACCTGGGTCCATCAGAGAA GCTCAGTGCCTGGACAAATGATGCCATGGCAGACAGTAGACAGAACAACACTTCCCTGAG GTCTGGGGGCCAGCGGCAGCGGGTCAGTCTGGCTCGAGCTGTTTACAGTGATGCCGATAT CAATGATCCAGTCACCTATGTGGTCCAGAAGCAGTTTATGAGACAGCTGAGTGCCCTGTC 3061 AGGCAGGTCAAGCTTTCCGTGTACTGGGACTACATGAAGGCCATCGGACTCTTCATCTC ----GCTGAGGCCAAGAAGGAGGACCTGGAAGCTGAAGGCGCAGAC GGTGCAGGTGACAGAGGCGAAGGCAGATGGGGCACTGACCCCAGGAGGAGAAAGCAGCAT TGGCACTGTGGAGCTCAGTGTGTTCTGGGATTATGCCAAGGCCGTGGGGGCTCTGTACCAC 2917 GCTGGCCATCTGTCTCTCTATGTGGGTCAAAGTGCGGCTGCCATTGGAGCCAATGTGT GCTGGGCGTCTATGCTGCTTTAGGAATTCTGCAAGGGTTCTTGGTGATGCTGGCAGCCAT GGCCATGGCAGCGGGTGGCATCCAGGCTGCCGGTGTGTTGCACCAGGCACTGCTGCACAA CAAGATACGCTCGCCACAGTCCTTCTTTGACACCACCACCATCAGGCCGCATCCTGAACTG CAATTCCTTCTTCAACGCCATCTCCACTCTTGTGGTCATCATGGCCAGCACGCCGCTCTT CTTCTCCAAGGACATCTATGTCGTTGATGAGGTTCTGGCCCCTGTCATCCTCATGCTGCT 2500 2680 2257 2317 2377 2437 2497 2557 2800 2860 2677 2896 2737 2797 3005 2857 3181 ( 2950 3121 3037 3481 2977 3241 3421 3097 3301 3157 3361 3217 3277 Q g g òγ Qγ Ω Op δy Db Qγ q  $Q_{Y}$ Ω δ qq δ Ω Qγ Op δy q g Op  $\delta$ δy Ω qq Qγ g δ g qq Ωp Qγ òγ ογ

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resistance protein; MRP; human; anthracycline; Vinca alkaloid;
                                                                       TGCAGCTAGAGGCATCTTCTACGGGATGGCCAGAGATGCTGGACTTGCCTAAAATATATT 4596
                                                                                        GCAGCAGAGAGGTCTTTTCTACAGCATGGCCAAAGACGCCGGCTTGGTGTGAGCCCCAGA 4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                         to at least two drug and Vinca alkaloids,
CAGGGTCCTGGTCCTGGACAAAGGAGTAGTAGCTGAATTTGATTCTCCAGCCAACCTCAT
                                                                                                                                                                                                                            Human multidrug resistance protein (MRP) nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated protein conferring multidrug resistance, selected from anthracyclines, epipodophyllotoxins on a drug sensitive mammalian cell -
                                                                                 epipodophyllotoxin; cancer; leukaemia; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Column 51-62; 78pp; English
                                                                                                                                                                       AAZ90192 standard; cDNA; 5011 BP
                                                                                                                                                                                                                                                                                                                                              92US-0966923.
93US-0029340.
93US-0141893.
95US-0407207.
                                                                                                                                                                                                                                                                                                                                                                                           QUEENS KINGSTON
                                                                                                                                                                                                                                                                                                                              95US-0461384
                                                                                                                                                                                                            (first entry)
                                                                                                          CCTGAGATTTC 4607
                                                                                                                            4801 GCTGGCATATC 4811
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This sequence represents a human multidrug resistance protein (MRP) nucleocide sequence. The human MRP encoded by this sequence confers multidrug resistance, including resistance to at least two drugs selected from anthracyclines, epipodophyllotoxins and vinca alkaloids, on a drug sensitive mammalian cell, when the protein is expressed in the cell. The multidrug resistance is not substantially reversed by chemosensitizers which reverse P-glycoprotein-mediated multidrug resistance. The MRP protein sequence can be used to generate antibodies against MRP. The MRP protein and nucleotide sequences can be used in compositions which are used to treat patients with tumours displaying multidrug resistance. The compositions and methods of the invention can be used particularly to treat breast cancer, leukaemias, fibrosarcomas, cervical cancer, gliomas, MRP can be used to inhibit the multidrug resistance of a multidrug

Sequence 5011 BP; 1064 A; 1497 C; 1394 G; 1056 T; 0 other;

resistant cell

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aps	84	144	398	264	324	384	444	504	564	624	684	744	788	840	885	1118 945	1178	1005
Match 34.2%; Score 1737.8; DB 21; Length 5011; Local Similarity 62.2%; Pred. No. 0; es 2882; Conservative 0; Mismatches 1662; Indels 87; G	S CGGGGAGCTCGGCTCCAAGTTCTGGGACTCCAACTGTGTGCACACAGAAAACCCGGA 	5 CCTCACTCCCTGCTTCCAGAACTCCCTGGTGGCCTGGGTGCCCTGCATCTACCTGTGGGT	5 CGCCCTGCCTGCTACTTGCTCTACCTGCGGCACCATTGTCGTGGCTACATCATCTCTC	5 CCACCTGTCCAAGCTCAAGATGGTCCTGGGTGTCCTGCTGTGGTGCGTCCCTGGGGGGGA   1	5 CCTTTTTTACTCCTTCCATGGCCTGGTCCATGGCCGGGCCCCTGCCCTGTTTTCTTTGT	5 CACCCCTTGGTGGTGGGGGTCACCATGCTGGTGGCCACCTGCTGATACAGTATGAGCG   1   1   1   1   1   1   1   1   1	5 GCTGCAGGGCTACAGTCTTCGGGGGTCCTCATTATCTTCTGGTTCCTGTGTGTG	5 CGCCATCGTCCCATTCCGCTCCAAGATCCTTTTAGCCAAGGCAGAGGTGAGATCTCAGA 	5 CCCCTTCCGCTTCACCACTTCTACATTTGCCCTGGTACTCTTGCCCTCATCTT	5 GGCCTGCTTCAGGGAGAAACCTCCATTTTCTCCGCAAAGAATGTCGACCCTAACCCCTA	5 CCCTGAGACCAGGGCTTTCTCTCCCGGCTGTTTTTCTGGTGGTTCACAAAGATGGC	5 CATCTATGGCTACCGGCATCCCCTGGAGGAGGACCTCTGGTCCCTAAAGGAAGAGGA   1   1   1   1   1   1   1   1   1	5 CAGATCCCAGATGGTGCAGCAGCTGCAGGGGATGGAGGA	on on		n w	σ	6 IGCCTGCTTCAAGCTTATCCAGGACCTGCTCTTCATCAATCCACAGCTGCTCAGCAT
Query M Best Lo Matches	25	275	33	39	45	325	385 579	445 639	505	565 759	625	685	745	78:	841	88	111	946
<b>-</b>	Qy Db	Qy Db	Qy Db	Qy Db	Qy Db	Qy Db	ογ Dp	QY Db	Oy Dp	oy D	Qy Db	Oy Db	QY Db	QY Db	δo	δά	Q .	O.y Db

1485 CCTGATCAGGTTTATCTCCAACCCCATGGCCCCCTCCTGGTGGGGCTTCCTGGTGGCTGG 1065 1425 1785 GGAGGGCATCAGGCAGGGTGAGGTCCAGCTGCCACGCGGGCTACCTCCACACCAC 1605 GGCCAGTGTGTCTCTGAAACGGATCCAGCAATTCCTGAGCCAAGAGGAACTTGACCCCCA 1845 2198 2318 1839 GGGCACCTTCACCTGGGTCTGCACCCCTTTCTGGTGGCCTTGTGCACTTTGCCGTCTA 1898 GAGTGTGGAAAGAAAGACCATCTCCCCAGGC-----TATGCCATCACCATACACAG 1896 GGCCTATGTGCCCCCAGCAGGCATGGATCCAGAACTGCACTCTTCAGGAAAACGTGCTTTT 2136 GCTGATGTTCCTGTGCTCCATGATGCAGTGGATCTTACAACACTATTACACTACAT CTTTGTGACTGGGGTGAAGTTTCGTACTGGGATCATGGGTGTCATCTACAGGAAGGCTCT CCTGCAAGTCATCCTTGCTCTCTACTCCTGTGGCTGAATCTGGGCCCTTCCGTCCTGGC 2019 GGCGAGTGTCTCCCTCAAACGCCTGAGGATCTTTCTCTCCCCATGAGGAGCTGGAACCTGA 1186 GGTTATCACCAACTCAGTCAAACGTGCGTCCACTGTGGGGGAAATTGTCAACCTCATGTC 1246 AGTGGATGCCCAGCGCTTCATGGACCTTGCCCCCTTCCTCAATCTGCTGTGGTCAGCACC CGCCTTCCAGGTAAAGCAAATGAAATTGAAGGACTCGCGCATCAAGCTGATGAGTAA CCTGAACGCCATCAAGGTGCTGAAGCTGTACGCCTGGGAGCCCAGCTTCCTGAAGCAGGT GTTTAATATCTTAAGACTTCCCCTCAACATGCTGCCCCAGTTAATCAGCAACCTGACTCA 1306 CCTGCAGATCATCCTGGCGATCTACTTCCTCTGGCAGAACCTAGGTCCCTCTGTCCTGGC TGGAGTCGCTTTCATGGTCTTGCTGATTCCACTCAACGGAGCTGTGGCCGTGAAGATGCG CCCGAAAGGGGCACTGGTGGCCGTGGTGGGCCTGTGGGCAAGTCCTCCTGGT AACCACCTTCACCTGGATGTGCAGCCCCTTCCTGGTGACCCTGATCACCCTCTGGGTGTA CGTGTACGTGGACCCAAACAATGTGCTGGACGCCGAGAAGGCCTTTGTGTCTGTGTCCTT 2079 CAGCATCGAGCGACGGCTGTCAAAGACGGCGGGGGGCACGAACAGCATCACCGTGAGGAA TGGCACCTTCACCTGGGCCCAGGACCTGCCCCCCACTCTGCACACACCCTAGACATCCAGGT 1139 TGCCACATTCACCTGGGCCAGGACCCTCCCACACTGAATGGCATCACCTTCTCCAT 1299 1006 1066 1126 1359 1539 1366 1599 1426 1659 1486 1546 1779 1606 1666 1899 1726 1959 1786 1846 2259 1897 2199 2017 1957 2077 ρp  $\dot{\Omega}$ οy qq ŏλ g ŏ QΩ qq q δ ò  $\Omega$ g ò g δ Dp ŏ q ŏ qq g ŏ qq QQ Dp Ω δ ò g δ qq g δ ò

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- E	GACTCTGGAGGCCTGTGCTAGC 21	AGAGATTGGAGAGGGCATTAACCT 22 	TCGAGCTGTŤTACAGTGATGCCGATAT 23	GA 2	CAAGACGCGAGTGCTGGTGACGCACGG 24	TGTGCTAGCTGATGGACAGGTGTCTGA 24:	GGGCTCCTTTGCCAACTTCTCTGCAA 25: 		ACTCAGCAACCACGGATCTGACAGA 267.	SITIATGAGACAGCTGAGTGCCCTGTC 273	CCGGAGGCACCTGGGTCCATCAGAGAA 27	ACTGACCCAGGAGAGAAAGCAGCCAT 28	3 2	3 2	<b>ω</b> ω	AGGGTTCTTGGTGATGCTGGCAGCCAT 309 	rGTGTTGCACCAGGCACTGCTGCACAA 31 (1111   1   1   1   1   1   1   1   1	PACACCATCAGCCGCATCCTGAACTG 32.
	CGGCAAAGCCCTGAACCCCAAGCGCTACCAGCAGACTCTGGAGGCCTGTGCCTTGCTAGC	TGACCTGGAGATGCTGCTGGTGGGGATCAGACAGAGATTGGAGAGAGA	GTCTGGGGGCCAGCGGGTCAGTCTGGCTCGAGCTGTŤTACAGTGATGCCGATAT 	TTTCTTGCTGGATGACCCACTGTCCGGGTGGACTCTCATGTGGCCAAGCACATCTTT 	CCACGTCATCGGGCCAGAAGGCGTGCTGGCAGGCAAGACGCGGGTGCTGGTGACGCACGG	CATTAGCTTCCTGCCCAGACAGACTTCATCATTGTGCTAGCTGATGACAGGTGTCTGA	GATGGGCCCGTACCCAGCCCTGCTGCAGCGCAACGGCTCCTTTGCCAACTTTCTCTGCAA	CTATGCCCCGATGAGGACCAGAGGCACTGGAGGACAGCTGGACGCGTTGGAAGGTGC	agaggataaggaggcactgctgattgaagacacactcagcaaccacggatctgacaga 	CAATGATCCAGTCACCTATGTGGTCCAGAAGCAGTTTATGAGACAGCTGAGTGCCCTGTC	CTCAGATGGGGACAGGGTCGGCCTGTACCCCGGAGGCACCTGGGTCCATCAGAGA	GGTGCAGGTGACAGAGGGAAGGCAGATGGGGCACTGACCAGGAGGAGAAAGCAGCAT 	TGGCACTGTGGAGCTCAGTGTGTTCTGGGATTATGCCAAGGCCGTGGGGCTCTGTACCAC	GCTGGCCATCTGTCTCTGTATGTGGGTCAAAGTGCGGCTGCCATTGGAGCCAATGTGTG	GCTCAGTGCCTGGACAAATGATGCCATGGCAGACAGTAGACAGAACAACTTCCCTGAG 	GCTGGGCGTCTATGCTGCTTTAGGAATTCTGCAAGGGTTCTTGGTGATGCTGGCAGCCAT	GGCCATGGCAGCGGGGGCATCCAGGCTGCCCGTGTGTTGCACCAGGCACTGCTGCACAA 	CAAGATACGCTCGCCACAGTCCTTGTTGACACCACCATCAGGCCGCATCCTGAACTG
2319	2137	2197	2257	2317	2377	2437 2679	2497 2739	2557 2799	2617 2859	2677 2895	2737	3004	2857	2917 3120	3180	3037	3097	3157
Q	Qy Db	Qy Db	Qy Db	Oy Db	oy Db	Qy Db	Oy Dp	Qy Dp	oy Db	Qy Db	60 G	Oy Dp	Oy Dp	oy Op	Oy Dp	oy Op	Oy Dp	, ολ

3636 3899 3456 3698 3816 4019 4079 3936 4199 4056 4116 3457 TTCGGAGACAGTGACTGGTGCCAGTGTCATCCGGGCCTACAACCGCAGCCGGGATTTGA 3516 3876 4439 CATCCTGCGGTCACCCATGAGCTTCTTTGAGCGGACCCCCAGTGGGAACCTGGTGAACCG 3419 CTACTCCTTGCAGGTGACATTTGCTCTGAACTGGATGATACGAATGATGTCAGATTTGGA 3756 GCATGTGCACGGTGGCGAGAAGGTGGGGATCGTGGGGCCACTGGGGGCTGGCAAGTCTTC 3996 CAATTCCTTCATCACGCCATCTCCATCTTGTGGTCATGGCCAGCACGCCGCTCTT CTTCTCCAAGGACATCTATGTCGTTGATGAGGTTCTGGCCCCTGTCATCCTCATGCTGCT CACTGTGGTCATCCTGCCCCTGGCTGTGCTCTACACCTTAGTGCAGCGCTTCTATGCAGC CACATCACGGCAACTGAAGCGGCTGGAATCAGTCAGCCGCTCACCTATCTACTCCCACTT CAACCGGTGGCTGAGCATCGGAGTTCGTGGGGAACTGCGTGCTGCTTTTGCTGC ACTATTTGCCGTCATCGGGAGGAGCAGCCTGAACCCGGGGCTGGTGGGCCTTTCTGTGTC 3757 ATCTAACATCGTGGCTGTGGAGAGGGTCAAGGAGTACTCCAAGACAGAGACAGAGGCGCC 3960 AACCAACATGTGGTGGAGAGGTCTCAAGGAGTATTCAGAGACTGAGAAGGAGGCGCC 3877 CCGGAATTATTCTGTGCGCTACCGGCCCGGGCCTAGACCTGGTGCTGAGAGACCTGAGTCT CATGACCCTTTGCCTGTTCCGCATCCTGGAGGCGGCAAAGGGTGAAATCCGCATTGATGG CCTCAATGTGGCCAGACATCGGCCTCCATGACCTGCGCTCTCAGCTGACCATCATCCCGCA GGACCCCATCCTGTTCTCGGGGACCCTGCGCATGAACCTGGACCCCTTCGGCAGCTACTC AGAGGAGACATTTGGTGGGCTTTGGAGCTGTCCCACCTGCACACGTTTGTGAGCTCCCA CTGGGTGGTGGAAGGCAGCCGCCCTCCCGAAGGTTGGCCCCCCACGTGGGGAGGTT 3480 3397 3660 3360 3420 3277 3337 3217 3577 3637 3697 3937 4260 3817 3997 4057 4117 4320 4177 g δy g Ω g Qγ Q δy g δ pp QΥ Q Οy Op Qγ g οy g οŻ qq Óλ QQ δŽ QQ δŻ qq QΥ qq οy Dp ОР g Ω q ò ð.

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The invention provides a method for identifying a substance which is a chemosensitizer that comprises, contacting a cell transfected with nucleic acid encoding multidrug resistance-associated protein (MRP) with
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                                                                                           CAGGGTCCTGGTCCTGGACAAAGGAGTAGTAGCTGAATTTGATTCTCCAGCCAACCTCAT 4536
                                                                                                                                     GCAGCAGAGAGGTCTTTTTTTATAGAGGCCAAAGACGCCGGCTTGGTGAGCCCCCAGA 4799
                                                                                                                                                                  TGCAGCTAGAGGCATCTTCTACGGGATGGCCAGAGATGCTGGACTTGCCTAAAATATATT 4596
                                                                                                                                                                                                                                                                                                                                                               Chemosensitizer; multidrug resistance-associated protein; MRP; human; therapeutic agent; P-glycoprotein-mediated multidrug resistance; lung;
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                                       GTTTGATACCTGCACTGTCCTGACCATCGCACCGGCTTAACACTATCATGGACTACAC
 GCAGCTCGTGTGCCTGGCCCGAGCCCTGCTCCGCAAGAGCCGCATCCTGGTTTTAGACGA
                                                                                                                                                                                                                                                                                                                                          Human multidrug resistance-associated protein (MRP) encoding cDNA.
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protein
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a therapeutic agent in vitro. The method is useful for identifying chemosensitizers which may then be used to treat cancer (especially lung cancer). The method allows the identification of chemosensitizers which do not reverse P-glycoprotein-mediated multidrug resistance. The present sequence represents a cDNA encoding a human MRP.
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                                                                                     34.2%; Score 1737.8; DB 21; Lengt ilarity 62.2%; Pred. No. 0; Conservative 0; Mismatches 1662; Indels
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	CAATCCACAGCTGCTCAG 	GIGGGCTTCCIGGIGGC 	ACAACACTATTACCACȚA 	TGTCATCTACAGGAAGGC 	GGAAATTGTCAACCTCAT 	CAATCTGCTGTGGTCAGC                   TAACATGATCTGGTCAGC	CCTAGGTCCCTCTGTCCT                         TCTGGGCCCTTCCGTCCT	AGCTGTGGCCGTGAAGAT 	CATCAAGCTGATGAGTGA 	GCCCAGCTTCCTGAAGCA 	GGCGCCTACCTCCACAC 	CCTGATCACCCTCTGGGT                   CTTGTGCACATTTGCCGT	GCCTTGTGTCTGTGTC 	GTTAATCAGCAACCTGAC 	CCAAGAGGAACTTGÁCCC 	-TATGCCATCACCATACACAG 	GCACAGCCTAGACATCCA 	CTGTGGGAAGTCCTCCTG
	AGGACCTCTCCTTCA:              NGACCTGATGATGTTTT	ACCCATGGCCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTC	GATGCAGTCGCTGATCT1 	TTCGTACTGGGATCATGGC i	ACGTGCGTCCACTGTGGC 	rgaccttccccttccr 	CTACTTCCTCTGGCAGAAA                       CTACCTCTGTGGCTGAA	GCTGATTCCACTCAACGC 	GAAATTGAAGGACTCGCC                   GAAGAGCAAAGACAATCC	GAAGCTGTACGCCTGGGA 	GCTCCAGCTGCTGCGCAC                 GCTGAAGGTGCTGAAGAA	CAGCCCTTCCTGGTGAC 	.rgrgcrggacgcgagaa 	CCTCAACATGCTGCCCA 	GATCCAGCAATTCCTGAG                  CCTGAGGATCTTTCTCTC	CTCCCCAGGC     III   CAAAGACGGGGGGGCAC	GGACCTGCCCCCACTCT 	GAAAGGGGCACTGGTGGCCGTGGGGCCTGTGGGAAGTCCTCC
	TGCCTGCTTCAAGGTTATCCAGGACCTGCTCCTTCATCAATCCAGGCTGCTCACAGTCTTCATCAAGGCCACAGGCCTGATGATGTTTTCCGGGCCGCAGATCTTAA	CCTGATCAGGTTTATCTCCAACCCCATGGCCCCCTCCTGGTGGGGCTTCCTGGTGGCTGG	GCTGATGTTCCTGTGCTCCATGATGCAGTCGTGATCTTACAACACTATTACCACTACAT	CTTIGTGACTGGGGTGAAGTTTCGTACTGGGATCATGGGTGTCATCTACAGGAAGGCTCT 	GGTTATCACCAACTCAGTCAAACGTGCGTCCACTGTGGGGGAAATTGTCAACCTCATGT/ 	AGTGGATGCCCAGCGCTTCATGGACCTTGCCCCTTCCTCAATCTGCTGTGGTCAGCAC 	CCTGCAGATCATCCTGGCGATCTACTTCCTGGCAGAACCTAGGTCCCTGTGTCCTGGC 	TGGAGTCGCTTTCATGGTCTTGCTGATTCCACTCAACGGAGCTGTGGCCGTGAAGATGCG 	CGCCTTCCAGGTAAAGCAAATGAAATTGAAGACTCGGGCATCAAGCTGATGAGTGAG	CCTGAACGGCATCAAGGTGCTGAAGGTGTACGCCTGGGAGCCCAGCTTCCTGAAGCAGGT 	GGAGGCATCAGGCAGGTGAGCTCCAGCTGCTGCGCACGGCGGCCTACCTCCACACCC 	AACCACCTTCACCTGGATGTGCAGCCCCTTCCTGGTGACCCTGATCACCCTCTGGGTGTA 	GTGTACGTGGACCCAAACAATGTGCTGGACGCCGAGAAGGCCTTTGTGTCTGTGTCCT 	GTTTAATATCTTAAGACTTCCCCTCAACATGCTGCCCCGGTTAATCAGCAACCTGACTGA	GCCAGTGTGTCTCTGAAACGGATCCAGCAATTCCTGAGCCAAGAGGAACTTGACCCCCA 	GAGTGTGGAAAGAACCATCTCCCCAGGCTATGCCATCACCATACAGG	TGGCACCTTCACCTGGGCCCAGGACCTGCCCCCCACTCTGCACAGCCTAGACATCCAGGT	cccgaaaggggcactggtggc 
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## ALIGNMENTS

	PRI 12-, TAN-1999	Complete cds	, , , , , , , , , , , , , , , , , , ,					; Euteleostomi:	E: Homo.		and Kruh, G.D.	of the MRP/CMOAT	
	AF104943 S079 bp mRNA linear	Homo sapiens ABC transporter MOAT-D (MOAT-D) mRNA, complete cds	AF104943	AF104943.1 GI:4140699		Homo sapiens.	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi:	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	1 (bases 1 to 5079)	Belinsky, M.G., Bain, L.J., Balsara, B.B., Testa, J.R. and Kruh, G.D.	Characterization of MOAT-C and MOAT-D, new members of the MRP/CMOAT	subfamily of transporter proteins
RESULT 1 AF104943	rocus	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM			REFERENCE	AUTHORS	TITLE	

us-09-647-140a-5.rge

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Belinsky, M.G., Bain, L.J. and Kruh, G.D.
Direct Submission
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. =	AGGICCCIC	TGTGGCCGT	CAAGCTGAT	CAGCTTCCT	GGCCTACCT 	GATCACCCT	CTTTGTGTC 	AATCAGCAA 	AGAGGAACT'                 AGAGGAACT'	CATACACAG'	CATCCAGGT	CTCCCTGGT(	GGCTCCGT(                     GGCTCCGT(	CGTGCTTTTC	CTTGCTAGC	CATTAACCTC	TGCCGATATE	CATCTTTGAC	SACGCACGG
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5117 bp mRNA linear PRI 08-SEP-1998
Homo sapiens canalicular multispecific organic anion transporter 2
(CMOAT2) mRNA, complete cds.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 5117)
Uchiumi,T., Hinoshita,E., Haga,S., Nakamura,T., Toh,S., Wada,M. and
Kuwano,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolation of a novel human canalicular multispecific organic anion transporter, cMOAT2/MRP3, and its expression in cisplatin resistant cancer cells with decreased ATP-dependent drug transport
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Uchiumi,T., Hinoshita,E., Haga,S., Nakamura,T., Toh,S., Wada,M. and
Kuwano,M.
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Submitted (11-AUG-1998) Department of Biochemistry, Kyushu
University School of Medicine, 3-1-1 Maidashi Higashiku, Fukuoka
                                                                                4681 ACACTGGGGGCACCTTAAGATTTTGCACCTGTAAAGTGCCTTACAGGGTAACTGTGCTGA 4740
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ó 240 313 360 420 433 480 GGTGCCCTGCATCTACCTGTGGGTCGCCCTGCTGCTACTTGCTCTACCTGCGGCACCA 180 300 540 373 553 Gaps 9 14 CCCCATGGACGCCCTGTGCGGGTTCCGGGGAGCTCGGCTCCAAGTTCTGGGACTCCAACCT 73 1 CCCCATGGACGCCCTGTGCGGTTCCGGGGAGCTCGGCTCCAAGTTCTGGGACTCCAACCT CACCCTGCTGATACAGTATGAGCGGCTGCAGGGCGTACAGTCTTCGGGGGGTCCTCATTAT TIGICGIGCIACAICAICCICICCCACCIGICCAAGCICAAGAIGGICCIGGGIGICCI GCTGTGGTGCGTCTCCTGGGCGGACCTTTTTACTCCTTCCATGGCCTGGTCCATGGCCG GGCCCCTGCCCCTGTTTTCTTTGTCACCCCCTTGGTGGGGGGTCACCATGCTGCTGGC CTICIGGITCCTGTGTGTGTCTGCGCCATCGTCCCATTCCGCTCCAAGATCCTTTTAGC CAAGGCAGAGGTGAGATCTCAGACCCCTTCCGCTTCACCACCTTCTACATCCACTTTGC Length 5117; ; 0 3; Indels DB 9; Score 5073.2; Pred. No. 0; 0; Mismatches Query Match 99.9%; Best Local Similarity 99.9%; Matches 5075; Conservative 194 121 181 241 361 434 301 421 481 셤 ò a qq ò δ а Ωÿ qq ò g ò g ò Q ò

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protein(MRP)-like protein-2 (MLP-2)"
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FEES Lett. 433 (1-2), 149-152 (1998)
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DQGHLEDSWTALEGAEDKEALLIEDTLSNHTDLTDNDPVTYVVQKQFMRQLSALSSDG
EGGGRPVPRRHLGPSEKVQVTEAKADGALTQEEKAAIGTVELSVFWDYAKAVGLCTTL
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/note="ATP-binding cassette transporter superfamily
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Kiuchi,Y., Suzuki,H., Hirohashi,T. and Sugiyama,Y.
Direct Submitssion
Submitted (12-FEB-1998) Yuichi Sugiyama, Graduate School of Pharmaceutical Sci., The University of Tokyo, Department of Pharmaceutics; Hongo 7-3-1, Bunkyo-ku, Tokyo 113, Japan (E-mail:BXG05433mniftyserve.or.jp, Tel:+81-3-3810-6449)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       multidrug resistance-associated protein(MRP)-like protein-2 (MLP-2).
Homo sapiens cell_line:Caco-2 cDNA to mRNA.
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                                                                                                                                          CAGCTGCTGGGTCAGGCCACCCCTAGGAACTCAGTCCTGTACTCTGGGGGTGCTGCCTGAA
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/db_xref="taxon:9606"
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ARALLEKSRILVLDERYAADIGFDNLIQATIRTQFDTCTVLTIAHRLNTIMDYTRVL
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1 GGFGGGCCTGTGGGCTGTGGAAGTCCTCCCTGGTGTCTGCCCTGCTGGAAGATGA 2040	GAAGCTAGAAGGCAAAGTGCACATGAAGGGCTCCGTGGCCTATGTGCCCCAGCAGCATG 21 	GATCCAGAACTGCACTCTTCAGGAAAAGGTGCTTTTCGGCAAAGCCCTGAACCCCAAGCG 216	CTACCAGCAGACTCTGGAGGCCTGTGCTTAGCTGACCTGGAGATGCTGCTGGTGG 222	GGATCAGACAGAGATTGGAGAGGAGTTAACCTGTCTGGGGGCCAGCGGCAGCGGT 1	CAGTCTGGCTCGAGCTGTTTACAGTGATGCCGATATTTTCTTGCTGGATGACCCACTGTC	CGCGGTGGACTCTCATGTGGCCAAGCACATCTTGACCACGTCATCGGGCCAGAAGGCGT 240	GCTGGCAGGCAAGAGGGGAGTGGTGACGCACGGCATTAGCTTCCTGCCCCAGACAGA	CTTCATCATTGTGCTGATGGACAGGTGTCTGAGATGGGCCCGTAGCCAGCC		. GCACCTGGAGACAGCTGGACCGCGTTGGAAGGTGCAGAGATAAGGAGCACTGCTGAT 2640	TGAAGACACACTCAGCAACCACGGATCTGACAGACAATGATCCAGTCAGT	CCAGAAGCAGTTTATGAGACAGCTGAGTGCCCTGTCCTCAGATGGGGAGGGA		<b>4</b> – <b>4</b>	CTGGGATTATGCCAAGGCCGTGGGGCTCTGTACCACGCTGGCCATCTGTCTCCTGTATGT 2940	GGGTCAAAGTGCGGCTGCCATTGGAGCCAATGTGTGGCTCAGTGCCTGGACAAATGATG 	CATGGCAGACAGTAGACAGAACACTTCCCTGAGGCTGGGCGTCTATGCTGCTTTAGG	. AATTCTGCAAGGGTTCTTGGTGATGCTGGCAGCCATGGCCATGGCAGCGGGTGGCATCCA 3120
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Hominidae; Homo.

Catarrhini;

Primates;

Eutheria;

Mammalia;

REFERENCE AUTHORS

Burgess, C.E., Conley, P.B., Grosse, W.M., Hart, M., Kekuda, R., Shimkets, R.A., Spytek, K.A., Szekeres, E.S., Tomlinson, J.E., Topper, J.N. and Yang, R.B.
Proteins and nucleic acids encoding same
Patent: WO 0216599-A 82 28-FEB-2002;
Curagen Corporation (US); COR THERAPEUTICS, INC. (US)

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ORGANISM

Euteleostomi;

Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;

Db 84	47 ATGGAGGAAGCAGGAAAAGCAGGCACGACGACAAAGGCTTCAGCAGCACCTGGGAAAAA 906		
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ACAGTA            ACAGTA	AAGGGT	GTGTGT" 	CCACACO              CCACACO	TTCTGG(                 TTCTGG(	TGGTCA:           TGGTCA:	ACACCT           ACACCT	TCAGCCC             TCAGCCC	GGGCCTZ	AGAGAA(          AGAGAA(	TGGGGA        TGGGGA	ACCCGG	GGATGA1         GGATGA1	AGTACTO           AGTACTO	STTGGCC            STTGGCC	ragacc1         ragacc1	resecce             resecce	CGGCAA	rgcgcrc
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3001 C	3061 AJ 1127 AJ	3121 GC 11 3187 GC		3241 TG 11 3307 TG		3361 TC     3427 TC	3421 GG 11 3487 GG	3481 TC 11 3547 TC	3541 TC     3607 TC	3601 GC     1   3667 GC	3661 CP 	3721 TC     1   3787 TC	3781 GC   1   3847 GC	3841 TC      3907 TC	3901 GC 11 3967 GC	3961 GG   1   4027 GG	4021 CC     1   4087 CC	4081 CC
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CTGTCCCACCTGCACACGTTTGTGAGCTCCCAGCCGGCAGGCCTGGACTTCCAGTG CTCCGCAAGAGCCGCATCCTGGTTTTAGACGAGGCCACAGGCTGCCATCGACCTGGA **IGGGGGCACCTTAAGATTTTGCACCTGTAAAGTGCCTTACAGGGTAACTGTGCTGA** CGCATGAACCTGGACCCCTTCGGCAGCTACTCAGAGGAGGACATTTGGTGGGCTTT 3AGGCGGGGAGAATCTCAGCGTGGCCAGAGGCAGCTCGTGTGCCTGGCCCGAGC 3CACACCGGCTTAACACTATCATGGACTACCAGGGTCCTGGTCCTGGACAAAGG 3CCAGAGATGCTGGACTTGCCTAAAATATATTCCTGAGATTTCCTCCTGGCCTTTC **TTTTCATCAGGAAGGAAATGACACCAAATATGTCCGCAGAATGGACTTGATAGCAA** CTAAAAGTTTCGTTTCTGTTTTTAATAAAAAGCTTTTTCCTCCTGGAACAAGA GCTGGGTCAGGCCACCCCTAGGAACTCAGTCCTGTACTCTGGGGTGCTGCCTGAA TAAAAATGGGAGTACTGATGAAATAAAACTACA 5078  7085690 5142 bp mRNA linear PRI 11-JAN-2000 sapiens multidrug resistance-associated protein 3 (MRP3) mRNA, omplete cds.

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ABGEISDPFRFTTFYIHFALVLSALILACFREKPPFFSAKNVDPNPYPETSAGFLSRL
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ALLNSFRDAGSTLVVIMASTPLETVVILDLAVLTATUQRFYAATSROLKRLESVSRSP
IXSHPSETVTGASTRAVNERDFEIISDTKVDANGRSYPYIISNRMLSIGVEFVGN
CVVLFAALFAVIGRSSLNPGLVGLSVSYSLOVYFFALNMMIRMMSDLESNIVAYBERVER
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VLDKGVVAEFDSPANLJAARGIFYGMARDAGLA"
1496 c 1399 g 1184 t
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                                                                                                                              Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                    1 (bases 1 to 5142)
Fromm, M.F., Leake, B., Roden, D.M., Wilkinson, G.R. and Kim, R.B.
Human MRP3 transporter: identification of the 5'-flanking region, genomic organization and alternative splice variants
Biochim. Blophys. Acta 1415 (2), 369-374 (1999)
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Submitted (24-Aug-1998) Pharmacology, Vanderbilt University, MRB1, Nashville, TN 37232, USA
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/protein_id="AAD02845.1"
/db_xref="GI:4106440"
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100.0%; Pred. No. 0;
+ive 0; Mismatches
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/db_xref="taxon:9606"
/chromosome="17"
                                                                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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1. .5142
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37. .4620
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                                                    TTGTCGTGGCTACATCCTCCTCCCACCTGTCCAAGCTCAAGATGGTCCTGGGTGTCCT
                                                                                                      GCTGTGGTGCGTCTCCTGGGCGGACCTTTTTTACTCCTTCCATGGCCTGGTCCATGGCCG
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Homo sapiens multidrug resistance-associated protein 3A (MRP3)
MRNA, complete cds.
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I (bases 1 to 5291)

Fromm, M.F., Leake, B., Roden, D.M., Wilkinson, G.R. and Kim, R.B. Human MRP3 transporter: identification of the 5'-flanking region, genomic organization and alternative splice variants
Biochim. Biophys. Acta 1415 (2), 369-374 (1999)
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Fromm,M.F., Leake,B., Roden,D.M., Wilkinson,G.R. and Kim,R.B.
Direct Submission
Submitted (24-A0G-1998) Pharmacology, Vanderbilt University, 572
MRBL, Nashville, TN 37232, USA
Location/Qualifiers
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/db_xref="GI:4106442"
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Qy Db	2701	CCAGAAGCAGTTTATGAGACAGCTGAGTGCCCTGTCCTCAGATGGGGAGGGA
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QY Db	3001	CATGGCAGACAGTAGACAGACAACACTTCCCTGAGGCTGGGCGTCTATGCTGCTTTAGG 3060
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Qy	3181 3213	CTTTGACACCACCACCATCAGGCGCATCCTGAACTGCTTCTCCAAGGACATCTATGTCGT 3240
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Qy Dp	3481	ACTAAGGT               ACTAAGGT
Qy Dp	3541	AGAAGO
Οy	3585	358
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ογ	585	
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Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3). Y17151.2 GI:4826562
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PVFFVTPLVVGVTMLLATLLIQYERLQGVQSSGVLIIFWFLCVVCAIVPFRSKILLAK
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IRFISNPMASBWGFLVAGLMFLCXMOSLILDHYYHTIFVTGVKFRFTGIMGYIYRK
ALVITNSVKRASPGEVVAGLWFLOXPARPMDLAPFLNLLMSAPLQIILAIYFLWONLGP
SVLAGVAFWVLLIPLNGAVAVKMRAFQVKQMKLKDSRIKLMSETLNGIKVLKLYAMEP
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Tumorbiochemie, Im Neuenheimer Feld, 280 D-69120 Heidelberg, FRG
On May 13, 1999 this sequence version replaced gi:3087793.
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                                               GTGAATGACACGCCTAAGGTCACAGCTAGTTTGAGCCAGTTAGACTAGT-CCCCGGTCTC
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Konig,J., Rost,D., Cui,Y. and Keppler,D.
Characterization of the human multidrug resistance pro
MRP3 localized to the basolateral hepatocyte membrane
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
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43. 4626
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1453 c 1364 g 1120 t

1011 COUNT BASE CO ORIGIN

Gaps ; 0 Length Indels 6 1; DB Score 4892.4; Pred. No. 0; 0; Mismatches Query Match 96.3%; Sco Best Local Similarity 100.0%; Pr Matches 4893; Conservative 0;

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     1 (bases 1 to 5346)
Fromm, M.F., Leake, B., Roden, D.M., Wilkinson, G.R. and Kim, R.B.
Human MRP3 transporter: identification of the 5'-flanking region, genomic organization and alternative splice variants
Blochim. Blochim. Blophys. Acta 1415 (2), 369-374 (1999)
                                                                                                                                                                              University, 572
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Fromm, M.F., Leake, B., Roden, D.M., Wilkinson, G.R. Burnect Submission
Submitted (24-AUG-1998) Pharmacology, Vanderbilt MRB1, Nashville, TN 37232, USA
Location/Qualifiers
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/gene="MRP3"
/note="MRP transporter family;
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Pred. No. 0;
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/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="17"

/tissue_type="liver"

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/gene="MRP3"

37. .1569
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                       CCTGGAGGCGCCAAAGGGTGAAATCCGCATTGATGGCCCTCAATGTGGCAAGACATCGGCCT
                                                                                                                                   CCTGCGCATGAACCTGGACCCCTTCGGCAGCTACTCAGAGGAGGACATTTGGTGGGCTTT
                                                                                                                                                   GGAGCTGTCCCACCTGCACACGTTTGTGAGCTCCCAGCCGGCAGGCCTGGACTTCCAGTG
                                                                                                                                                                                                                                                                  CTCAGAGGCCGGGAGAATCTCAGCGTGGGCCAGAGGCAGCTCGTGTGCCTGGCCCGAGC
                                                                                                                                                                                                                                                                                  GACTGACAACCTCATCCAGGCTACCATCCGCACCCAGTTTGATACCTGCACTGTCCTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCATGACCTGCGCTCTCAGCTGACCATCATCCCGCAGGACCCCATCCTGTTCTCGGGGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GATGGCCAGAGATGCTGGACTTGCCTAAAATATATTCCTGAGATTTCCTCCTGGCCTTTC
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DEFINITION

RESULT 8 AF085692

ACCESSION

VERSION KEYWORDS SOURCE

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480	540	600	660	678	725	785	845 932	905	965 1052	1025	1085	1145 1232	1205	1265 1352	1325	1385	1445	0
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qq	2613	GCAACGCTCCTTTGCCAACTTTCTCTGCAACTATGCCCCGATGAGGACCAAGGGCACC 2672	
Οy		SGAGGACAGCTGGACGCTTGGAAGGTGCAGAGGATAAGGAGGATGCTGCTGATTGAAG 264:	
Q	2673	TGGAGGACACTGGACCGCGTTGGAAGGTGCAGAGGATAAGGAGGCACTGCTGATTGAAG 2732	
δŏ	646	ACACACTCACCACCACCGCATCTGACAGACAATGATCCAGCTCACCTATGTGGTCCAGA 2705	
qq	33	CACTCAGCAACCACGGATCTGACAGACAATGATCCAGTCACCTATGTGGT	
Oy Dp	2706	AGCAGTTTATGAGACAGCTGAGTGCCCTGTCCTCAGATGGGGACAGGGACAGGGTCGCCTG 2765 	
δ δ	766	82	
3 3	500	ASSECTATE THE STATE OF THE STATE OF THE STATE OF THE STATE OF STAT	
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Oy Dp	2886	ATTATGCCAAGGCCGTGGGGCTCTGTACCACGCTGGCCATCTGTCTCCTGTATGTGGGTC 2945 	
δy	2946	SGACAAATGATGCCATG	
g	3033	AAAGTGCGGCTGCCATTGGAGCCAATGTGTGGCTCAGTGCCTCGACAAATGATGCCATGG 3092	
Š S	3006	90	
3 ,	26.0	SAATTC 315	
oy D	3153	TGCAAGGGTTCTTGGTGATGCTGGCCATGGCCATGGCGGGTGGCGTGCCAGGCTG 3125 	
δλ	126	CCCGTGTGTTGCACCAGGCACTGCTGCACAACAAGATACGCTCGCCACAGTCCTTCTTG 3185	
Dp	3213 (	CCGTGTGTTGCACCACGCGCTGCTGCAAAAAAATACGCTCGCCACAGATCCTTTTT	
Oy Db	3186 A	ACACCACACCATCAGGCCGCATCCTGAACTGCTTCTCCAAGGACATCTATGTCGTGATG 3245 	
οy	3246	AGGTTCTGGCCCCTGTCATCTCATGCTGCTCAATTCCTTCAACGCCATCTCCACTC 3305	
Dp.	3333 7	CTGCTCAATTCCTTCTTCAACGCCATCTC	
Oy Db	3393 1	TIGIGGICAICAIGGCCAGCACGCCGCTCITCACTGTCATCCTGCCCCTGGCTGGC 3365 	
ΟŸ	3366 1	CTACACCTTAGTGCAGGGCTTCTATGCAGCCACATCACGGCAACTGAAGGGGCTG	
QQ	3453 1	51	
0y	426	CAGTCAGCCGCTCACCTATCTACTCCCACTTTTCGGAGACAGTGACTGGTGCCAGTGTCA 3485	
qq	513	*AGCCGCTCACCTATCTACTCCCACTTTTCGGAGACAGTGACTGGTGCCAGT	
οy	3486 1	TCCGGGCCTACAACCGCAGCCGGGATTTTGAGATCATCAGTGATACTAAGGTGGATGCCA 3545	
ф	3573 1	CATCAGTGATACTAAGGTG	
δλ	546	358	
3	650	TIGUTACCUTACATCATCTCCAAC	
οy	3582 -	3581	
QQ	3693	CCTGCTCCTCCAGGAATTCCCAGCAGGTCTCTGGTGTTCAGGGTCCTTGTCCCTCCTTT 3752	

Qy	3582		3581
QΩ	3753	CCCCTAAGCAGAAAACTGGCCCTGCCCTGCCCTGCCCATTTCCTCCTCATCTGATCCC	$\overline{}$
QY	3582	GTGGCTGAGCATCGGAGTGGAGTTCGTGGGGAACTGCGTGGTGCTCTTTGCTGC	3636
qa	3813		87
Qy	3637	CGGGGCTGGTGGCCTTTCTGTGTC	69
qa	3873	CTATITICCGTCATCGGGAGGAGCACCTGAACCCGGGGCTGGTGGGCCTTTCTGTGTC	m
Qy	3697	TTTGCTCTGAACTGGATGATGATGTCAGATTGA	3756
qa .	3933	ACTCCTTGCAGGTGACATTTGCTCTGAACTGGATGATACGAATGATGTCAGATTTGGA	6
Οy	3757	GGTCAAGGAGTACTCCAAGACAGAGACAGAGGCGCC	3816
qa	3993	TCTAACATCGTGGGCTGTGGAGGGTCAAGGGTGTCTCCAAGACAGAGACAGAGGGGCGC	05
Qγ	3817	GGCCCCCACGTGGGGGGGGTGGAGTT	7
qq	4053	TGGTGGTGGAGGCAGCCGCCCCCCGAGGTTGGCCCCCCACGTGGGGGAGGTGGGTT	11
φy	3877	CTGGTGCTGAGAGCCTGAGTCT	93
QQ	4113	CGGAATTATTCTGTGCGCTACCGGCCGGCCTAGACCTGGTGCTGTGTTTTTTTT	4172
οy	3937	GGTGGCGAGAAGGTGGGATCGTGGGCCGCACTGGGGCTGCCAAGTCTTC	6
qq	4173	ATGTGCACGGTGGCGAGAAGGTGGGGATCGTGGCCCGCACTGGGGCTGGCCAGTGTTTC	4232
Οy	3997	CATCCTGGAGGCGGCAAAGGGTGAAATCCGCATTGATGG	ഗ
ΩD	4233	ATGACCCTTTGCCTGTTCCGCATCCTGGAGGGGGCGAAGGGTGAAATCCGCATTGATGG	29
Qγ	4057	CGCTCTCAGCTGACCATCATCCCGCA	4116
qq	4293	CTCAATGTGGGAGACATCGGCCTCCATGACCTGCGCTCTCAGCTGACCATCATCCCGCA	4352
QΥ	4117	SCGCATGAACCTGGACCCCTTCGGCAGCTACT	17
Dp	4353	GACCCCATCCTGTTCTCGGGGACCCTGCGCATGAACCTGGACCCCTTCGGCAGCTACTC	4412
ΟŸ	4177	GCTTTGGAGCTGTCCCACCTGCACGTTTGTGAGCTCCC	23
qa	4413	GAGGAGGACATTTGGTGGCTTTGGAGCTGTCCCACCTGCACCTGTTTGTGAGCTCCCA	4472
Qγ	4237	GGGAGAATCTCAGCGTGGGCCAGAG	6
qq	4473	CCGCCAGGCCTGCACTTCCAGTGCTCAGAGGCGGGGAGAATCTCAGCGTGGGCCAGAG	~
δ	4297	CAAGAGCCGCATCCTGGTTTTAGACGA	1356
qq	4533	CAGCTCGTGTGCCTGGCCCTGCTCCGCAAGAGCCGCATCCTGTTT	59
Qy	4357	CAGCTGCCATCGACCTGGAGACTGACAACCTCATCCAGGCTACCATCCGCACCCA	4416
qa	4593	GCCA	65
Qy	4417	TITGATACCIGCACTGTCCTGACCATCGCACACCGGCTTAACACTATCATGGACTAC	47
qq	4653	GTTTGATACCTGCACTGTCCTGACCATCGCACACGGCTTAAACACTATCATGGACTACAC	7
Qy	4477	TCCTGGTCCTGGACAAAGGAGTAGCTGAATTTGATTCTCCAGCCAACCTCA	53
qq	4713	AGGGTCCTGGTCCTGGACAAAGGAGTAGCTGAATTTGATTCTCCCAGCCAACCTCAT 4	1772
Qy	4537	TGGCCAGAGATGCTGGACTTGCCTAAAATATATT 4	965
QQ	4773	CAGCTAGAGGCATCTTCTACGGGATGGCCAGAGATGCTGGACTTGCCTAAAATATATT 4	832

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LWYALPCYLLYLYLRHHCRGYTLLSALLSARWINGSWLANTERPLDIFFCURALLHGRAPA
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ENGEVSYSLWILLSLANMAPOLISNITGASSSVSKRROOFLOGGELDOGVSERRTISP
GYATITHSGFTWAQDLPPTHSLDIQVPRGALVAVVGPVGGGKSSLVSALLGEMEKL
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GEGGGREDSARGARSALLEDTLSDTLANDLENDVYCOPNROLSSLS
GEGGGREDSARTALEGSBERSALLGDTLSNTTODEKAANTOGCATT

***TOTTENTALLEGSBERSALLATENDVANTODEKAALTONNOVCOPNROLSSLSSD
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****TOTTENTALLEGSBERSALDGATSNTTODEKAATTODEKAATTONNOVCOPNROLSSLS
GEGGGREDSARGANTALGSSTANDGATTODEKAANTOGCATT
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AMAMAAGGIQAARVLHOALLHINKIRSPQSFEDTTPSGRILINCFSKDIY VVDEVLAPVI
LMLLUSFFUAL STLVVIMASTPLFTVVULPLAVITTUORRFAATSROLGKRIESSVSRS
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NCVVLFAALFAVIGRSSLNPGLVGLSVSYSLQVTFALNWHIRMSDLESNIVAVERVK
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CARALLRKSRILIVLDEATAAIDLETPULIQATIRTOFDTCTVLTIAHRLNIINDYTRV
                                                                                                                                                                                        /translation="MDALCGSGELGSKFWDSNLSVHTENPDLTPCFQNSLLAWVPCIY
                                                                    the multidrug resistance-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTCTGTGCACACAGAAAACCCGGACCTCACTCCCTGCTTCCAGAACTCCCTGCTGGCCTG 120
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/db_xref="GI:4102188"
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                                               /gene="MRP3"
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Kool,M., de Haas,M., Ponne,N.J., Baas,F. and Borst,P.
Direct Submission
Submitted (22-JUN-1997) Molecular Biology, The Netherlands Cancinstitute, Plesmanlaan 121, Amsterdam 1066 CX, The Netherlands
Location/Qualifiers
  CCTGAGATTTCCTCCTGGCCTTTCCTGGTTTTCATCAGGAAAGGAAATGACAAAAATG
                                                                                                                                                                                                                                                                                                                                                                                                                 TCCGCAGAATGGACTTGATAGCAAACACTGGGGGGCACCTTAAGATTTTGCACCTGTAAAG
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                                                                                                                                                                                    AAGCTTTTTCCTCCTGGAACAGAAGACAGCTGCTGGGTCAGGCCACCCCTAGGAACTCAG
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/organism="Homo sapiens"
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AAAGAATGECGACCCTAACCCCTGAGACCAGCGCTGGCTTTCTCTCCCGGCTGT. 
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AGACTICCCCTCAACATGCTGCCCCAGTTAATCAGCAACCTGACTCAGGCCAGTGTGTC CTGAAACGGATCCAGCAATTCCTGAGCCAAGAGGAACTTGACCCCCAGAGTGTGGAAAG GAGAAGCTAGAAGGCAAAGTGCACATGAAGGGCTCCGTGGCCTATGTGCCCCAGCAGGC GACCTGCCCCCACTCTGCACAGCCTAGACATCCAGGTCCCGAAAGGGGCACTGGTGGC rgatccagaactgcactcttcaggaaaacgtgcttttcggcaaagccctgaaccccaa 3GGGATCAGACAGAGTTGGAGGAGAGGGCATTAACCTGTCTGGGGGCCAGCGCCAGCG #TGCTGGCAGGCAAGACGCGAGTGCTGGTGACGCACGGCATTAGCTTCCTGCCCCAGAC GCTACCAGCAGACTCTGGAGGCCTGTGCCTTGCTAGCTGACCTGGAGATGCTGCCTGG STCAGTCTGGCTCGAGCTGTTTACAGTGATGCCGATATTTTCTTGCTGGATGACCCACT | CCGCGGTGGACTCTCATGTGGCCAAGCACATCTTTGACCACGCGTCGTCGGGCCAGAAGG 

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        Bosma, P.J.,
                                                             Other publication AU 1736697 19970910
Location/Qualifiers
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/db_xref="taxon:32644"
1423 c 1325 g 107:
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1 (bases 1 to 4762)
Oude, E.R., Paulusma, C.C.,
                                                                                                                                      Query Match 90.3%;
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Q	1925	AGAAAGACCATCTCCCCAGGCTATGCCATCACCATACACAGTGGCACCTTCACCTGGGCC 1984		
ò	1916	CAGGACCTGCCCCCACTCTGCACAGCCTAGACATCCAGGTCCCGAAAGGGGCACTGGTG 19	Qγ	299
q	8	CAGGACCTGCCCCCCACTCTGCACAGCCTAGACATCCAGGTCCCGAAAGGGGCACTGGTG 204	QΩ	306
ò	1976	GCCGTGGTGGGGCTTGTGGAAAATTCTTCTTGTGAAAATTCTTGGTGTATCTTGGTGGTGTATCTTGGTGAAAATTCTTGGTGAAAATTCTTGGTGGTGTATGGTGAAAATTCTTGGTGAAAATTCTTGGTGGTGTGTGGTGGTGTGTGGTGGTGTGTGGTGG	Qy	305
ි _{සි}			QQ	312
ò	2036	ATGGAGAAGCTAGAAGGCAAAGTGGACATGAAGGGCTCCGTGGCCTATGTGCCCCAGCAG 209	Qy	311
9	2105	ATGGAGAAGCTAGAAGGGAAAGTGCACATGAAGGGCTCCGTGGCCTATGTGCCCCAGCAG 216	qq	318
ò	2096	GCATGGATCCAGAACTGCACTCTTCAGGAAAACGTGTTTTTCGGGAAAACCTTCAACAAAAAAAA	Qy	317
g 8	2165		qq	324
ò	2156	- 「「「	QY	323
D Q	0	AGGCTACCAGCAGCAGCTCTGGAGGCCTTGCTAGCTAGCT	qa	330
ΛO	2216	GGIGGGGATCAGACAGAGTIGGAGAGAGAGATIPACCIGICIIGGAGGGGCCAGCAG	δλ	329
q q	2285		Db	336
ò	2276		Qy	335
. a	2345		Dp	342
ò	2336	CTGTCCGCGGTGGACTCTCATGTGGCCAAGCACATCTTTGACCACGTCATGGGCCAGAA 239	ογ	341
g	2405		qq	348
ò	2396	GGCGTGCTGGCAGGCAAAGGCGAAGTGCTGGTGACGCACGGCATTAGCTTCTGCTCACACAA	ΟŸ	347
음	46		QQ	354
ò	2456	ACAGACTTCATCATTGTGTAAGTAGGAAGGACAGGAGGAGGAGGAGGATGTTCATTGTTGATTGTTGATTGTAGTAGGAGGAGGAGGAGGAGG	Qγ	353
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2 A	58		Db	366
.0	57	CAAGGGCACTTGGAAGACACACCTCGCTTTTGGAAGATGCAGATGAAGATTAAAGATAAACAACAACAACAACAACAACAACAACAACAACAACA	Οy	365
, E	2645		qq	372
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7 A	2705		qa	378
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연	2765	82	DP	384
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2		0 0	οy	3896
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ò	2876	203	QŸ	3956
전	94		qq	4025
ò	2936	299	Qy	4016
g qq	3005	90	qq	408

QY	2996	GATGCCATGGCAGACAGTAGACAGAACACTTCCCTGAGGCTGGGCGCTCTATGCTGCT 3055 
QY	05(	AGGAATTCTGCAAGGGTTCTTGGTGATGCTGGCAGCCATGGCCATGGCCAGGGGGGGG
qa	3125	
Qy	3116	ATCCAGGCTGCCCGTGTGTGCACCAGGACTGCTGCACAACAAGATACGCTGCCACAG 3175
qa	3185	SCAGGCTGCCCGTGTTGCACCAGGCACTGCTGCACAACAAGATACGCTCGCCACAG 3
Qy	3176	TTGACACCACCATCAGGCCGCATCCTGAACTGCTTCTCCCAAGGACATCTAT 32
qa	3245	CCTTCTTTGACACCACCACCATCAGCCGCATCCTGAACTGCTTCTCCCAAGGACATCTTGT 330
Qy	3236	GGTTGATGAGGTTCTGGCCCCTGTCATCCTCATGCTGCTCAATTCCTTCTTCAACGCC 32
qq	3305	TGATGAGGTTCTGGCCCCTGTCATCCTCATGCTGAATTCCTTCTTCAACGCC 336
QY	3296	TCTCCACTCTTGTGGTCATCATGGCCAGGCGCGCTCTTCACTGTGTGTCATCCTGCCC 335
qa		ACTCTTGTGGTCATCATGGCC
Qy	3356	CTGTGCTCTACACCTTAGTGCAGCGCTTCTATGCAGCCACATCACGGCAACTGAAG 341
qq	3425	
QY	3416	AGTCAGCCGCTCACCTATCTACTCCCACTTTTCGGAGACAGTGACTGGT 347
qq		GGCTGGAATCAGTCAGCCGCTCACCTATCTACTCCCACTTTTCGGAGACAGTGACTGGT 35
δλ	3476	CATCCGGGCCTACAACCGCAGCCGGATTTTGAGATCATCATGATACTAAG 353
qq	3545	CCAGTGTCATCCGGGCCTACAACCGCGGGATTTTGAGATCATCATCAGTGATACTAAG 360
Qy	3536	CAACCAGAGAAGCTGCTACCTACATCATCTCCAACCGGTGGCTGAGCATC 359
qq		GGATGCCAACCAGAGAAGCTGCTACCCCTACATCATCTCCAACCGGTGGCTGAGCATC 36
QY	3596	3TGGGGAACTGCGTGGTGTTTTGCTGCACTATTTGCCGTCATCGGG 36
QQ	3665	GAGTGGAG
οy	3656	CCTGAACCCGGGGCTGGTGGCCCTTCCTGTGCTCCTTGCAGGTGACA 37
QQ	3725	3AGCAGCCTGAACCCGGGGCTGGTGGGCCTTTCTGTGTCCTACTCCTTGCAGGTGACA 37
QY	3716	GCTCTGAACTGGATGATACGAATGATGTCAGATTTGGAATCTAACATCGTGGCTGTG 37
Db	3785	TICCICIGAACIGGAIGAIACGAAIGAIGIGIIIIIIIIII
Οy	3776	STACTCCAAGACAGAGAGGGGCGCCCTGGGTGGTGGAAGGCAG
ΩP	3845	AGAGGGTCAAGGAGTACTCCAAGAGAGACAGAGGGCGCCCTGGGTGGTGGAGGCAGC 390
Qy	3836	TCCCGAAGGTTGGCCCCCACGTGGGGAGGTGGAGTTCCGGAATTATTCTGTGCC 3
QQ	3905	GCCCTCCCGAAGGTTGGCCCCCCACGTGGGGAGGTGGAGTTCCGGAATTATTCTGTGCGC 3
Οy	3896	CCGGCCGGGCCTAGACCTGGTGCTGAGACACCTGAGTCTGCATGTGTGCACGTGGCGAG 3
QQ	3962	ACCGGCCGGCCTAGACCTGGTGTTTTTTTTTTTTTTTTT
Qy	3956	ATCGTGGGCCGCACTGGGGCTGGCAAGTCTTCCATGACCCTTTGCCTGTTC 4
QQ	4025	GTGGGGATCGTGGGCCCCACTGGGCTGGCAAGTCTTCCATGACCCTTTGCTTC
QY	4016	CAAAGGGTGAAATCCGCATTGATGGCCTCAATGTGGCAGACATC 4
qa	4085	ATCCTGGAGGCGGCAAAGGGTGAAATCCGCATTGATGGCCTCAATGTGGCAGACATC 4

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Submitted (14-JAN-1998) Tomoko Hirohashi, Faculty of Pharmaceutical
Submitted (14-JAN-1998) Tomoko Hirohashi, Faculty of Pharmaceutical
Sciences, Tokyo University, Department of Pharmaceutics; Hongo
7-3-1, Bunkyo-ku, Tokyo 113, Japan
(E-mail:hirohasi@seizai.f.u-tokyo.ac.jp, Tel:81-3-5802-2045,
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Hirohashi,T., Suzuki,H., Ito,K., Ogawa,K., Kume,K., Shimizu,T. and
Sugiyama,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatic expression of multidrug resistance-associated protein-like proteins maintained in eisai hyperbilirubinemic rats Mol. Pharmacol. 53 (6), 1068-1075 (1998)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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               4145 GGCCTCCATGACCTGCGCTCTCAGCTGACCATCATCCCGCAGGACCCCATCCTGTTCTCG
                                                                                4205 GGGACCTGCGCATGAACCTGGACCCCTTCGGCAGCTACTCAGAGGAGGACATTTGGTGG
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                                                               GGGACCCTGCGCATGAACCTGGACCCCTTCGGCAGCTACTCAGAGGAGGACATTTGGTGG
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AGGKILDPERETTYTYTERAUNGAREMSOVALLE WHALLCYOFALD IPERSET LIALLA AGGKILDPERETTYTYTYTERAUNGAREMSOVALLE WHALLCYOFA SAGFERAL SFEWRFTKAILGFREDSDLWSLSEEDCSHKVORLLEAWOKOOTOASGPOTAALE PKIAGEBED LIAGEMSTERALVETSTSLLWGACFKLIQDLLSFINDOLLSTINDOLLSTINDOLLSTINDOLLSTINDOLLSTINDOLLSTINDOLLSTINDOLLSTINDOLLSTINDOLLSTINDOLLSTINDOLLSTINDOLLSTINDOLLSTINDOLLSTINDOLLSTINDOLLSTINDOLLSTINDOLLSTINDOLLSTINDOLLSTINDOLLSTINDOLLSTINDOLLSTINDOLLSTINDOLLSTINDOLLSTINDOLLSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTINDOLTSTIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ETBAPWVLESNRAPEGWPRSGVVEFRNYSVRYRPGLELVLKNLTLHVOGGEKVGIVGR
GRGKSSMTLCLFRILDABAGGERIDIOLUNAHIGLHDLRSQLTIIPODPILFSGTIRM
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LRKSRVLVLDBATAAIDLETDDLIQGTIRTQFEDCTVLTIAHRURINDYNRVLVLDR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 GGCCCCTGCCCTGTTTCTTTGTCACCCCCTTGGTGGGGGGGTCACCATGCTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 5174;
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                                                                                                                                                                                                                                                                                                    (MLP-2)"
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0; Mismatches
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                                                                                                                                                                                                                                                       /product="multidrug resi:
(MRP)-like protein-2 (MLK
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"Sprague-Dawley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="18 a nucleotides'
1439 c 1352 g. 128
                              /db_xref="taxon:10116"
/sex="male"
                                                                                                          /tissue_type="colon"
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                                                                                                                                                /dev_stage="adult"
19. .4620
                                                                                                                                                                                                                     /codon_start=1
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Best Local Similarity 81.4%;
Matches 3761; Conservative
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464	ω α	540	644	9	720 764	780 824	840 881	900 941	960 1001	1020 1061	1080	1140	1200 1241	1260	32	1380 1421	1440	1500
	1 CTTCTGGTTCCTGTGTGTGTGCGCCATCGTCCCATTCCGCTCCAAGATCCTTTAG	1 CAAGGCAGAGGGTGAGATCTCAGACCCCTTCCGCTTCACCCCTTCTACATCCACTTTGC	1 CCTGGTACTCTGCCCTCATCTTGGCCTGCTTCAGGAGAAACCTCCATTTTTCTCGC	1 AAAGAATGTCGACCCTAACCCTGAGACCAGGGCTGGCTTTC	1 TTTCTGGTGGTTCACAAAGATGGCCATCTATGGCTACCGGCATCCCCTGGAGAGAAGGA	1 CCTCTGGTCCCTAAAGGAAGAGACAGATCCCAGATGGTGGTGCAGCAGCTGCTGGAGGC	1 ATGGAGGAAGCAGGAAAAGCAGGACGACACAAGGCTTCAGCAGCACCTGGGAAAAA	1 TGCCTCCGGCGAGGACCGGGTGCTGGGTGCCCGGCCCAGGCCCCGGAAGCCCTCCTT	1 CCTGAAGGCCCTGCTGGCCACCTTCGGCTTCCTCATCAGTGCCTGCTTCAAGCT	1 TATCCAGGACCTGCTCCTTCATCAATCCACAGCTGCTCAGCATCCTGATCAGGTTTAT	1 CTCCAACCCCATGGCCCCCTCCTGGTGGGGCTTCCTGTGGCTGGC	1 CTCCATGATGCAGTCGCTGATCTTACCACTATTACCACTACATCTTTGTGACTGGGGT	1 GAAGTITCGTACTGGGATCATGGGTGTCATCTACAGGAAGGCTCTGGTTATCACCAACTC	1 AGTCAAACGTGCGTCCACTGTGGGGAAATTGTCAACCTCATGTCAGTGGATGCCAGGG	1 CTTCATGGACCTTGCCCCTTCCTCAATCTGCTGGGTCAGCACCCCTGCAGATCATCC	1 GGCGATCTACTTCCTCTGGCAGAACCTAGGTCCCTCTGTCCTGGCTGG	1 GGTCTTGCTGATTCCACTCAACGGAGCTGTGGCCGTGAAGATGCGCGCCTTCCAGGTAAA	GCAAATGAAGGACTCCCGCATCAAGCTG
b 40	4 4	48	54.	64	99 /	72	78	84	90	96	102	108	114	120	126	132	138	144
ដ	Oy Db	Q Dp	Qy Dp	Q D	Q D	Q Q	Q D	Qy Dp	Oy Db	Q D	Qy Db	OY Db	ζς α	Oy Db	QY Db	Qy Db	Qy Db	δ

1661 1740 1920 1980 2040 2100 2280 2400 1601 1800 1841 1860 1901 1961 2021 2141 2160 2220 2381 2441 2618 2081 2201 2261 2321 GCAAATGAAGTICAAAGACTCCCGCATCAAACTGATGAGTGAGATCCTGAATGGCATCAA 1541 GGGTGAGCTCCAGCTGCGCACGGCGGCCTACCTCCACACCACAACCACCTTCACCTG GATGTGCAGCCCTTCCTGGTGACCCTGATCACCCTCTGGGTGTACGTGTACGTGGACCC CCTGCCCCCCCACTCTGCACAGCCTAGACATCCAGGTCCCGAAAGGGGCCACTGGTGGCCGT GAAGCTAGAAGGCAAAAGTGCACATGAAGGGCTCCGTGGCCTATGTGCCCCCAGCAGGCATG CTACCAGCAGACTCTGGAGGCCTGTGCCTAGCTGACCTGGAGATGCTGCTGGTGG AAACAATGTGCTGGACGCCGAGAAGGCCTTTGTGTCTGTGTCCTTGTTTAATATCTTAAG ACTICCCCTCAACAIGCTGCCCCAGTTAATCAGCAACCTGACTCAGGCCAGTGTGTCTCT GGTGGGGCCTGTGGGGAAGTCCTCCCTGGTGTCTGCCCTGCTGGGAGATGGA GATCCAGAACTGCACTCTTCAGGAAAACGTGCTTTTCGGCAAAGCCCTGAACCCCAAGCG GGATCAGACAGAGATTGGAGAGAGGGCATTAACCTGTCTGGGGGGCCAGCGGCAGCGGGT CTTCATCATTGTGCTAGCTGATGGACAGGTGTCTGAGATGGGCCCGGTACCCAGCCCTGCT GCAGCGCAACGGCTCCTTTGCCAACTTTCTCTGCAACTATGCCCCCGGATGAGGACCAAGG 1482 1542 1561 1602 1621 1662 1681 1741 1842 1902 1921 1962 1981 2041 2082 2101 2142 2161 2202 2262 2281 2322 2382 2562 1501 1722 1782 1801 1861 2022 2221 2341 2401 2442 2502 2521 2461 g οy ŏ Db g Óγ q δ q Ω ò d οy g Qγ q Ω Ω δŻ g Ω QQ ò Op Qγ do δy 5 g g g ōy Ω Ω δ δý

T 2640 I 2669	GT 2700     GT 2729	3 276 1 3 278	281 284	T 2877 1 T 2909	A 2937     A 2969	A 2997     A 3029	T 3057   T 3089	T 3117   T 3149	c 3177   c 3209	T 3237   T 3269	3297	3357	G 3417   G 3449	3477	353	3597 3629	3657 3689
NGGATAAGGAGCACTGCTGA/ 	GATCCAGTCACCTATGTG 	CAGATGGGGAGGACAGGGTC                            CTGAAGGAGGGCCAGAACC	GGTGCAGGTGACAGAGGCGAA 	FGGCACTGTGGAGCTCAGTG 	GCTGGCCATCTGTCTCCTGT 	GGCTCAGTGCCTGGACAATG 	TGAGGCTGGCGTCTATGCTGCTT: 	ATGGCAGCGGGTGGCA	GCTGCACAACAAGATACGCTCGCCACAGT( 	AGGACATCTATG 	ICAATTCCTTCTTCAACGCCAT	ACTGTGGTCATCCTGCCCCT	GAAGC       GAAGA	TCGGAGACAGTGACTGGTGC 	atcatcagtgatactaaggt 	CCAACCGGTGGCTGAGCATCGG	CTATTGCCGTCATCGGGAG 
GGAGGACAGCTGGACGGTTGGAAGGTGCAGA             GGAGGCCATGAAGGAGTCTTGCAACATGCA	CAACCACACGGATCTGACAGACAATI 	'GAGACAGCTGAGTGCCCTGTCTC1 	.CCTGGGTCCATCAGAGAAGG 	CAGATGGGGCACTGACCCAGGAGGAAAGCAGCCATTGGCACT 	SCCAAGGCCGTGGGGCTCTGTACCACG 	SCCATTGGAGCCAATGTGT 	GCAGACACAGAACAACACTTCCCTGAGG 	CTTGGTGATGCTGGCAGCCATGGCC 	CACCAGGCACT	CATCAGGCCGCATCCTGAACTGC 	CCTGTCATCCTCATGCTGC: 	CTIGIGGICATCATGGCCAGCACGCGCTCTTCACTGTGGTCATCC 	CTACACCTTAGTGCAGCGCTTCTATGCAGCCACATCACGGCAACT. 	TCACCTATCTACTCCACTTTTCGGAGACAGT 	ACAACCGCAGCCGGGATTTTGAGAT 	ACATCATCT              catcgcct	SGTGCTCTTTGCTG
GCACCT	TGAAGACACACTCAG	CCAGAAGCAGTTTAT                       CGCCAAGCAGTTCAT	GCCTGTACCCGGAGGCACCTG 	GGCAGATGGGCCACTGAC                       AGACTGGTGCATTAAT	GTTCTGGGATTATGCCAA 	TGTGGGTCAAAGTGCGGCT( 	TGCCATGGCAGACAGTAG 	AGGAATTCTGCAAGGGTTCTTG 	CCAGGCTGCCCGTGTGTTG	CTTCTTGACACCACACCC	CGTTGATGAGGTTCTGGCC	CTCCACTCTTGTGGTCATC	GGCTGTGCTCTACACCTT/ 	GCTGGAATCAGTCAGCCGCTC	CAGTGTCATCCGGGCCTAC	GGATGCCAACAGAAGCTGCTACCCT. 	AGTGGAGTTCGTGGGGAACTGCGT 
2581	2641	2701	2761	2818	2878	2938	3030	3058	3118	3178	3238	3298	3358	3418 3450	3478 3510	3538 3570	3598
Qy Db	Qy Dp	Oy Dp	Qy Dp	Qy Db	Q O	Oy Dp	Qy Dp	Qy Dp	Oy Dp	Oy Dp	Qy Dp	Oy Db	Qy Dp	Oy Dp	Qy	Qy Dp	Qy Db

3777 3809 3837 3869 3897 3929 3957 3989 4049 4077 4137 4169 4017 4109 4197 4229 4317 AGCCCTGCTCCGCAAGAGCCGCATCCTGGTTTTAGACGAGGCCACAGCTGCCATCGACCT 4377 4350 AGCCTGCTCCGAAAGAGCCGTGTCCTGGTTTTAGACGAGGCCACCGCTGCCATTGACCT 4409 TGCTCTGAACTGGATGATACGAATGATGTCAGATTTGGAATCTAACATCGTGGCTGTGGA CCCTCCCGAAGGTTGGCCCCCACGTGGGGAGGTGGAGTTCCGGAATTATTCTGTGCGCTA CCGGCCGGGCCTAGACCTGGTGCTGAGAGCCTGAGTCTGCATGTGCACGTGGCGAGAA CATCCTGGAGGCGGCAAAGGGTGAAATCCGCATTGATGGCCTCAATGTGGCAGACATCGG CCTCCATGACCTGCGCTCTCAGCTGACCATCCCGCAGGACCCCCATCCTGTTCTCGGG GACCCTGCGCATGAACCTGGACCCCTTCGGCAGCTACTCAGAGGAGGACATTTGGTGGGC GGTGGGGATCGTGGGCCGCACTGGGGCTGGCAAGTCTTCCATGACCCTTTTGCCTGTTCCG GTGCTCAGAGGGCGGGAGAATCTCAGCGTGGGCCAGAGGCAGCTCGTGTGCCTGGCCCG 4651 CT 4617 =5 3750 4078 3718 3778 3810 3838 4110 3898 3930 3958 3990 4018 4050 4138 4258 4318 4616 4650 qq δý ò QQ δý g οy QQ ò Ob οqα Qγ δ pp ò g δ q á g δ q δ g ٥ÿ qq q рp ŏ ò ŏ g ά

AF072816 5107 bp mRNA linear ROD 02-JUL-1998 Rattus norvegicus ABC-type transporter MRP3 (mrp3) mRNA, complete

RESULT 12
AF072816
LOCUS
DEFINITION

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LWAALDCYLEYLRHHIACYTULOYERLEGURSDELDENCHUNDELYSCHGUNGGSDA

LWAALDCYLEYLRHHIACYTULOYERLEGURSDELDENCHUNDELYSCHGUNGGSDA

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SFWAFFKLAICKRRPLEDSDLWALESEDCGHKVORELLEAWGROOTOGASGPOTAALE

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SGLFRHEDVWMGFELLAGLMYSSTWOTLILHGHYHTLTVWALERTRAILGYTYRKAL

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TITNSYKRETYGEWINTASYDAORRHUNSPSRINTLTGATVCYNCHNUNDARKA

FVSLGLENILKIPLANLPOLLSGWOOTSVELKPRODELDPGCVERKTITSPGRA

TITNNGTFSWSKDLPPTLHSINIQIPRGALVAVGPVGGKSSLVSALLGEMEKLEGA

VSVKGSVAYVPOGANTQUCTLGEDTSTFTWATGATSTLADLDLUFGGOOT

EIGERG INLSGGGRORVSLARAYSDANIFLLDDDELDPCAYBYRKHIPDQVIGPEGVL

GKTRVLYTHCISFLPOTDFIIVLDFBPAITENTYRCHIPWV

GKTRVLYTHCISFLDOTDFIIVLADGOTTENGHYSKELGURDSCHORD

ENGERGULDHYLLEDPILSTHDLTDEPAITSTRYRCPRESSLSSEGEGONRP

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YGGONAVALGHNUSAMMTDVEHGGONNTSVRLGYYATLGTLGLGGLLYMLSAFTWV

GALDAARLLHTALLHNQIRAPCSFFULDATDSTRYRCYVATLGTLGLGGLLYMLSAFTWV

STALFRYTGRYGRYCHAUSTSTRYRCYNGYRYTSTRYRCHYRYSTSTRYRCYNGYRYTSTRYRCYNGYRYTSTRYRCYNGYRYTSTRYRCYNGYRYTSTRYRCYNGYRYTSTRYRCYNGYRYTSTRYRCYNGYRYTSTRYRCYNGYRYTSTRYRCYNGYRYTSTRYRCYNGYRYTSTRYRCYNGYRYTSTRYRCYNGYRYTSTRYRCYNGYRYTSTRYRCYNGYRYTSTRYRCYNGYRYTSTRYRCYNGYRYTSTRYRCYNGYRYTSTRYRCYNGYRYTSTRYRCYNGYRYTSTRYRCYNGYRYTSTRYRCYNGYRYTSTRYRCYNGYRYTSTRYRCYNGYRYTSTRYRCYNGYRYTSTRYRCYNGYRYTSTRYRCYNGYRYTSTRYRCYNGYRYTSTRYRCYNGYRYTSTRYRCYNGYRYTSTRYRCYNGYRYTSTRYRCYNGYRYTSTRYRCYNGYRYTSTRYRCYNGYRYTSTRYRCYNGYRYTSTRYRCYNGYRYTSTRYRCYNGYRYTSTRYRCYNGYRYTSTRYRCYNGYRYTSTRYRCYNGYRYTSTRYRCYNGYRYTSTRYRCYNGYRYTSTRYRCYNGYRYTSTRYRCYNGYRYTSTRYRCYNGYRYTSTRYRCYNGYRYTSTRYRCYNGYRYTSTRYRCYNGYRYTSTRYRCYNGYRYTSTRYRCYNGYRYTSTRYRCYNGYRYTSTRYRCYNGYRYTTRYRCYNGYRYTTRYRCYNGYRYTTRYRCYNGYRYTTRYRCYNGYRYTTRYRCYNGYRYTTRYRCYNGYRYTTRYRCYNGYRYTTR
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GAGKSSMILCLFRILEAAGETFIDGLNVAHIGHDIRSQLTII TOPDFILFSGTIRMN
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RKSRVLVLDEATAAIDLETDDLLQGTIRTQFEDCTVLTIAHRLNTIMDYNRVLVLDKG
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                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                             1 (bases 1 to 5107)
Ortiz,D.F., Li,S. and Iyer,R.
ABC-type protein upregulated in TR-, EHBR and cholestatic liver
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (16-JUN-1998) Physiology, Tufts, 136 Harrison Ave,
Boston, MA 02111, USA
Location/Qualifiers
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/protein_id="AAC25416.1"
/db_xref="G1:3283977"
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/db_xref="taxon:10116"
/tissue_type="liver"
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ilarity 81.2%;
Conservative
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Ortiz, D.F.
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Horrigan, S., Soppet, D.R. and weaver, \omega. Cancer gene determination and therapeutic screening using signature
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           3134 TIGCACCAGGCACTGCTGCACAACAAGATACGCTCGCCACAGTCCTTCTTTGACACCACA
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 AGGAGTAGTAGCTGAATTTGATTCTCCAGCCAACCTCATTGCAGCTAGAGGCATCTTCTA
                                                CGGGATGCCCAGAGATGCTGGACTTGCCTAAAATAT - - ATTCCTGAGATTTGCTCCTGGC
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Patent: WO 0194629-A 3831 13-DEC-2001;
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/db_xref="taxon:9606"
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Location/Qualifiers
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7 CGTGGGGAACTGCGTGGTGCTCTT 	7 GAACCCGGGGCTGGTGGGCCTT	7 CTGGATGATACGAATGATGTCA 	7 GGAGTACTCCAAGACAGAGACAGAGGGGG 	AGGTTGGCCCCCACGTGGG 	0-0			0-0			0 0	0-0					
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Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horrigan, S., Soppet, D.R. and Weaver, Z.
Cancer gene determination and therapeutic screening using signature
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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GCCAGTTAGACTAGTCCCCGGTCTCCCGATTCCCAACTGAGTGTTATTTGCACACTGCAC
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Sequence 6335 from Patent W00194629.
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Avalon Pharmaceuticals (US)
Location/Qualifiers
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/db_xref="taxon:9606"
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-TACACCTTAGTGCAGCGTTCTATGCAGCCACATCAGGCAACTGAAGCGGCTGGAATC 3	CCAGAGAAGCTGCTACCTACATCTCCCAACCGGTGGCTGAGCATCGGAGTGGAGTT 3	CTGGATGATACGAATGATGACAATTTGGAATCTAACATCGTGGCTGTGGAGAGGGTCAA 3  [11111111111111111111111111111111111	CCTAGACCTGGTGCTGAGAGCCTGAGTCTGCATGTGCACGTGGCGAGAAGGTGGGGAT 31	1 4 L 4 L 4 L 4 L
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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					SENCOURT	ZD451H	52634 MA	26419 MA	12913152	02054722
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	oР	Query	Match		14.5	13.8	9.6	9.2	8.8	8.7
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## ALIGNMENTS

		AGENCOURT_8414907 NIH_MGC_100 Homo sapiens cDNA clon	)', mkna sequence. Nr Bo645685			human.		_	1 (bases 1 to 947)	SS		_	Contact: Robert Strausberg, Ph.D.	Email: cgapbs-r@mail.nih.gov	Tissue Procurement: CGAP (Stanford)	CDNA Library Preparation: Rubin Laboratory	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	DNA Sequencing by: Agencourt Bioscience Corporation	Clone distribution: MGC clone distribution information can be	found through the I.M.A.G.E. Consortium/LLNL at:	http://image.llnl.gov	Plate: LLCM2449 row: j column: 04	High quality sequence start: 18	nign quailty sequence stop: 645.	
RESULT 1 BQ645685	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM		REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT											FEATURES	

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EST 14-AUG-2001
                                                                                 655 bp mRNA linear EST 14-AUG-2007 (synonym: hlccl) spinal cord Homo sapiens cDNA
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No s1 sequence available.

This clone (DKFZp451H201) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                            Email: poustkaemping berlin-dahlem.mpg.de
This is the 5' sequence of the clone insert
Clone from S. wiemann, Molecular Genome Analysis, German Canox
Research Center (DKF2); Email s.wiemann@dkf2- heidelberg.de;
sequenced by DKF2 (German Cancer Research Center,
Heidelberg/Germany) within the CDNA sequencing consortium of
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Poustka,A., Wellenreuther,R., Mewes,H.W., Weil,B. and Wiema EST (Poustka,A., Wellenreuther,R., Mewes,H.W., Weil,B. and .S.)
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/tissue_type="human spinal cord"
                                                                                                                                                                                                                                                                                                                   Contact: Poustka A.J.
Department Lehrach
Max-Planck-Institute for Molecular Genetics
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Tel: +49-30-84131623
Fax: +49-30-84131128
                                                                                                               mRNA sequence.
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/db_xref="taxon:9606"
/clone="DKFZp451H201"
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clone DKFZp451H201 5'
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Mammalia; Eutheria;
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                                                                         /tissue_type="hepicocilular carcinoma, cell line"
/tab_nost="DHIOB (phage-resistant)"
/note="Organ: liver; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-dr priming. Directionally cloned
into ECORIX/AhoI sites using the following 5, adaptor:
GGCAGCAG(G). Size-selected >500bp for average insert size
1:8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
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Pred. No. 6.4e-142;
0; Mismatches 27; Indels
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             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6271971"
                                                            /clone_lib="NIH_MGC_100"
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Best Local Similarity 95.3%;
Matches 738; Conservative
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PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Exa: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
and _minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                 EST 25-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Casas, E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E. Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for
                                                                                                                                                                                                                                                                                                                                                                                                                                     Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: Sall; Library made from pooled tissue from day 11, 13, 15, 20 and 30 embros:"
                                                                                                                                                          540
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                                                                                                                                                                                                                       Design and use of two pooled tissue normalized cDNA libraries
      CAGAGCGACCCTGTCCGCCACCTGTCCACCTATGCCTGTCTCTGGTGGTGGTGGCACAG
                                                        CTGATTCACACCGAGAGGAAAAAGGGAGTCCAGTCATCTGGAGTGCTGTTTGGTTACTGG
                                                                                                         CTTCTCTGCTTTGTCTTGCCAGCTACCAACGCTGCCCAGCAGGCCTCCGGAGCGGGCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 434.4; DB 12; Length 566; Pred. No. 7.4e-91;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae,
1 (bases 1 to 566)
                                                                                                                                                                                                                                                                                                                                             352634 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence. BG834418
BG834418.1 GI:14199678
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/tissue_type="pooled"
/lab_host="DH10B"
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BACKWARD: GTTTCCCAGTCAGGACG
Blate: 113 row: H COLUMN: 23
Seq primer: ATTTAGGTGACACATATAG
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Best Local Similarity
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Sus:
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VERSION
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COMMENT
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BG834418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine Unpublished (2000)
Contact: Smith TPL
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Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Reele, J.W.
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                               2772 CATCCAATACGGCAGGGTGAAGGCCACAGTGCACCTGGCCTACCTGCGTGCCGTGGGCAC 2831
                                                                                                                                                                                                                          AGCCCTGCGTGGCGGGATCTTCGGGCTCTCGGCTGTCTCCAAGCCATTGGCTGTTTGC 3011
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                                               GGGCTACTGGCTGAGCCTGTGGGCGGACGACCTGCAGTAGGTGGGCAGCAGACGCAGGC
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 Indels
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PO Box 166, Clay Center, NE 68933-0166, USA
TTEL: 402 762 4356
Fax: 402 762 4359
 81;
 Mismatches
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                                                                                                                                                                                                                                          FORWARD: AGGAAACAGCTATGACCAT BACKWARD: GTTTTCCCAGTCACGACG
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PCR PRimers
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Conservative
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BG610482.1
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AUTHORS
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COMMENT
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KEYWORDS
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FEATURES

BASE COUNT

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3974 TCGACGGGTCCCCATTGCCCACGTGGGCTGCACACACTGCGCTCCAGGATCAGCATCA 4033
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 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: capabs-rémail.nih.gov.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MCC clone distribution information can http://imagel.lnl.gov.

Anniet. Travallin.gov.
                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone="IMAGE:5054244"
/clone=lib==Nib==NorEdAP_Lig"
/lab_host="DBIOB (Tl phage-resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: Site_2: Sall; Cloned unidirectionally. Primer: Oli: Average insert is ze 1.9 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
a 203 c 211 g 133 t
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85.0%; Pred. No. 1e-81;
Nicmatches 79;
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High quality sequence stop: 699.
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                                                                                                                                                                                                                                                                                                 /strain="FVB/N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           454; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BF539254
                                                                                                                                                                                                                                                                                                                                                                                                                                                       154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                               source
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
BF539254
LOCUS
                                                                                                                                                                                                                                             FEATURES
                                                      COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δλ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            701 bp mRNA linear EST 05-JUL-2001
Mus musculus cDNA clone IMAGE:5054244 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 701)
                                                                                                               /tissue_type="pooled"
/lab host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1;
Librar made from pooled tissue from day 11, 13, 15, 20, and 30 embryos."
                                                                                                                                                                                                                                                                                                                              2972
                                                                                                                                                                                                                                                                                                                                                                                                   3032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240
                                                                                                                                                                                                                                                                                                                                                                                                                                   120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  420
                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                           2913 GGCGGACGCTGCAGTAGGTGGCCAGCAGGCAGGCAGCCCTGCGTGGCGGGATCTT
                                                                                                                                                                                                                                                                                                                                                           1 GGCAGACGACCTACCGTGGACGGACGCAGACACAGGCAGCCTGCGGGCTGGGTCTT
                                                                                                                                                                                                                                                                                                                                                                                             2973 CGGGCTCTCGGCTGTCTCCAAGCCATTGGGCTGTTTGCCTCCATGGCTGCGGGTGCTCCT
                                                                                                                                                                                                                                                                                                                                                                                                               3033 AGGTGGGCCCCGGCCATCCAGGTTGCTTTCCAGAGGCTCCTGTGGGATGTGGTGCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCCCATCAGCTTCTTTGAGCGGACACCCATTGGTCACCTGCTAAACCGCTTCTCCAAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GACAGACACGGTTGACGTGGACATTCCAGACAAACTCCGGTCCCTGCTGATGTACGCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3213 TGGACTCCTGGAGGTCAGCCTGGTGGTGGCAGTGGCTACCCCCACTGGCCACTGTGGCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3273 CCTGCCACTGTTTCTCCTCTACGCTGGGTTTCAGAGCCTGTATGTGGTTAGCTCATGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 CCTGCCTCTGCTCTCTATGCTGGGTTTCAGCGCCTGTATGTGGCCAGCTCGTGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3393 CCAGGGCACACAGTGGTCCGGGCATTCCGAACCCAGGCCCCCTTTGTGGCTCAGAACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTGAGACGCTTGGAGTCAGCCAGCTACTCGTCTGTCTGCTCCCACATGGCTGAGACGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCTCAGACGCCTGGAGTCAGCCAGGTACTCATTCGTGTTTCCCACGTGGCTGAGACATT
                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                            Length 558;
                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                          DB 12;
                                                                                                                                                                                                                                                                                          89;
                                                                                                                                                                                                                                                      Score 415.6; DB 1
Pred. No. 1.9e-86;
                                                                                                                                                                                                                                                                                        0; Mismatches
                                                               /organism="Sus scrofa"
                                                                                 /db_xref="taxon:9823"
/clone_lib="MARC 1PIG"
       r: ATTAGGTGACACTATAG.
Location/Qualifiers
1. .558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus
                                                                                                                                                                                                      174 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             602913152F1 NCI_CGAP_Li9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA sequence.
BI147240
BI147240.1 GI:14607241
                                                                                                                                                                                                                                                        9.2%;
84.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3453 TGCTCGCGTAGATGAAAG 3470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGCACGCGTGGATGAAAG 558
                                                                                                                                                                                                                                                                                        Matches 469; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
              Seq primer:
                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BI147240
                                                                                                                                                                                                    88
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1;

Gaps

Indels

701;

9

Oligo

180

EST 11-DEC-2000

linear

4393

419

4453

DEFINITION

RESULT 5 BI147240

ACCESSION VERSION KEYWORDS SOURCE

541

ORGANISM

REFERENCE

999

720

099 685

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (bases 1 to 603)
Fahrenkrug/S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E. Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Reele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.9809004.e. Vector identified by cross_match with the -minscore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-"Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1; Library made from pooled tissue from day 11, 13, 15, 20,
                                                                                                                                          pooled tissue normalized cDNA libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGTCAGGAGCCCCTCCACCA-CTGGCCACCTACCTGTGCTTGTCCCTGGTGGTGG-TGAG
                                                                                                                   541 TTTGTGCTGTCCTGCCGGATCAACCCCCTTCTTCCTTGAAGACCCCCAGCAGTCT
       CTGCTCTGCTGCATCTTGCCAGGAATCAACACTGTGCAGCAGGCCTCTGCAGGGAACTTC
                                                                                                                                                                                               AACCCCTGTCCAGAGACTGGGGCAGCCTTCCCCTCCAAAGCCACGTTCTGGTGGGTTTCT
                                                                                                                                                                                                                   GGCCTGGTCTGGAGGGGATACAGGAGGCCACTGAGACCAAAAGACCTCTGGTCGCTTGGG
                                           481 CAGAGCGACCCTGTCCGCCACCTGTCCACCTATGCCTGTCTCTGGTGGTGGCACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 392.8; DB 13
Pred. No. 4.3e-81;
); Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BI338028 603 bp
361675 MARC 1PIG Sus scrofa cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC lPIG"
/issue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plate: 129 row: N column: 14
Seq primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
1. .603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BACKWARD: GTTTTCCCAGTCACGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BI338028.1 GI:15031311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and 30 embryos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Design and use of two p
EST discovery in swine
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               206
                                                                                                                                                                                                                                                                                                                                                                  HILLILLILL
AGAGAAACTC 756
                                                                                                                                                                                                                                                                                                                                                  AGAGAAAACTC 731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BI338028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Simil
Matches 461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                              509
                                                                                                                                                                                               601
                                                                                                                                                                                                                                   626
                                                                                                                                                                                                                                                                        661
                                                                                                                                                                                                                                                                                                                                                721
                                                                                                                                                                                                                                                                                                                                                                                   746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 7
BI338028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
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QQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="NCI_CGAP_SG2"
-/Lab_host="DH100 (T] phage-resistant)"
/note="Organ: salivary qland; Vector: pcMv-SPORT6; Site_l:
NotI; Site_2: Sali; Cloned unidirectionally. Primer: Oligo
Mt. Average insert size 1.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. E 1 (bases 1 to 83a)

NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Email: Gapbs-rémail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
Contact: Robert Strausberg, Ph.D.
Email: Gapbs-rémail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CONA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9526 row: l column: 05
High quality sequence stop: 663.
                                                                                                                                                        Murinae; Mus.
   musculus cDNA clone IMAGE:4193812 5'
                                                                                                                                     Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 GGCTACCTCCGGATGTCCCCACTCTTCAAAGCCAAGATGGTGCTTGGATTCGCCCTCATA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          271 CTTCTGTATACCTTCAACGTGGCCGTGCCTTCTGTGGAGGATCCACCAGGGCGTGCCCCAG 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCTGCCGCCACCAGCCTGTGAGCCTGTGCTTCCTGAGAACAGCAGGGGTCTGGGTACCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCCATGIACCICTGGGICCTIGGICCCAICTACCICCICTICAICCACCACCAIGGCCGG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   211 TGCTACCTCCGGATGTCCCACCTCTTCAAAACCAAAATGGTGCTGGGGCTTGGCCCTCATC 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 GCCCCAGAATTCCTCATTCATCCTACTGTGTGGCTCACCACGATGAGCTTCGCAGTGTTC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 GTCCTGTGTACCTCCAGCGTGGCTGTCGCTCTTTGGAAAATCCAACAGGGAACGCCTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361 CTGATTCACACCGAGAGAAAAAGGGAGTCCAGTCATCTGGAGTGCTGTTTGGTTACTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTTCTCTGCTTTGTCTTGCCAGCTACCAACGCTGCCCAGCAGGCCTCCGGAGCGGGCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.7%; Score 393.4; DB 12; Length 838; 76.5%; Pred. No. 3.7e-81; ive 0; Mismatches 166; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:4193812"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:10090"
 602054722F1 NCI_CGAP_SG2 Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="FVB/N"
                                                    BF539254.1 GI:11626635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. 838
                   mRNA sequence.
BF539254
                                                                                                             Mus musculus
                                                                                             house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     160
                                                                          EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             559;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loca
Matches
                                                                                                             ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
ORIGIN
                                                                                                                                                                                      AUTHORS
TITLE
JOURNAL
COMMENT
                                     ACCESSION
                                                    VERSION
KEYWORDS
SOURCE
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EST 30-JUL-2001

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Allikmets, R., Gerrard, B., Hutchinson, A. and Dean, M. Characterization of the human ABC superfamily: isolation and mappling of 21 new genes using the expressed sequence tags dat 4Hum. Mol. Genet. 5 (10), 1649-1655 (1996)
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CCTGCCGCACCAGCCTGCTGAGCCTCCTGAGAACAGGGGGTCTGGGTACCC
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                                                                       GGCTACCTCGGGATGTCCCCACTCTTCAAAGCCAAGATGGTGGTTGGGATTCGCCCTCATA
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/db_xref="taxon:9606"
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Direct Submission
Submitted (12-MC) Human Genetics Section,
Institute, NGI-FCRDC, Frederick, MD 21702, USA
Location/Qualifiers
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sequence.
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Homo sapiens clone EST90757 mRNA
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Seg primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
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88.0%;
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Unpublished (2000)
Contact: Smith TPL
                                             Query Match 8.5
Best Local Similarity 88.0
Matches 417; Conservative
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Fax: 402 762 4390
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Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Smith, T.P.L., Casas, E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (bases 1 to 474)
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1; Library made from pooled tissue from day 11, 13, 15, 20, and 30 embryos."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Design and use of two pooled tissue normalized cDNA libraries for
                                             4375
1021 ACCTGGACCCCTTCGGCAGCTACTCAGAGGAGGACATTTGGTGGGCTTTTGGAGCTGTCCC 1080
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                            AGCTCAAAGCCTTGGTGGCCAGCCTGCCCGGCCAGCTGCAGTACAAGTGTGCTGACCGAG
                                                                                      GCGAGGACCTGAGCGTGGGCCAGAACAGCTCCTGTGTCTGGCACGTGCCCTTCTCCGGA
                                                                                                                                                                                                        AGATGCAGGCCATGCTCGGGAGCTGGTTTGCACAGTGCACTGTGCTGCCCATTGCCCACC
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USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TPL: 402 762 4360
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 1PIG"
/tissue_type="pooled"
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FORWARD: AGGAAACAGCTATGACCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the .minscore
and -minmatch 12 options.
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                                                               Length
                                                          Score 382.8; DB 10; Length
Pred. No. 8.3e-79;
0; Mismatches 57; Indels
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PO Box 166, Clay Center, NE 68933-0166, USA
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Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
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Single pass s
v0.980904.e.
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Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E. Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Keele, J.W.
Design and use of two pooled tissue normalized cDNA libraries for Unpublished (2000)

Contact: Smith TPL
                                                                                /note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1; Library made from pooled tissue from day 11, 13, 15, 20,
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352285 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
BG834171
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NE 68933-0166, USA
                                                                                                                                                           Score 360.6; DB 12;
Pred. No. 1.3e-73;
                                                                                                                                                                                                 0; Mismatches
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         /organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 1PIG"
                                                   /tissue_type="pooled"
/lab_host="DH10B"
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PO Box 166, Clay Center, NE
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                          159
                                                                                                            and 30 embryos:
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                                                                                                                                                                    Query Match 8.0%;
Best Local Similarity 85.4%;
Matches 402; Conservative
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Sus scrofa
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source
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pass sequencing. Bases called and alt_trimmed with phred 04.e. Vector identified by cross_match with the -minscore 18
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                                                                                                                                                                                                                                                                                                                   /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI; Library made from pooled tissue from day 11, 13, 15, 20, and 30 embryos."
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Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 570)
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Pred. No. 3.1e-73;
0; Mismatches 70;
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                                                                                                                                                                                                                                                                                                                                                                                   100
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/db_xref="taxon:9823"
/clone_lib="MARC 1PIG"
/tissue_type="pooled"
/lab_host="DH108"
                                     and -minmatch 12 options.
PCR PRimers
FORWARD: AGGAAACAGGTATGACCAT
BACKWARD: GTTTTCCCAGTCAGGAC
Plate: 112 row: N column: 22
Seq primer: ATTTAGGTGACACTAGG.
                                                                                                                                                                       Location/Qualifiers
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85.1%;
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1 (bases 1 to 518)
Kim.N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
                                                                                                                                                                                                                                                                                                                           BM826384 512SNU16n1 Homo sapiens cDNA clone S22SNU16n1-120-G07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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    TTGCCAGCTACCAACGCTGCCCAGCAGGCCTCCGGAGCGGGCTTCCAGAGCGACCCTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.3%; Score 327.8; DB 14; Length 518; 99.4%; Pred. No. 6.7e-66; 1ve 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eceun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4409
Fax: +82-42-860-4409
                                                                                                                                                                                     533 CACCACCTGGCCACCTGTGCTTGTCCTTGTGGTGGT 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="Ascites"
/cell_type="Lyphoblast-like"
/cell_tine="SNU-16"
/lab_host="DH10B"
                                                                                                                                                              496 CGCCACCTGTCCACCTACCTATGCCTGTCTCTGGTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21C Frontier Korean EST Project 2001
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:9606"
/clone="$22$NU16n1-120-G07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: yongsung@mail.kribb.re.kr
Plate: 120 row: G column: 07
High quality sequence stop: 518.
Location/Qualiflers
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                                                                                                                                                                                                                                                                                                                                                                  5', mRNA sequence.
BM826384
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BM826384
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: kidney; Vector: pWE18S-FL3; Site_1: braIII (CACGTGTGT); Site_1: braIII (CACGTGTGTG); Lst strand cDNA was primed with an oligo(dT) primer is strand cDNA (ATGTGGCCTTTTTTTTTTTTTTTT); double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pWE18S-FL3 vector (S' site CACGTGTG, 3' site CACGTGTG). XhoI should be used to isolate the CDNA insert. Size selection was
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                         Ritter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     performed to exclude fragments 41.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5. end primer CTTGCTCTAAAAGCTGCG and 3. end primer CTACTGCTCTAAAAGCTGCG and 3. end primer CTACTGCTCTAAAAAGCTGCG and 3.
                                                                                                                                                                                                                                                                 Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76 CTGCTGAGCCTGTGCTTCCTGAGAACAGCAGGGTCTGGGTACCCCCCATGTACCTCTGG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 TIGCTCAGCCTGTGCTTTGTGAGAGCCGCCAGCAGCAGCTGCCCCCCATGTACCTCTGG 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTCCTTGGTCCCATCTACCTCCTCTTCATCCACCATGGCCGGGGCTACCTCCGGATG 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCCCCACTCTTCAAAGCCAAGATGGTGCTTGGATTCGCCCTCATAGTCCTGTGTACCTCC 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   256 AGCGTGCCTCTCTTTGGAAATCCAACAGGAACGCCTGAGGCCCCAGAATTCCTC 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          293 AACGTGGCCGTGCCTCTGTGGAGGATCCACCAGGCGTGCCCCAGGCCCCAGAGCTTCTA 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  376 AGGAAAAAGGGAGTCCAGTCATCTGGAGTGCTGTTTGGTTACTGGCTTCTCTGCTTTGTC 435
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                                                                                                                                                                               Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
  Theising, B., Allen, M., Bowers, Y., f., Pape, D., Harvey, N., Schurk, R.,
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
'E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
Waterston,R. and Wilson,R.
The WashUrNCI Mouse BST Project 1999
Unpublished (1999)
Other_ESTS: un08e11.x1
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0
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Pred. No. 2.5e-67;
0; Mismatches 115; Indels
                                                                                                                                                       Contact: Marra M/WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/strain="557BL"
/db_xref="taxon:10090"
/clone="IMAGE:2373260"
/clone_lib="Sugano mouse kidney mkia"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                         Seq primer: custom primer used
High quality sequence stop: 518.
Location/Qualiflers
1. .570
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/lab_host="DH10B"
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Best Local Similarity 77.8%;
Matches 403; Conservative C
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                                                                                                                                                                                                                          Tel: 314 286 1800
Fax: 314 286 1810
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FOR PRIMERS
FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                               EST 09-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Casas, E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                              Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E. Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W. and Keele,J.W.
Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine Unpublished (2000)
Contact: Smith FPL
                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 541)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="pooled"
/lab_nost="bH10B"
/note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1;
Library made from pooled tissue from day 11, 13, 15, 20,
                                                                                                                       CAAGGGGCAGGTGGCAGAGAGCGGCAGCCCGGCCCAGCTGCTGGCCCAGAAGGGCCTGTT 4478
                 240
                                                                                                                                      CCTGCCGCCACCAGCCTGCTGAGCCTGTGCTTCCTGAGAACAGCAGGGGTCTGGGTACCC 120
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                                                                           181 GCTGCTCATTGCCCACCGCCTGCGCTGATGGACTGTGCCCGGGTTCTGGTATGGA
4299 CCCTGGCACGAGCTGCAGATGCAGGCCATGCTCGGGAGCTGGTTTGCACAGTGCACTGT
                                                           GCTGCCCATTGCCCACCGCCTGCGCTCCGTGATGGACTGTGCCCGGGTTCTGGTCATGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 10; Length 541;
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Pred. No. 6.4e-64;
0; Mismatches 72; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TTE1: 402 762 4390
Fax: 402 762 4390
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                                                                                                                                                                                 4479 TTACAGACTGGCCCAGGAGTCAGGCCTGGTC 4509
                                                                                                                                                                                                   301 TTACAGACTGGCCCAGGAGTCAGGCCTGGTC 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BACKWARD: GTTTTCCCAGTCACGACG
Plate: 53 row: B column: 22
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC lPIG"
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170 c 15
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Best Local Similarity 83.33
Matches 375; Conservative
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BE014336
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1 (bases 1 to 314)

1 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagal, M.A., da Sllva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&t2=CM3·NT0245-Seq primer: puc 18 forward High quality sequence start: 3 High quality sequence story: 314.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                      300
                                                                                                       121 CCCATGTACCTCTGGGTCCTTGGTCCCATCTACCTCCTCTTCATCCACCACCATGGCCGG 180
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                                                                                                                                                                    241 GTCCTGTGTACCTCCAGCGTGGCTGTCGTTTTGGAAAATCCAACAGGGAACGCCTGAG
                                                                                                                                                                                                                                                                                                                                         181 GGCTACCTCCGGATGTCCCCACTCTTCAAAGCCAAGATGGTGCTTGGATTCGCCCTCATA
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/db_xref="taxon:9606"
/clone_lib="NT0245"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  421 CTTCTCTGCTTTGTCTTGCCAGCTACCAAC 450
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
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No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions.
                                                                                                                              ;
0
                                                                                                                                                    TGCCAGCTACCAACGCTGCCCAGCAGGCCTCCGGAGCGGGCTTCCAGAGCGACCCTGTCC 496
                                                                                                                                                                                                                                                                             121 TGCCAGCTACCAACGCTGCCAGCAGCCTCCGGAGCGGCCTTCCAGAGCGACCCTGTCC 180
                                                                                                                                                                                                                                                                                                                   IGGCGGATCAACCCCCCTTCTTCCCTGAAGACCCCCAGCAGTCTAACCCCTGTCCAGAGA 616
                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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0
                                                                                              Query Match 7.0%; Score 314; DB 13; Length 314; Best Local Similarity 100.0%; Pred. No. 8.9e-63; Matches 314; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 617 CTGGGCCAGCCTTC 630
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Search completed: December 18, 2002, 21:26:58 Job time : 3852.31 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

December 18, 2002, 07:49:35; Search time 109.187 Seconds (without alignments) 16388.716 Million cell updates/sec Run on:

US-09-647-140A-7 4509 Perfect score:

Title:

1 atggccgcgcctgctgagcc.......cccaggagtcaggcctggtc 4509 Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

356696 seqs, 198428768 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

/cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq: //cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq: //cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq: //cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq: //cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq: 6/ptodata/1/pubpna/USO7_NEW_PUB.seq: 6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq: 6/ptodata/1/pubpna/USO8_NEW_PUB.seq: 6/ptodata/1/pubpna/USO8_PUBCOMB.seq: /ptodata/1/pubpna/US06_NEW_PUB.seq:/ /ptodata/1/pubpna/US06_PUBCOMB.seq: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:/cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seg Published_Applications_NA: /cgn2_6/ /cgn2_

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		dР				
Result No.	Score	Query Match	Query Match Length DB	DB	DI	Description
						CSC TPCTOIL
Н	3030	67.2	5728	10	US-09-917-800A-479	Sequence 479. Ann
7	1076.8	23.9	1936	10	US-09-880-107-3832	
æ	713	15.8	5300	10	US-09-880-107-3373	Sequence 3373. An
4	693	15.4	4918	10	US-09-917-800A-1578	Sequence 1578. An
S	384.6	8.5	1977	10	US-09-954-456-804	Seguence 804, App
Q	384.6	8.5	1977	10	US-09-880-107-3407	3407
7	384.6	8.5	1977	10	US-09-967-768A-190	Sequence 190, App
œ	350.2	7.8	1448	10	US-09-925-299-157	Sequence 157, App
σ	336.6	7.5	4551	σ	US-09-938-842A-1674	
10	271.4	9.0	3786	6	US-10-012-896-1006	Sequence 1006. Ap
11	271.4	0.9	4395	6	US-10-012-896-1007	Sequence 1007. Ap
12	271.4	0.9	6140	σ	US-10-012-896-536	Sequence 536. App
13	271.4	0.9	6140	10	US-09-759-143-536	Sequence 536, App
14	271.4	0.9	6140	10	US-09-780-669-536	Sequence 536, App
15	271.4	9.0	6140	10	US-09-822-827-536	Sequence 536, App
16	264.2	5.9	6082	6	US-10-012-896-535	Sequence 535, App
17	264.2	5.9	6082	10	US-09-759-143-535	Sequence 535. App
18	264.2	5.9	6082	10	US-09-780-669-535	Sequence 535. App
19	264.2	5.9	6082	10	US-09-822-827-535	Sequence 535, App

Sequence 436. App	Sequence 1392. An	Segmence 247 Ann	Sequence 55. Appl	Sequence 4147. An	Sequence 293 App	Segmence 1. Apply	Sequence 18. Appl	Sequence 16, Appl	Sequence 1, Appli	Sequence 4038, Ap	Sequence 824. Ann	Segmence 824 App	Sequence 824 Ann	Sequence 824. App	Sequence 613. Ann	Segmence 11 Aprol	Seguence 11 Aprol	Sequence 5. Appli	Sequence 1560. An	Sequence 1. Appli	Segmence 3. Appli	Sequence 1424 An	Sequence 13. Annl	Sequence 7. Appli	Sequence 105, App
US-09-938-842A-436	US-09-938-842A-1392	US-09-925-297-247	US-09-938-842A-55	US-09-815-242-4147	US-09-833-381-293	US-09-976-059-1	US-09-795-693-18	US-09-795-693-16	US-10-072-621-1	US-09-815-242-4038	US-10-012-896-824	US-09-759-143-824	US-09-780-669-824	US-09-822-827-824	US-09-925-300-613	US-09-739-254-11	US-09-904-615-11	US-09-866-866A-5	US-09-917-800A-1560	US-09-769-097-1	US-09-769-097-3	US-09-917-800A-1424	US-09-764-884-13	US-09-866-866A-7	US-09-756-095-105
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4872	4869	1019	4545	1812	744	88421	2298	3408	3512	2172	1074	1074	1074	1074	1427	3289	3289	4189	3912	4369	4425	4254	1076	4788	3069
5.8	5.5	5.1	4.4	3.6	3.5	3.5	3.0	3.0	3.0	2.9	2.8	2.8	2.8	2.8	2.8	2.7	2.7	5.6	2.5	2.5	2.5	2.5	2.4	2.4	2.4
262.4	246.6	229	196.8	161.6	158.6	156	133.4	133.4	133.4	130.4	128.2	128.2	128.2	128.2	125.8	121.6	121.6	118.4	113.2	112.8	112.8	110.8	110.2	108	107.8
20	21	22	23	24	c 25	c 26	27	28	29	30	. 31	32	33	34	32	36	37	38	39	40	. 41	42	43	44	45

## ALIGNMENTS

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; OTHER INFORMATION: Genbank Accession No. US20020119462A1 AB010466 US-09-917-800A-479
                                                                                                                                                                                                                                            APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5938-US
                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/917,800A CURRENT FILING DATE: 2001-07-31 PRIOR APPLICATION NUMBER: US 60/222,040 PRIOR FILING DATE: 2000-07-31
                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 60/222,880
PRIOR FILING DATE: 2000-11-02
PRIOR APPLICATION NUMBER: US 60/290,029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: US 60/292,336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/295,798
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US 60/297,457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,884
PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/303,459
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 1740
                            Sequence 479, Application US/09917800A Patent No. US20020119462A1
                                                                                                                                                     APPLICANT: Johnson, Kory
APPLICANT: Castle, Arthur
APPLICANT: Elashoff, Michael
APPLICANT: Gene Logic, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Ver. 2.1
                                                                             GENERAL INFORMATION:
APPLICANT: Mendrick, Donna
                                                                                                                                             Porter, Mark
US-09-917-800A-479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 479
LENGTH: 5728
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Hest Local Similarity 80.3%; Pred. No. 0; Matches 3629; Conservative 0; Mismatches 850; Indels 39; Gaps 1 ATGGCGGGCCTGGTGAGCCTGGGGGGGGGGGGGGGGGGG	61 CCTGCCGCCACCAGCCTGTGAGCCTGTGAGAACAGCAGGGGGTCTGGGTACCC 120	121 CCCATGTACCTCTGGGTCCTTGGTCCCATCTACCTCCTCTTCATCCACCATGGCCGG 180	181 GGCTACCTCCGGATGTCCCCACTCTTCAAAGCCAAGATGGTGCTTGGATTCGCCCTCATA 240	241 GTCCTGTGTACCTCCAGCGTGGCTGTCGCTCTTTGGAAAATCCAACGGAACGCCTGAG 300	301 GCCCCAGAATTCCTCATCATCTGTGTGGCTCACCAGGTGAGCTTCGCAGTGTTC 360 	361 CTGATTCACACCGAGAGAAAAGGGAGTCCAGTCATCTGGAGTGCTGTTTGGTTACTGG 420 	421 CTTCTCTGCTTTGTCTTGCCAGCTACCAACGCTGCCCAGCAGCCTCCGGAGCGGCTTC 480	481 CAGAGCGACCTGTCCGCCACCTACCTACCTGTCTCTGTGGTGGTGGCACAG 540	541 TTTGTGCTGCCTGCCTGGGGGATCAACCCCCCTTGTTCCCTGAAGACCCCGAGCAGTCT 600	601 AACCCTGTCCAGAGACTGGGGCAGCCTTCCCCTCCAAAGCCACGTTCTGGTGGGTTTCT 660	661 GGCCTGGTCTGGAGGGGATACAGGAGGCCACTGAGACCAAAAGACCTCTGGTCGCTTGGG 720	721 AGAGAAACTCCTCAGAAGAACTTGTTCCCGGCTTGAAAGGAGTGGATGAGGAACCGC 780 	781 AGTGCAGCCCGGAGGCACAACAAGGCAATAGCATTTAAAAGGAAAGGCGGCAGTGGCATG 840 	841 AAGGTICCAGAGACCGAGCCTICCTACGGCAAGAGGAGCCAGTGGCGCCCACTGCTG 900	901 AAGGCCATCTGGCAGGTGTTCCATTCTACCTTCCTCGGGGACCCTCAGCCTCATCATC 960	961 AGTGATGTCTTCAGGTTCACTGTCCCCAAGCTGCTTTTCCTGGAGTTTATTGGT 1020 11 1111 11111111 11111111 1111111 11 11
Oy Mag	Qy Db	Oy Dp	Qy Db	Qy Db	Oy Op	oy ob	0y .	oy Op	oy Ob	Oy Dp	ολ Dp	Qy Db	Qy Dp	Qy Dp	Oy Dp	Qy

1200 1440 1500 1260 1278 1338 1380 1458 1518 1560 1098 1320 1578 1620 1638 1677 1737 1758 1797 1818 1857 1878 1917 1935 1977 1995 2037 2055 2097 2157 GATCCCAAGCCTCCAGCCTGGAAGGGCTACCTCCTCGCCGTGCTGATGTTCCTCTCAGCC ATCAACTTCCATGGCTGGGAGGGCTTTCTGGACAGACTCTGGGCATCCGGGCATCCGGGCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCTTCTGGACAGACTCTGCAGACTCTGCAGGCGACTCCTGCAGACTCCTGCAGACTCCTGCAGACTCCTGCAGACTCCTGCAGACTCCTGCAGACTCCTGCAGACTCCTGCAGACTCCTGCAGACTCCTGCAGACTCCTGCAGACTCCTGCATATCCGGGGCCAG CAGGAAAGCCCTCCCTCCACAGAATAAACCTCACGGTGCCCCAGGGCTGTTGCTG AGAAAGGCCAGTGCGTGGTGATGTGGTCAATCTGGTGTCCGTGGACGTGCAGCGCCTG ATGAGGCAGAAGGACTCACGGGCACGGCTCACCAGCTCTTATCCTCAGGAACTCGAAGACC GCCTGGGTGCAGAACACCTCTGTGGTAGAATGTGTGCTTCGGGCAGGAGCTGGACCCA TTGCGGTCGGCCATCACTGGCCTGGTGTACAGAAAGGTCCTGGCTCTGTCCAGCGGCTCC ACCGAGAGCGTCCTCTACCTCAACGGGCTGTGGCTGCCTCTCGTCTGGATCGTGGTCTGC **AATGCTATGAATGCAGAGAAAGCCTTTGTGACTCTCACAGTTCTCAACATCCTCAACAAG** GCCCAGGCTTTCCTGCCCTTCTCCATCCACTCCTCGTCCAGGCCCGGGTGTCCTTTGAC 1039 1081 1159 1099 1141 1219 1261 1321 1381 1399 1441 1459 1519 1201 1279 1339 1579 1639 1678 1879 1501 1561 1621 1699 1738 1759 1798 1819 1858 1918 1936 1978 1996 2038 2056 2098 qq Qy Db οy g οy Оþ δ Db ò g οy qq QΥ g οy q οy Dp ò QQ ò g οy g Qγ g qq a δ ŏ qq qq Qγ ΩŸ

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Oy         4312         CTGCAGATGCAGGCCATGCTCGGGAGCTGGTTTCCACAGTGCACTGTGCTGCCCATTGCC         4371           I	13832 32, Application US/06 USJO020142981a1 ORMATION: UCKLEY, JOSEPH G. SCHET, UWE GENE LOGIC, INC. NVENTION: GENE EXPIES ENCE: 44921-5028-WO LING DATE: 2001-06-1 ICATION NUMBER: US 6( TO DATE: 2000-06-14 ICATION NUMBER: US 6( TO DATE: 2000-06-14 ICATION NUMBER: US 6( TO DATE: 2000-10-02 SEQ ID NOS: 3950 SEQ ID NOS: 3950 HOMO SAPIENS P36 HOMO SAPIENS P3832	

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0; Mismatches 1695;
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APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Scherf, Uwe
TITLE OF INVENTION: Gene Expression Profiles in Live
TITLE OF INVENTION: Gene Expression Profiles in Live
FILE REPRENCE: 44921-5028-WO
CURRENT FILING DATE: 2001-06-14
PRIOR PPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PALENTIN Ver. 2.1
SSOFTWARE: PALENTIN Ver. 2.1
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15.8%; Score 713;
Best Local Similarity 51.4%; Pred. No. 8e
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US-09-917-800A-1578
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                                                                                                                                                                                                               APPLICANT: POLICE, MAILA
APPLICANT: Castle, Arthur
APPLICANT: Castle, Arthur
APPLICANT: Elashoff, Michael
APPLICANT: Elashoff, Michael
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE FEFERNCE: 44921-5038(02)
CURRENT APPLICATION NUMBER: US 60/222,040
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR FILING DATE: 2000-10-11
PRIOR APPLICATION NUMBER: US 60/290,029
PRIOR FILING DATE: 2001-05-15
PRIOR FILING DATE: 2001-05-15
PRIOR FILING DATE: 2001-05-15
PRIOR FILING DATE: 2001-05-15
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-16
PRIOR FILING DATE: 2001-06-19
PRIOR FILING DATE: 2001-07-09
SOFTWARE: PATENTIN VON: 1740
4675 CTGGACCCTTTTATGGCTAAGGAAGCTGGCATTG 4713
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Pred. No. 6.6e-161;
0; Mismatches 1670;
                                                                                                                      Sequence 1578, Application US/09917800A
Patent No. US20020119462A1
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Conservative
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                                                                                                                                     Patent No. US20020113462A1
GENERAL INFORMATION:
APPLICANT: Mendrick, Donna
APPLICANT: Porter, Mark
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Matches 1867; Conserva
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                                                                                                                                                 APPLICANT: Young, Paul

TITLE OF INVENTION: Paul

TITLE OF INVENTION: Sets

FILE REFERENCE: 689290-76

CURRENT PAPLICATION NUMBER: US/09/954,456

CURRENT PAPLICATION NUMBER: US/60/233,617

PRIOR PLING DATE: 2000-09-18

PRIOR PLING DATE: 2000-09-20

PRIOR PLING DATE: 2000-09-20

PRIOR PLING DATE: 2000-09-20

PRIOR PLING DATE: 2000-09-20

PRIOR PLING DATE: 2000-09-26

PRIOR PLING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: US/60/235,710

PRIOR PLING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: US/60/235,840

PRIOR PLING DATE: 2000-09-27

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8.5%; Score 384.6; DB 10;
llarity 55.8%; Pred. No. 4.1e-85;
Conservative 0; Mismatches 631;
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; OTHER INFORMATION: n=a, t,g or
US-09-954-456-804
                                                                                                                        Sequence 804, Application
Patent No. US20020115057A1
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ORGANISM: Homo sapiens
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Sequence 190, Application US/09967768A Patent No. US20020150877A1 GENERAL INFORMATION:
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55.8%; Pred. No. 4.1e-85;
ive 0; Mismatches 631; Indels 12;
                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Horne, Darci T.
APPLICANT: Horne, Darci T.
APPLICANT: Cockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
APPLICANT: Gene Expression Profiles in Liver Cancer:
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer:
FILE REFERENCE: 44921-5028-W0
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-16
PRIOR FILING DATE: 2000-06-16
SOFTWARE: PATCHING DATE: 2000-06-16
SOFTWARE: PATCHING DATE: 2000-10-02
SOFTWARE: PATCHING DATE: 2000-06-16
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Patent No. US20020142981A1
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Best Local Similarity 55.8<sup>†</sup>
Matches 811, Conservative
                            1441 ATGCTGGACTTGCC 1454
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485 GGAACTGCGTGGTGCTCTTTGCTGCACTATTTGCCGTCATCGGGAGGAGCAGCCTGAACC 544
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            664 ACTCCAAGACAGAGAGAGGCGCCCTGGGTGTG---GAACAGCCGCCCTCCCGAAGGT 720
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CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: PATCHIN VET: 2.0
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; Patent No. US20020055627A1
; GENERAL INFORMATION:
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TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using $\) FILE REFERENCE: $69290-72
CURRENT APPLICATION NUMBER: US/09/967,768A
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: US/60/236,109
PRIOR FILING DATE: 2000-09-28
PRIOR PELING DATE: 2000-09-28
PRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 325
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
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55.8%; Pred. No. 4.1e-85;
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CCATION: (1)...(1977)

OTHER INFORMATION: n=a,t,g or c

US-09-967-768A-190
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Matches 811; Conservative
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                                                                                         Sequence 1674, Application
Patent No. US20020160378A1
GENERAL INFORMATION:
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APPLICANT: Kreps, Joel
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                                                                                                                                                                                                                                                GCAGTGGGTTGTTCGCAACTGGACAGACCTAGAGAACAGCATCGTGTCAGTGGAGCGGAT 3707
                                                                                                                                                                                                                                                                                                                                                                     3768 GCCCCCCTGGCCTCAGGGCGGGCAGATCGAGTTCCGGGACTTTGGGCTAAGATGCCGACC 3827
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                                                                                                                                                                                                                                                                           243 GGCCTAGACCTGGTGCTGAGACCTGAGTCTGCACGTGGCGARAAGGTGG 302
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                                                                                                                                                                                                                3 CCTGAACCCGGGGCTGGTGGGCCTTTCTGTGTCCTACTCCTTGCAGGTGACATTTGCTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGTGGCAGAGAGCGGCAGCCCGGCCCAGCTGCTGCCCCAGAAGGGCCCTGTTTTACAGACT
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                                                                                                                     Score 350.2; DB 10; Length
Pred. No. 1.1e-76;
3; Mismatches 357; Indels
                                                                            ^{\rm or}
                                                        ; LOCATION: (456)
; OTHER INFORMATION: n equals a,t,g,
US-09-925-299-157
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                                                                                                                      7.8%;
                                                                                                                                   Best_Local Similarity 61.03
Matches 562; Conservative
        ORGANISM: Homo sapiens
FEATURE:
                                           NAME/KEY: misc_feature
                                                                                                                      Query Match
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PLANTS, TRANSGENIC PLANTS CONTAINING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1074 CTCAGCCTGCCTGCAAACGCTGTTTGAGCAGCAGGAACATGTACAGGCTCAAGGTGCCGCA 1133
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Pred. No. 4e-73;
0; Mismatches 1944;
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
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Page

2012 2513 CTCTGGAGCACGCCAGTGCTTATCTCTGCTCTCACCTTGGCCACGCCCTTGCCTTGGG 1718 GGAGGCCTGGGTGCAGAACACCTCTGTGGTAGAGAATGTGTGCTTCGGGCAGGAGCTGGA 2153 2154 CCCACCCTGGCTGGAGAGATACTAGAAGCCTGTGCCCTGCAGCCAGATGTGGACAGCTT 2213 2373 TGTTTTAGCGCAGTGGATGCTCATACCGGTTCAGATATATTCAA-----GAAATGTT 2426 GCGAGTCATCAAGTTTCAGGCTTGGGAGAATCATTTAACAAGAGGATCCTCAAATTCAG 1598 GGACATGGAGTTTGGTTGGCTATCCAAGTTTCTTTACTCCATTGCTGGCAATATTATTGT 1658 CGAGAATGCTATGAATGCAGAGAAAGCCTTTGTGACTCTCACAGTTCTCAACATCCTCAA 1733 CAAGGCCCAGGCTTTCCTGCCTTCTCCATCCACTCCTTGTCCAGGCCCGGGTGTCCTT 1793 TGACCGTCTGGTCACCTTCCTCTGCCTGGAAGAAGTTGACCCTGGTGTCGTAGACTCAAG 1853 TICCICIGGAAGCGCIGCCGGGAAGGAIIGCAICACCAIACACAGTGCCACCIICGCCIG 1913 2393 AGCCCTGGGTTGTGATGGTAATACTGCCGTGGAGGTCAGAGATGGAAGCTTTAGTTGGGA 1952 TGGGAGACTGGACTCATACATGAGCAAAGAGCTGTCGGAAGATGCTGTGGA---GAG GGAGCTGTCAAAGGTGGAGGGGTTCGTGAGCATCGAGGGTGCTGTGGCCCTACGTGCCCCA AGGCCAGGAGCTGGGGCCCTTGCGGACCTCCGGCCTCCTCTTCTCTGTGTCGCTGGTGTC CTTCCAAGTGTCTACATTTCTGGTCGCACTGGTGTTTTGCTGTCCACACTCTGGTGGC GTCCCAGGAAAGCCCTCCCTGCCTCCACAGAATAAACCTCACGGTGCCCCAGGGCTGTCT 1953 TGATGAGGACAACGAACCTGCTCTCAGTGATATCAACTTCAAGGTTAAGAAAGGTGAGCT GCTGGCTGTTGTCGGTCCAGTGGGGGCAGGGAAGTCCTCCCTGCTGTCCGCCCTCCTTGG GCAGCGGCTGAGCCTGGCCCGGGCTGTATACAGAAAGGCAGCTGTGTACCTGCTGGATGA CCCCCTGGCGCCCTGGATGCCCACGTTGGCCAGCATGTCTTCAACCAGGTCATTGGGCC AAGAGGAGCTCTGAAAGGCAAGACCGTATTACTCGTTACCCATCAAGTGGATTTCTTGCA CCAGGCTGATTGGATCATAGTGCTGGCAAATGGGGCCATCGCAGAGATGGGTTCCTACCA GGAGCTTCTGCAGAGGAAGGGGGCCCTCGTGTCTTCTGGATCAAGCCAGACAGCCAGG AGATAGAGGAGAAGGAGAAACAGGACCTGGGACCAGCACCAAGGACCCCAGAGGCACCTC 2274 2607 1554 1614 1659 1674 1719 1734 1776 1794 1836 1854 1893 1914 1974 2034 2073 2094 2193 2334 2394 2427 2454 2487 2514 2574 δ g g Qγ Q ò Q ò g qq ογ g ò g ŏ g οy δ 셤 οy δ g ά g ò g QΥ q οŽ Q δý g Qγ g Ω

3137 3173 3197 3233 3413 3437 3497 3533 3617 GTCTCCCCATGCAAGCTCTCCGAGA----ACGTCAATGGAGTCTCCTCACTTAAGTGA 2720 GTGGCAGGGATCTCTAATGGCCAGCGATTACTGGCTTGCATACGAAACATCAGCCAAAAA 2957 TGCAATATCATTTGATGCTTCCGTTTTCATTCTCGGATATGTAATTATTGCACTTGTTTC 3017 AGCCATTGGGCTGTTTGCCTCCATGGCTGCGGTGCTCCTAGGTGGGGCCCCGGGCATCCAG 3053 CATCGTTTTGGTGAGCATCCGGTCATATACGTCACCCACTTGGGACTCAAGACGGCTCA 3077 3257 GGTGGTGGCAGTGGCTACCCCACTGGCCACTGTGGCCATCCTGCCACTGTTTCTCCTCTA 3293 CGCTGGGTTTCAGAGCCTGTATGTGGTTAGCTCATGCCAGCTGAGACGCTTGGAGTCAGC 3353 GGCATTCCGAACCCAGGCCCCCTTTGTGGCTCAGAACAATGCTCGCGTAGATGAAAGCCA 3473 3557 CAGTGCTGGCCTCGTGGGCTTCTCTGTCTGCTGCCCTCCAGGTGACCCAGACACTGCA 3650 GTGGGTTGTTCGCAACTGGACAGACCTAGAGAACAGCATCGTGTCAGTGGAGCGGATGCA 3710 3678 CTTTGCCATATACATGAGCTGCTTTGTCGAGAACAAGATGGTTTCAGTTGAAAGGATCAA 3737 GCTCATCAAAGAAGAAAAGGGAAAACGGACAAGCTTAGGAGTTTACAAACAGTA CCGTACCACTTCAGAAGCCCAGACAGAGGTTCCTCGGATGACCCTGACAGGGCAGGATG 2721 TCTAAACGATGAGCATATCAAATCATTTCTCGGTTCTCACATCGTAGAAGATGGCTCGAA GCCAGCAGGAAAGGACAGCATCCAATACGGCAGGGTGAAGGCCACAGTGCACCTGGCCTA CT---GCACTGAGGCTTATGGCTGGTGGGGAATTGTGCTTGTTCTTCTTCTCTGAC AGTGGCCTCCTTCTGCCGGGGCTACTGGCTGAGCCTGTGGGCGGACGACCCTGCAGTAGG TGGGCAGCAGCCAGGCAGCCCTGCGTGGCGGGATCTTCGGGCTCCTCGGCTGTCTCCA GTTGCTCTTCCAGAGGCTCCTGTGGGATGTGGTGCGATCTCCCATCAGCTTCTTTGAGCG CATTCCAGACAAACTCCGGTCCCTGCTGATGTACGCCTTTGGACTCCTGGAGGTCAGCCT GAGGATCAGTTTCCCGCGACTGGTGGCTGACAGGTGGCTTGCGGCCAATGTGGAGCTCCT 3138 CACGCCATCGGGAAGAATTCTCAGTCGGCATCGACTGATCAGACCAATGTCGATATCCT 3198 TATTCCGTTTATGCTCGGACTTGTGGTCTCAATGTACACCACTCTGCTGAGCATTTTCAT GGGGAATGGCCTGGTGTTTGCAGCCGCCACGTGT---GCTGTGCTGAAGCCCACCT 3558 TGGGAGCTGGGTGCTCTGCATCTCGGCTTTATGGTATTGTTACCCAGCAACGTTAT 3498 CAGGATGGACTTCCACAACAATGGCTCCAACGAATGGCTCGGGTTTCGGCTGGAGCTGGT 2667 2874 2898 2994 3258 3378 2754 2781 2958 3018 3114 3234 3318 2634 2694 2934 3054 3078 3294 3354 3414 3438 3618 3651 , dg δy pp δ qq QQ Ωý Op QQ Qγ qq qq Db Qy QΥ Ω Ω Óγ δy Qγ qq ÓΥ ò Db Qy QQ Qγ QQ δy g δ q Db qq òγ Qγ

Houghton, Raymond L. Vinals de Bassols, Carlota Hural, John McNeill, Patricia D. Henderson, Robert A. Hural, John Wang, Aijun Skeiky, Yasir A.W. Hepler, William T.

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APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Madeleline Joy
TITLE OF INVENTION: DIAGNOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
CURRENT APPLICATION NUMBER: US./10/10/2/896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 6.0%;
Best Local Similarity 46.0%;
Matches 1185; Conservative
                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-896-1006
                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 1006
LENGTH: 3786
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                             GCTCCCCCTGGCTGTGCAGGCCTGTCCTTCAAGATCCACGCAGGAGAAGGTGGGCAT
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Pred. No. 4.3e-57;
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Sequence 1006, Application US/10012896 Publication No. US20020183251A1 GENERAL INFORMATION:

US-10-012-896-1006

APPLICANT: XW, Jiangchun APPLICANT: XW, Jiangchun APPLICANT: Mitcham, Jennifer L. APPLICANT: Harlocker, Susan L. APPLICANT: Harlocker, Susan L. APPLICANT: Kalos, Michael D. APPLICANT: Ralos, Michael D. APPLICANT: Retter, Marc W. APPLICANT: Stolk, John A. APPLICANT: Vedvick, Thomas S. APPLICANT: Vedvick, Thomas S. APPLICANT: Carter, Darrick

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Publication No. US20020183251A1
GENERAL INFORMATION:
APPLICANT: W. Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Alang, Yuqiu
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Carter, Marc W.
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick US-10-012-896-1007 2878 2938 3676 3736 3796 3856 3916 3115 3976 3172 3232 3292 4216 4036 4096 4156 3352 3412 4276 4396 4453 ò qq g οy δ qq οy qq ŏ ρp ò g qq Q g qq g QY ò ò g Qγ ò qq g qq δ δ

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                                       APPLICANT: MENUELSON, ADDELL A.
APPLICANT: HURAL JOHN
APPLICANT: HOUGHLON, RAYMOND L.
APPLICANT: HOUGHLON, RAYMOND L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Wandeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
FILE REFERENCE: 210121.427C27
CURRENT APPLICATION NUMBER: US/10/012, 896
CURRENT APPLICATION NUMBER: US/10/012, 896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SSOFTWARE: FASELSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                               Score 271.4; DB 9;
Pred. No. 4.6e-57;
0; Mismatches 1366;
        Skeiky, Yasir A.W.
Hepler, William T.
Henderson, Robert A.
                                                                                                                                                                                                                                                                                                 6.0%;
46.0%;
                                                                                                                                                                                                                                                                                                           Best Local Similarity 46.0
Matches 1185; Conservative
Wang, Aijun
                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-10-012-896-1007
                                                                                                                                                                                                                          SEQ ID NO 1007
                                                                                                                                                                                                                                                  TYPE: DNA
                                APPLICANT:
                                                                                                                                                                                                                                                                                                  Query Match
                      APPLICANT:
           APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                           1996
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2416 ACTCCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTG-----GTCTCAACAAT
                                                                                                                                                                                                                                          2716 ACAGAGGTTCCTCTGGATGACCCTGACAGGGCAGGATGGCCAGCAGGAAAGGACAGCATC
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                                                                                                                                                                                2471 CTTCTAGACCCTCCTTGAAGATGGTGCTCTGGAGAGCCAAGATACAGAGAATGTCCCAG
                                                                                                                                                                                                                                                                                                          2531 TTACACTATCAGAGGAGAACCGTTCTGAAGGAAAGTTGGTTTTCAGGCCTATAAGAATT
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                                                                                                                             AGACGCGAGAGGTCCATCAAGTCAGTCCCTGAGAAGGACCGTACCACTTCAGAAGCCCAG
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TCCTTCAAGATCCACGCAGGAGAAGGTGGGCATCGTTGGCAGGACCGGGGCAGGGAAG 3915
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                                                       TCCTCCCTGGCCAGTGGGCTGCTGCGGCTCCAGGAGGCAGCTGAGGGTGGGATCTGGATC 3975
                                                                                                                                                                                                                                                                                        GACGGGGTCCCCATTGCCCACGTGGGGCTGCACACTGCGCTCCAGGATCAGCATCATC 4035
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CTAGAGAACAGCATCGTGTCAGTGGAGCGGATGCAGGACTATGCCTGGACGCCCAAGGAG
                                                                         4156 AGCCTGCCCGGCCAGCTGCAGTACAAGTGTGCTGACCGAGGCGAGGACCTGAGCGTGGGC
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RESULT 12
US-10-012-896-536
Sequence 536, Application US/10012896
Fublication No. US20020183251A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Kalos, Michael D.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Carter, Marc W.
APPLICANT: Carter, Day, Craig H.
APPLICANT: Carter, Thomas S.
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1936 CICCACAGAATAAACCTCACGGIGCCCCAGGGCTGTCTGCTGGTGTTGTCGGTCCAGTG 1995
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                                                APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Moneill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Mantanabe, Yoshihiro
APPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2176 CTAGAAGCCTGTGCCCTGCAGATGTGGACAGCTTCCCTGAGGGAATCCACATTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 271.4; DB 9
Pred. No. 5.3e-57;
                             Skeiky, Yasir A.W.
Hepler, William T.
Henderson, Robert A.
Hural, John
MCNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: n = A,T,C or US-10-012-896-536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.0%;
46.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: 4535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 536
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                                APPLICANT
APPLICANT
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Thu Dec 19 10:40:58

2866 CACTIGICALCITCICCAGGGGCTCTGGACCAICCGGGCAIACAAAGCAGAAGAAGG 2925 TTACACTATCAGAGGAGAACCGTTCTGAAGGAAAAGTTGGTTTTCAGGCCTATAAGAATT 2269 CAATACGGCAGGGTGAAGGCCACAGTGCACCTGGCCTACCTGCGTGCCGTGGGCACCCCC 2835 ACAACGTCCCGCTGGTTCGCCGTCCGTCTGGATGCCATCTGTGCCATGTTTGTCATCATC 3045 GCCCTCGTGTGTCTTCTGGATCAAGCCAGACAGCCAGGAGATAGAGGAGAAGGAAACA GATTTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAAGTGAACAACCTCCAGTTCCAGGA 2095 ACTCCCACACTAAGGAATCGTACCTTCTAGAGTCTTCGGTTTG-----GTCTCAACAAT 2716 ACAGAGGTTCCTCTGGATGACCCTGACAGGGCAGGATGGCCAGCAGGAAAGGACAGCATC 2508 TCTATTGGTATTCTACGTCCTTGTTAACTCTTCACAAACTT - TGCACAACAAAATGTTT CTTCTAGACCCTCCTTGAAAGATGGTGCTCTGGAGAGCCAAGATACAGAATGTCCCAG AGACGCGAGAGGTCCATCAAGTCAGTCCCTGAGAAGGACCGTACCACTTCAGAAGCCCAG ACTICAGAGCIGGIGCICACTGGATIGICTICATITICCTTATICICCTAAACACTGCAG CTCTGCCTCTACGCACTCTTCCTCTTCCTCTGCCAGCAAGTGGCCTCCTTCTGCCGGGGC CTGCGTGGCGGGATCTTCGGGCTCCTCGGCTGTCTCCAAGCCATTGGGCTGTTTGCCTCC 2448 GTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTGGCATAGCAAGATC TGGGATGTGGTGCGATCTCCCATCAGCTTCTTTGAGCGGACACCCATTGGTCACCTGCTA GAGTCAATTCTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGAATTTTA **AACCGCTTCTCCAAGGAGACAGACACGGTTGACGTGGACATTCCAGACAAACTCCGGTCC** 3196 CTGCTGATGTACGCCTTTGGACTCCTGGAGGTCAGCCTGGTGGTGGCAGTGGCTACCCCA 2686 TTCATCCAGACATTGCTACAAGTGGTTGGTGTGGTCTCTGTGGCTGTGGCCGTGATTCCT 3256 CTGGCCACTGTGGCCATCCTGCTTTCTCTCTTACGCTGGGTTTCAGAGCCTGTAT 2746 TGGATCGCAATACCCTTGGTTCCCCTTGGAATCATTTTCATTTTCTTCGGCGATATTTT CACATGGCTGAGACGTTCCAGGGCAGCACAGTGGTCCGGGCATTCCGAACCCAGGCCCCC TITGIGGCTCAGAACAATGCTCGCGTAGATGAAAGCCAGAGGATCAGTTTCCCGCGACTG 2926 TGTCAGGAACTGTTTGATGCACCAGGATTTACATTCAGAGGCTTGGTTCTTGTTTTTG GTGGCTGACAGGTGGCTTGCGGCCAATGTGGAGCTCCTGGGGAATGGCCTGGTGTTTGCA ATGCCTGCGGTGCTCCTAGGTGGGGCCCGGGCATCCAGGTTGCTTCCAGAGGCTCCTG 2806 TTGGAAACGTCAAGAGATGTGAAGCGCCTGGAATCTACAACTCGGAGTCCAGTGTTTTCC GCCGCCACGTGTGCTGTGCTGAGCAAAGCCCACCTCAGTGCTGGCCTCGTGGGCTTCTCT 2035 2656 2150 2776 2270 2836 2330 3016 3076 2626 3376 3436 3496 3046 2896 2390 2956 3316 2986 3136 qq g δý g οy g οy a οy a Ω g οy Ω 셤 ογ g οy g οχ qq ò g ò a δ qq ŏ 윱 ò g δ q å

4035 4155 4215 4335 4452 3616 GTCTCTGCTGCCTCCAGGTGACCCAGACACTGCAGTGGGTTGTTCGCAACTGGACAGAC 3675 TCCTTCAAGATCCACGCAGGAGAAGAGGTGGCCATCGTTGGCAGGACCGGGGCAGGGAAG 3915 3343 ACAGCACTCATTAAATCACAAGAAAAGGTTGGCATTGTGGGAAGAACCGGAGCTGGAAAA 3402 3403 AGTICCCTCATCTCAGCCCTTTTTAGATT---GTCAGAACCCGAAGGTAAAATTTGGATT 3459 GCTCCCTGGAGGCTGCCCACATGTGCAGCTCAGCCCCCTGGGCTCAGGGCGGGGGAGATC 3676 CTAGAGAACAGCATCGTGTCAGTGGAGCGGATGCAGGACTATGCCTGGACGCCCAAGGAG 3880 AGCGACAAGATAATGGTTTTAGATTCAGGAAGACTGAAAGAATATGATGAGCGTATGTT 3283 ATCTTTGACAATGTGAACTTCATGTACAGTCCAGGTGGGCCTCTGGTACTGAAGCATCTG 3916 TCCTCCCTGGCCAGTGGGCTGCTGCGGCTCCAGGAGGCAGCTGAGGGTGGGATCTGGATC 3976 GACGGGGTCCCCATTGCCCACGTGGGGCTGCACACACTGCGCTCCAGGATCAGCATCATC 4096 CACTCGGACGAGGCTATCTGGCCAGCCCTGGAGACGGTGCAGCTCAAAGCCTTGGTGGCC 3640 GATCTTCCTGGTAAAATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGGA CAGAAACAGCTCCTGTGTCTGGCACGTGCCCTTCTCCGGAAGACCCAGATCCTGTCTCTG 3700 CAAAGACAACTGGTGTGCCTTGCCAGGGCAATTCTCAGGAAAAATCAGATATTGATTATT GACGAGGCTACTGCTGCCGTGGACCCTGGCACGGAGCTGCAGATGCAGGCCATGCTCGGG CCCCAGGACCCCATCCTGTTCCCTGGCTCTCTGCGGATGAACCTCGACCTGCTGCAGGAG 4156 AGCCTGCCCGGCCAGCTGCAGTACAAGTGTGCTGACCGAGGCGAGGACCTGAGCGTGGGC 4336 AGCTGGTTTGCACAGTGCACTGTGCTGCCCATTGCCCACCGCCTGCGCTCCGTGATGGAC 3940 TIGCTGCAAAATAAAGAGGCCTATTTTACAAGATGGTGCAACAACTGGGCAAGG 3994 4453 CAGCTGCTGCCCAGAAGGCCCTGTTTACAGACTGGCCCAGGAGTCAGGCCTGG 4507 3736 4036 4216 4276 ò g Qγ g δ qq ò qq οy g δ Ωp δ g ΟŊ QQ δy g δý Dp g qq ò ŏ δ δ

RESULT 13
US-09-759-143-536
US-09-759-143-536
Satent No. US2002002248A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqui
APPLICANT: Haenderson, Robert A.
APPLICANT: Handerson, Robert A.
APPLICANT: Kalos, Michael D.

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                                                                                                                          THE THERAPY AND
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                                                                                                                                                                                                                                                                                                                                 Score 271.4; DB 10; Length
Pred. No. 5.3e-57;
0; Mismatches 1366; Indels
     APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Carter, Danrick
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Gamuel
APPLICANT: Rang, Aijun
APPLICANT: Hepler, William
APPLICANT: Hepler, William
APPLICANT: Hepler, William
APPLICANT: Holer, William
APPLICANT: Holer, William
APPLICANT: Holer, William
APPLICANT: DINVENTION: DAMONSIS OF PROSTATE CANCER
TITLE OF INVENTION: DAMONSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DAME: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FRASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION: (1)...(6140)
; OTHER INFORMATION: n=A,T,C or G
US-09-759-143-536
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
                                                                                                                                                                                                                                                                                                                                   Query Match 6.0%;
Best Local Similarity 46.0%;
Matches 1185; Conservative 0
                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature LOCATION: (1)...(6140)
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3015 2447 2035 GATTITGGCTCCCTTTTAAAGAAGGATAATGAGGAAAGTGAACAACCTCCAGTTCCAGGA 2094 2210 TTACACTATCAGAGGAGAACCGTTCTGAAGGAAAAGTTGGTTTTCAGGCCTATAAGAATT 2269 2507 TCTATIGGTATICTACGTCCTTGTTAACTCTTCACAAACTT--TGCACAACAAAATGTTT 2565 3135 3315 2805 3375 AACCGCTTCTCCAAGGAGACAGGACACGGTTGACGTGGACATTCCAGACAAACTCCGGTCC 3195 GTGGCTGACAGGTGGCTTGCGGCCAATGTGGAGCTCCTGGGGAATGGCCTGGTGTTTGCA 3555 GTCTCTGCTGCCCTCCAGGTGACCCAGACACTGCAGTGGGTTGTTCGCAACTGGACAGAC 3675 2095 ACTCCCACACACAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTG-----GTCTCAACAAT 2656 AGACGCGAGAGGTCCATCAAGTCAGTCCCTGAGAAGGACCGTACCACTTCAGAAGCCCAG 2150 CTTCTAGACCCTCCTTGAAAGATGGTGCTCTGGAGAGCCAAGATACAGAGAATGTCCCAG ACAGAGGTTCCTCTGGATGACCCTGACAGGGCAGGATGGCCAGCAGGAAAGGACAGCATC CTCTGCCTCTACGCACTCTTCCTCTTCCTCTGCCAGCAAGTGGCCTCCTTCTGCCGGGGC CTGCGTGGCGGATCTTCGGGCTCTCGGCTGTCTCCAAGCCATTGGGCTGTTTGCCTCC TGGGATGTGGTGCGATCTCCCATCAGCTTCTTTGAGCGGACACCCATTGGTCACCTGCTA 2270 ACTICAGAGCIGGIGCICACIGGAIIGICITCATITICCITATICICIAAACACIGCAG 2448 GTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTGGCATAGCAAGATC ATGGCTGCGGTGCTCCTAGGTGGGGCCCGGGCATCCAGGTTGCTCTTCCAGAGGCTCCTG GAGTCAATTCTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGAATTTTA CTGCTGATGTACGCCTTTGGACTCCTGGAGGTCAGCTGGTGGTGGCTACCCCA CTGGCCACTGTGGCCATCCTGCCACTGTTTCTCCTCTACGCTGGGTTTCAGAGCCTGTAT CACATGGCTGAGACGTTCCAGGGCAGACAGTGGTCCGGGCATTCCGAACCCAGGCCCCC TTTGTGGCTCAGAACAATGCTCGCGTAGATGAAAGCCAGAGGATCAGTTTCCCGCGACTG 2686 TTCAICCAGACATIGCTACAAGIGGITGGIGTGGTCTCTGIGGCIGIGGCGGAATICCT GCCGCCACGTGTGCTGTGTGTGAGCCCACCTCAGTGCTGGCCTCGTGGGCTTCTCT

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             3226 GCACCTTGGGAATATCAGAAACGCCCACCA---CCAGCCTGGCCCATGAAGGAGTGATA 3282
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CTAGAGAACAGCATCGTGTCAGTGGAGCGGATGCAGGACTATGCCTGGACGCCCAAGGAG
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RESULT 14
US-09-780-669-536
Fatent No. US20020051977A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
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                                                                                APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Hepler, William
APPLICANT: Hural, John
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TILE REFERENCE: 210121.427024
CURRENT APPLICATION NUMBER: US/09/780,669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: Fastseq for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 6.0%; Score 271.4; DB 10; Best Local Similarity 46.0%; Pred. No. 5.3e-57; Matches 1185; Conservative 0; Mismatches 1366;
                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: (1)...(6140)
; OTHER INFORMATION: n=A,T,C or G
US-09-780-669-536
Day, Craig H.
Vėdvick, Thomas S
Carter, Darrick
Li, Samuel
                                                                       Wang, Aijun
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                                                                                  3226 GCACCTTGGGAATATCAGAAACGCCCACCA---CCAGCCTGGCCCCATGAAGGAGTGATA
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Batent No. US20020081680A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY PITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REPERENCE: 210121,534C1
CURRENT APPLICATION NUMBER: US/09/822,827
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 982
SOFTWARE: EsstSEQ for Mindows Version 3.0
SEQ ID NO 536
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                                                                              Length 6140;
                                                                                                    Indels
                                                                           Score 271.4; DB 10;
Pred. No. 5.3e-57;
0; Mismatches 1366;
                                             O
                                             or
                                                                           Query Match
Best Local Similarity 46.0%;
Matches 1185; Conservative
          FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(6140)

OTHER INFORMATION: n=A,T,C
US-09-822-827-536
ORGANISM: Homo sapiens
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3403 AGTTCCCTCATCTCAGCCCTTTTTAGATT --- GTCAGAACCCGAAGGTAAAATTTGGATT 3459
                                       3976 GACGGGGTCCCCATTGCCCACGTGGGGCTGCACACTGCGGTTCCAGGATCAGCATCATC 4035
                                                                            3460 GATAAGATCTTGACAACTGAAATTGGACTTCACGATTTAAGGAAGAAATGTCAATCATA 3519
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Search completed: December 18, 2002, 21:44:23 Job time: 202.187 secs

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Sequence 3, Application US/08463092B
Patent No. 5766880
GENERAL INFORMATION:
APPLICANT: Cole, Susan P.C.
APPLICANT: Deeley, Roger G.
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING
TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: PAREQ RESEARCH & DEVELOPMENT INNOVATIONS
STREET: Queen's University at Kingston
US-08-476-900A-4
US-08-488-546A-4
US-08-488-546A-4
US-08-404-531B-7
US-08-404-531B-8
US-08-476-900A-7
US-08-488-546A-7
US-08-488-546A-7
US-08-488-546A-30
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US-09-605-785-536
US-09-605-785-535
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                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTMARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,092B
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/966,923
FILING DATE: 27-0CT-1992
CLASSIFICATION ATA:
APPLICATION NUMBER: 08/029,340
FILING DATE: 8-MAR-1993
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/029,340
FILING DATE: 8-MAR-1993
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
CLASSIFICATION DATA:
FILING DATE: 26-0CT-1993
FILING DATE: 26-0CT-1993
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REFERENCE/DOCKET NUMBER: Q1546
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/407,207
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NAME: Steeg, Carol Miernicki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (613) 545-2342
TELEFAX: (613) 545-6853
INFORMATION FOR SEQ ID NO: 3:
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CLASSIFICATION: 435
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CITY: Kingston
STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: CANADA ZIP: K7L 3N6
                                          US-08-463-092B-3
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Copyright (c) 1993 - 2002 Compugen Ltd.
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US-08-461-1384B-3
US-08-461-1384B-1
US-08-460-907B-1
US-08-460-907B-1
US-08-461-907A-1
US-08-461-907A-1
US-08-461-908-5
US-08-463-109A-5
US-08-463-109A-5
US-08-461-384B-1
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US-08-461-384B-5
US-08-461-384B-5
US-08-461-400-1
US-08-401-51B-4
US-08-404-531B-4
US-08-404-531B-4
US-08-404-531B-4
US-08-404-531B-4
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Match Length DB
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                                                                                       27.2%; Score 1227.6; DB 1;
55.8%; Pred. No. 4e-281;
iive 0; Mismatches 1934;
     LENGTH: 5011 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
SEQUENCE CHARACTERISTICS:
                                                                                                        Conservative
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196..4788
                                      MOLECULE TYPE: CDNA FEATURE:
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Matches 2538; Conserv
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US-08-463-092B-3
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1977 GGCTGTTGTCGGTCCAGTGGGGCCAGGGAAGTCCTCCTGCTGCTGCTCCTCCTTGGGGAGTCCTCCTGCTGCTCTCTTGGGGAGTCGTCGTGGTGGGCTGCTGCTGCTGCTGCTGCTGCTGTTGGCTGGCTGGCTGGTGG	2037 GCTGTCAAAGGTGGAGGGTTCGTGAGCATCGAGGGTGCTGTGGCCTACGTGCCCCAGGA	2097 GGCCTGGGTGCAGAACACCTCTGTGGTAGAGAATGTGTGTG	2157 ACCCTGGCTGGAGAGTACTAGAAGCCTGTGCCCTGCAGCCAGATGTGGACAGCTTCCC	2217 TGAGGGAATCCACACTTCAATTGGGGAGCAGGCATGAATCTCTCCGGAGGCCAGAAGCA 1	2277 GCGCTGAGCCTGGCCCGGGCTGTATACAGAAAGGCAGCTGTGTACCTGCTGGTGATGACCCCCCCC	2337 CCTGGCGCCCTGGATGCCCACGTTGGCCAGGTGTCTTCAACCAGGTCATTGGGCCTGG	2397 TGGGCTACTCCAGGGAACAACAACGATTCTCGTGACGCACGC	2457 GGCTGATTGGATCATAGTGCTGGCAAATGGGGCCATCGCAGAGATGGGTTCCTACCAGGA	2517 GCTTCTGCAGAGGGGGCCCTCGTGTGTCTTCTGGATCAAGCCAGACAGCCAGGAGACAGCTGGTGTCTTCTGGATCAAGCCAGGAGGGGCCTTCG-CTGAGTTCCTGCGTACCTATGCCAGCAGAGGGCGCTTCG-CTGAGTTCCTGCGTACCTATGCCAGCAGAGG	2577 TAGAGGAGAAGGAGAACCGGGACCAGGCACCAAGGACCCCGAGAGGCACCTCTGC	2637 AGGCAGGAGCCCGAGCTTAGACGCGAGAGGTCCATCAAGTCAGTC	2692	2717 CAGAGGTICCTCTGGATGACCCTGACAGGGCAGGATGGCCAGCAGGAAAGGACAGCATCC	2777 AATACGGCAGGGTGAAGGCCACAGTGCACTGGCCTACCTGCGTGCG	2837 TCTGCCTCTACGCACTCTTCCTCTGCCAGCAAGTGGCCTCCTTCTGCCGGGGCT	2897 ACTGGCTGAGCCTGTGGGCGACGACCTGCAGTAGGTGGGCAGCAGCAGAGAGCCCGGGGCAGCCCCGTGGAGCTAGGCAGCAGCAGCAGCAGGAGCCCATCGTCAACGGGACTCAGGAGCACAGGAAGACCCCATCGTCAACGGGACTCAGGAGCACAGGAAG	2957 TGCGTGGCGGGATCTTCGGGCTCCTCCGAGCCATTGGCCTGTTTGCCTCCAA 
Qy Db	Qy Dp	Oy Db	Qy Db	Qy Dp	Qy Db	Oy Db	Q Dp	Oy Dp	9y 0b	oy Op	Qy Dp	Qy Db	Qy Dp	Qy Dp	75 Ga G	Qy Db	Oy Dp

3076 3136 3415 3475 3296 CCATGGCCGTGTCCATCGGGGGGATCTTGGCTTCCCGCTGTGCACGTGGACCTGCTGC 3355 3256 3316 3436 3715 3496 3775 ACCECTTCTCCAAGGAGACAGACACGGTTGACGTGGACATTCCAGACAAACTCCGGTCCC 3196 3376 3655 3556 3595 3835 3616 3955 3736 4015 3796 4075 3856 3916 3976 4036 CTGCCCTGTTTGCGGTGATCTCCAGGCAACGCTCAGTGCTGGCTTGGTGGGCCCTCTCAG 3895 TCTCTGCTGCCCTCCAGGTGACCCAGACACTGCAGTGGGTTGTTCGCAACTGGACAGACC 3676 CCCAGGACCCCATCCTGTTCCCTGGCTCTCTGCGGATGAACCTCGACCTGCTGCAGGAGC 4096 4097 ACTCGGACGACGAGGCTATCTGGGCAGCCCTGGAGACGGTGCAGCTCAAAGCCTTGGTGGCCA 4156 3017 IGGCIGCGGTGCTCCTAGGIGGGCCCCGGGCATCCAGGTTGCTCCTACAAGGCTCCTGT ACAGCATCCTGCGGTCACCCATGAGCTTCTTTGAGCGGACCCCCAGTGGGAACCTGGTGA ACATGGCTGAGACGTTCCAGGGCAGCACAGTGGTCCGGGCATTCCGAACCCAGGCCCCCT 3656 ATTTCAACGAGACCTTGCTGGGGGTCAGCGTCATTCGAGCCTTCGAGGAGCAGGAGCCCT TIGTGGCTCAGAACAATGCTCGCGTAGATGAAAGCCAGAGGATCAGTTTCCCGCGACTGG 3716 TCATCCACCAGAGTGACCTGAAGGTGGACGAGAACCAGAAGGCCTATTACCCCAGCATCG GGGATGTGGTGCGATCTCCCATCAGCTTCTTTGAGCGGACACCCATTGGTCACCTGCTAA TGCTGATGTACGCCTTTGGACTCCTGGAGGTCAGCCTGGTGGTGGCAGTGGCTACCCCAC TGGCCACTGTGCCATCCTGCCACTGTTTCTCCTCTACGCTGGGTTTCAGAGCCTGTATG 3596 TGCTTCCTCCCGGCAGCTGAAGCGCCTCGAGTCGGTCAGCCGCTCCCCGGTCTATTCCC TGGCTGACAGGTGGCTTGCGGCCAATGTGGAGCTCCTGGGGAATGGCCTGGTGTTTGCAG CCGCCACGTGTGCTGAGCAAAGCCCACCTCAGTGCTGGCCTCGTGGGCTTCTCTG AGTICCGGGACITIGGGCTAAGATGCCGACCTGAGCTCCCGCTGGCTGTGCAGGGCGTGT CCTCCCTGGCCAGTGGGGCTGCTGCGGGAGGCAGCTGAGGGTGGGATCTGGATCG ACGGGGTCCCCATTGCCCAACGTGGGGCTGCACACACTGCGCTCCAGGATCAGCATCATCC CCTTCAAGATCCACGCAGGAGGAAGGTGGGCATCGTTGGCAGGACCGGGGCAGGGAAGT 3077 3416 3197 3317 3836 3137 3257 3377 3557 3617 3886 3956 4016 4076 3857 4136 3917 3977 4256 4037 4316 3437 3497 3677 3737 3797 g QQ ò Óγ gg Qγ qq οy Q Dp οy Ω Ω ద δ QQ δy ΩQ 9 9 9 90 64 64 Qy Dp οy qq Óχ g ò Ω οy pp δy qq Óγ 7;

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                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08462109A
Patent No. 5882875
GENERAL INFORMATION:
APPLICANT: Cole, Susan P.C.
APPLICANT: Deeley, Roger G.
TITLE OF INVENTION: METHODS FOR IDENTIFYING
TITLE OF INVENTION: MULTIDRUG RESISTANT TUMOR CELLS
MINDER OF SEQUENCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,109A
FILING DATE:
CLASSIFICATION: 435
PROOR APPLICATION OF 435
PRIOR APPLICATION NUMBER: 08/029,340
FILING DATE: 27-OCT-1992
APPLICATION NUMBER: 08/029,340
FILING DATE: 26-OCT-1993
APPLICATION NUMBER: 08/141,893
FILING DATE: 26-OCT-1993
APPLICATION NUMBER: 08/141,893
FILING DATE: 26-OCT-1993
APPLICATION NUMBER: 08/141,893
FILING DATE: 20-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Deconti, Giulio A. Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PQI-002CP4
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: LAHIVE & COCKFIELD
60 State Street, suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 3:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE &
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STATE: Massack
COUNTRY: USA
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                                                                                                                                                                                                     Length 5011;
                                                                                                                                                                                              Score 1227.6; DB 2; Length
Pred. No. 4e-281;
0; Mismatches 1934; Indels
                                                                                                                                                                                                   27.2%;
55.8%;
                                                                                                                                                                                            Query Match 27.28
Best Local Similarity 55.8°
Matches 2538; Conservative
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                            CDS
196..4788
                                         TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                         , NAME/KEY:
, LOCATION:
US-08-462-109A-3
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oy D	900	GAAGGCCATCTGGCAGTGTTCCATTCTACCTTCCTCGGGGACCCTCAGCCTCATCAT 959	
Oy Db	960	CAGTGATGTCTTCAGGTTCACTGTCCCCAAGCTGCTTTTCCTGGAGTTTATTGG 1019	
Qy Db	1020 1257	IGATCCCAAGCCTCCAGCCTGGAAGGCCTACCTCCCGCCGTGCTGATGTTCCTCTCAGC 1079	
Qy	1080	CTGCCTGCAAACGCTGTTTGAGCAGCAGAACATGTACAGGCTCAAGGTGCCGCAGATGAG 1139 	
Oy Dp	1140	GTTGCGGTCGGCCATCACTGGCTGGTGCAGAAAGGTCCTGGCTCTGCCAGGGCTC 1199	
Qy Db	1200	CAGAAAGGCCAGTGGGTGATGTGGTCAATCTGGTGTCCGTGGACGTGCAGCGGCT 1259 	
QY Dp	1260	GACCGAGAGCGTCCTCTACCTCAACGGGCTGTGGCTCTCTCT	
Oy Dp	1320	CTTCGTCTATCTCTGGCAGCTCCTGGGCCCTCCCCTCACGCCATCGCTGTCTTCCT 1379	
g G	1380	GAGCCTCCTCTGAATTTCTTCATCTCCAAGAAAGGAACCACCATCAGGAGGAGCA 1439 	
Qy Db	1440	AATGAGGCAGAAAGGACTCACGGCTCACCAGCTCTATCCTCAGGAACTCGAAGAC 1499 	
oy Op	1500	CATCAAGTTCCATGGCTGGGAGCCTTTCTGGACAGAGTCCTGGGCATCCGAGCCA 1559 	
Qy Dp	1560	161 185	
QY	1620 1857	AGTGTCTACATTTCTGGTCGCACTGGTGTTTGCTGTCCACACTCTGGTGGCCGAGAA 1679	
Qy Db	1680	TGCTATGAATGCAGAGAAAGCCTTTGTGACTCTCACAGTTCTCAACATCCTCAACAA 1736 	
Oy Op	1737	GGCCCAGGCTTTCCTGCCTTCTCCATCCACTCCTCGTCCAGGCCCGGGTGTCCTTGA 1796	
Qy Db	1797		
o y	1857	CTCTGGAAGGCTGCCGGGAAGGATTGCATCACCATACACAGTGCCACCTTCGCCTGGTC 1916 TGTGAAAAGAACGCGCGCGAACAACAACAACAACAACAACAAC	
δy	1917	197	
qq	2157	CAGGAGCGACCTCCCACACTGATGGCATCACCTTCTCCATCCCCGAAGGTGCTTTGGT 2216	
οy	1977	GGCTGTTGTCGGTCCAGTGGGGGCAGGGAAGTCCTCCTGCTGTCCGCCCTCCTTGGGGA 2036	

2456 2156 2396 2216 2276 2336 2396 2636 2516 2756 2576 2716 2815 2636 2935 3017 TGGCTGCGGTGCTCCTAGGTGGGGCCCGGGCATCCAGGTTGCTTCCAGAGGCTCCTGT 3076 TCAGCAGCTCCTCCTCTATAGTGGGGACATCAGCAGGCACCACAACAGCACCGCAGAAC 2995 GGCCTGGGTGCAGAACACCTCTGTGGTAGAAATGTGTGTTCGGGCAGGAGCTGGACCC ACCCTGGCTGGAGAGAGTACTAGAAGCCTGTGCCCTGCAGCCAGATGTGGACAGCTTCCC TGAGGGAATCCACACTTCAATTGGGGAGCAGGGCATGAATCTCTCCGGAGGCCAGAAGCA CCTGGCGGCCCTGGATGCCCACGTTGGCCAGGTCTTCAACCAGGTCATTGGGCCTGG GCTTCTGCAGAGGAAGGGGCCCCTCGTGTGTCTTCTGGATCAAGCCAGACAGCCAGGAGA TAGAGGAGAAGGAGAAACAGAACCTGGGACCAGCACCAAAGGACCCCAGAGGCACCTCTGC AGCAAATGGAGAATGGCATGCTGGTGACGGACAGTGCAGGGAAGCAACTGCAGAGACCAGG CAGAGGTTCCTCTGGATGACCCTGACAGGGCAGGATGGCCAGCAGGAAAGGACAGCATCC TCTGCCTCTACGCACTCTTCCTCTCTGCCAGCAAGTGGCCTCCTTCTGCCGGGGCT 2957 IGCGIGGCGGGAICTICGGGCTCCTCGGCTGTCTCCAAGCCATTGGGCTGTTTGCCTCCA GCTGTCAAAGGTGGAGGGTTCGTGAGCATCGAGGGTGCTGTGGCCTACGTGCCCCAGGA GGCTGATTGGATCATAGTGCTGGCAAATGGGGCCCATCGCAGAGATGGGTTCCTACCAGGA TGCAGAAAGCTGAGGCCAAGAAGGAGGAGCATGGAAGCTGATGGAGGCTGACAAGGCGC TCCGGCTGAGCGTCTATGGAGCCCTGGGCATTTCACAAGGGATCGCCGTGTTTGGCTACT 2037 2277 2337 2157 2397 2217 2457 2517 2577 2637 2697 2757 2577 2876 2936 2717 2996 2777 3116 3176 3236 2217 2097 2277 2337 2397 2457 2517 2637 2692 3056 2837 2897 ΩD Ω Db Óγ Ω δ Ω g δ qα οy Op οy a ò g ò g δ Dp ŏ qq ŏ g Qγ qq ò 셤 δ ga ò ద δy OG δ

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REFERENCE/DOCKET NUMBER: 01:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: K7L 3N6 .. COMPUTER READABLE FORM: MEDIUM TYPE: Floppy (
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
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SOFTWARE: ASCII to
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3296 CCATGGCCGTGTCCATCGGGGGATCTTGGCTTCCCGCTGTCTGCACGTGGACCTGCTGC
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                                      ACAGCATCCTGCGGTCACCCATGAGCTTCTTTGAGCGGACCCCCAGTGGGAACCTGGTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/08460907B
Patent No. 5891724
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Deeley, Roger G.
APPLICANT: Cole, Susan P.C.
TITLE OF INVENTION: METHODS FOR CONFERRING ITILE OF INVENTION: RESISTANCE ON A CELL NUMBER OF SEQUENCES: 9
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APPLICATION NUMBER: US/08/460,907B
FILLING DATE: 05-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/966,923
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CLASSIFICATION: 424
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APPLICATION NUMBER: 08/029,340
FILING DATE: 8-MAR-1993
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APPLICATION NUMBER: 08/141,893
FILING DATE: 26-0CT-1993
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NAME: Steeg, Carol Miernicki
REGISTRATION NUMBER: 39,539
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                                                                                                                                                                                               DB 2;
                                                                                                                                                                                             Score 1227.6; DB 2;
Pred. No. 4e-281;
0; Mismatches 1934;
TELEPHONE: (613) 545-2342
TELEFAX: (613) 545-6853
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5011 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                             Query Match 27.2%;
Best Local Similarity 55.8%;
Matches 2538; Conservative
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196..4788
                                                                                                                                        NAME/KEY:
                                                                                                                                                  ; LOCATION:
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               077 TGAGGAGGTGGAGGCTTTGATCGTCAAGAGGAGGAGGGAACCCCTCTGTT
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                                                                                               CAGTGATGTCTTCAGGTTCACTGTCCCCAAGCTGCTCAGCCTTTTCCTGGAGTTTATTGG
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---GAGACCGAGCCCTTCCTACGGCAAGAAGGGAGCCAGTGGCGCCCACTGCT
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                                                GAAGGCCATCTGGCAGGTGTTCCATTCTACCTTCCTGGGGACCCTCAGCCTCATCAT
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3436 3496 3376 3655 3595 3616 3736 4075 3556 3676 3955 3796 3856 3916 3976 4096 3236 TCCGGCTGAGCGTCTATGGAGCCCTGGCCATTTCACAAGGGATCGCCGTGTTTGGCTAT ACAGCATCCTGCGGTCACCCATGAGCTTCTTTGAGCGGACCCCCAGTGGGAACCTGGTGA ACCECTTCTCCAAGGAGACAGGCTTGACGTGGACATTCCAGACAAACTCCGGTCCC 3017 TGGCTGCGGTGCTCCTAGGTGGGGCCCGGGCATCCAGGTTGCTCTTCCAGAGGCTCCTGT GGGATGTGGTGCGATCTCCCATCAGCTTCTTTGAGCGGACACCCCATTGGTCACCTGCTAA TGCTGATGTACGCCTTTGGACTCCTGGAGGTCAGCCTGGTGGTGGCAGTGGCTACCCCAC TGGCCACTGTGGCCATCCTGCCACTGTTTCTCCTCTACGCTGGGTTTCAGAGCCTGTATG TTGTGGCTCAGAACAATGCTCGCGTAGATGAAAGCCAGAGGATCAGTTTCCCGCGACTGG TGCCTGACAGGTGGCTTGCGGCCCAATGTGGAGCTCCTGGGGAATGGCCTGGTGTTTGCAG CCGCCACGTGTGCTGTGCTGAGCCAAAGCCCACCTCAGTGCTGGCCTCGTGGGCTTCTCTG TAGAGAACAGCATCGTGTCAGTGGAGCGGATGCAGGACTATGCCTGGACGCCCAAGGAGG CCATGGCCGTGTCCATCGGGGGATCTTGGCTTCCCGCTGTCTGCACGTGGACCTGCTGC ACATGGCTGAGACGTTCCAGGGCAGCACAGTGGTCCGGGCCATTCCGAACCCAGGCCCCCT TCTCTGCTGCCCCTCCAGGTGACCCAGACACTGCAGTGGGTTGTTCGCAACTGGACAGACC TGGAAACCAACATCGTGGCCGTGGAGAGGCTCAAGGAGTATTCAGAGACTGAGAAGGAG AGTICCGGGACTITGGGCTAAGATGCCGACCTGAGCTCCCGCTGGCTGTGCAGGGCGTGT CCTTCAAGATCCACGCAGGAGAAGGTGGGCATCGTTGGCAGGACCGGGGCAGGGAAGT CCTCCCTGGCCAGTGGGCTGCTGCGGCTCCAGGAGGCAGCTGAGGGTGGGATCTGGATCG ACGGGGTCCCCATTGCCCACGTGGGGCTGCACACTGCGCTCCAGGATCAGCATCATCC 3077 3137 3416 3197 3476 3257 3536 3317 3596 3656 3716 3776 3377 3437 3497 3557 3836 3617 3896 3677 3956 4016 4076 3857 3917 3977 3737 3797 4136 4196 4256 4037 pp Ω Ωp Q qq g Óγ Ω ò δ φ ŏ Ω g οy g ò g δ g Qγ g ò D δy qq δŻ g δ g οy QQ QΥ d Ω

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                               ACTCGGACGAGGCTATCTGGGCAGCCCTGGAGCGTGCAGCCTCAAAGCCTTGGTGGCCA 4156
                                                                                                                                                                                                                                          4556 ATGAGGCCACGGCAGCCGTGGAACGGACGACCTCATCCAGTCCACCATCCGGA 4615
                                                                                                               GCTGGTTTGCACAGTGCACTGTGCTGCCCATTGCCCACCGCCTGCGCTCCGTGATGGACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/08463179A
Patent No. 6001563
GENERAL INFORMATION:
APPLICANT: Cole, Susan P.C.
APPLICANT: Deeley, Roger G.
TITLE OF INVENTION: METHODS FOR IDENTIFYING CHEMOSENSITIZERS NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: DeConti, Giulio A. Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PQI-002CP8
TELECOMMUNICATION INPORMATION:
TELEFAN: (617) 227-7400
TELEFAN: (617) 227-5941
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: LAHIVE & COCKFIELD 60 State Street, suite 510
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APPLICATION NUMBER: 07/966,923
FILING DATE: 27-0CT-1992
APPLICATION NUMBER: 08/029,340
FILING DATE: 8-MAR-1993
PILING DATE: 26-0CT-1993
APPLICATION NUMBER: 08/141,893
FILING DATE: 26-0CT-1993
APPLICATION NUMBER: 27-0CT-1993
APPLICATION NUMBER: 08/407,207
FILING DATE: 20-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-463-179A-3
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Pred. No. 4e-281;
0; Mismatches 1934; Indels
                                                                                                                                                                                                        27.2%;
55.8%;
SEQUENCE CHARACTERISTICS:
LENGTH: 5011 base pairs
               LENGTH: 5011 base pair:
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                          Best Local Similarity 55.8
Matches 2538; Conservative
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196..4788
                                                                                                                                ; NAME/KEY:
; LOCATION:
US-08-463-179A-3
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OY Db	960	10	on 10
Qy Dp	1020	10	മെയ
Qy Db	1080	CTGCCTGCAAACGCTGTTTGAGCAGCAGAACATGTACAGGCTCAAGGTGCCGCAGATGAG 113	6 9
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Qy Db	1200	CAGAAAGGCCAGTGGGGGGGGTGATGTGGTCAGTGTCCGTGGACGTGCAGGGGCT 125 	ъ v
Oy Dp	1260 1497	GACCGAGAGCGTCCTCTACCTCAACGGGCTGTGGCTGCCTCTCGTCTGGATCGTGGTCTG 131	on vo
93 Dp	1320	CTTCGTCTATCTCTGGCGCCTCCGCCCTCACTGCCATCGCTGTCTT 137-	σφ
Qy Dp	1380	GAGCCTCCTCCTGAATTCTTCATCTCCAAGAAAGGAACCACCATCAGGAGGAGGA 143'	. 6 9
₹ Q.	1440	AATGAGGCAGAAGGACTCACGGCCACGCTCACCAGCTCTATCCTCAGGAACTCGAAGAC 149 	6 9
0y Db	1500	CATCAAGITCCATGGCTGGGAGGGAGCCTTCTGGACAGAGTCCTGGGCATCCGAGGCCA 155	o vo
Qy Db	1560	GGAGCTGGGGCCTTCGGGACCTCCTCTTCTCTGTGTCGCTGGTGTCCTTCCA 161	on w
Qy Dp	1620 1857	AGTGTGTACATTTCTGGTCGACTGGTGGTGTTTGCTGTCCACACTCTGGTGGCCGAGAA 167- 	6 V
Qy	1680	TGCTATGAATGCAGAGAAAGCCTTTGTGACACTCTCACAGTTCTCAACATCCTCAACAA 173	9 9
op Op	1737	GGCCCAGGCTTTCCTGCCTTCTCCATCCACTCCTCGTCCAGGCCCGGGTGTCCTTTGA 179	9 9
Qy Db	1797 2037	CCGTCTGGTCACCTTCCTCTGCCTGGAAGAAGTTGACCCTGGTGTGTGGACTCAAGTTC 1850	9 9
Qy Db	1857	CTCTGGAAGCGCTGCCGGGAAGGATTGCATCACCATACACAGTGCCACCTTCGCCTGGTC 1911	y y
Q. Q.	1917	CCAGGAAAGCCCTCCCTGCCTCCACAATAAACCTCACGGTGCCCCAGGGCTGTTGT 1976	9 9

2096 2156 2396 2576 2396 2636 2516 2276 2336 2756 2776 GGCTGTTGTCGGTCCAGTGGGGCAGGGAAGTCCTCCCTGCTGTCCGCCCTCCTTGGGGA 2036 2815 2636 2875 2716 3055 2836 3175 2691 2995 2956 GCTTCTGCAGAAGGGGGCCCTCGTGTGTCTTCTGGATCAAGCCAGACAGCCAGGAGA 2576 CCTGGCGCCCCTGGATGCCCACGTTGGCCAGCATGTCTTCAACCAGGTCATTGGGCCTGG 2217 GCCCGTGGTGGCCAGGTGGCCTGCTGAAGTCGTCCCTGCTCTCAGCCCTCTTGGCTGA GGCCTGGGTGCAGAACACCTCTGTGGTAGAATGTGTGTTCGGGCAGGAGCTGGACCC CAGTGGGGATGGGACAGACTTGGCGAGAAGCA CTGTCTGGGGGACAGAAGCA 2757 GCTGCTGGGCTCGAGACGCGCCTTCG-CTGAGTTCCTGCGTACCTATGCCAGCACAGAGC ----GACCGTACCACTTCAGAAGCCCAGA--2936 TCAGCAGCTCCTCCTCTATAGTGGGGACATCAGCAGGCACCACAACAGCACGCAGAAC 2717 CAGAGGITCCICTGGATGACCCTGACAGGGCAGGATGGCCAGCAGGAAAGGACAGCATCC AATACGGCAGGGTGAAGGCCACAGAGGCACCTGGCCTACCTGCGTGCCGTGGGCACCCCC TGCGTGGCGGGATCTTCGGGCTCCTCGGCTGTCTCCAAGCCATTGGGCTGTTTGCCTCCA 2217 TGAGGGAATCCACACTTCAATTGGGGAGCAGGCATGAATCTCTCCGGAGGCCAGAAGCA GCGGCTGAGCCTGGCCCGGGCTGTATACAGAAAGGCAGCTGTGTACCTGCTGGATGACCC 2577 TAGAGGAGAAGGAGAAACAGAACCTGGGACCAGCACCAAGGACCCCAGAGGCACCTCTGC AGCAAATGGAGAATGGCATGCTGGTGACGGACAGTGCAGGGAAGCAACTGCAGAGACAGC 2996 TGCAGAAAGCTGAGGCCAAGAAGGAGGAGCACGCAGGAGCTGATGGAGGCTGACAAGGCGC TCTGCCTCTACGCACTCTTCCTCTTCTGCCAGCAAGTGGCCTCCTTCTGCCGGGGCT 2157 2692 1977 2277 2397 2457 2277 2517 2337 2577 2397 2457 2697 2876 2777 3056 3176 2957 3236 2037 2097 2517 2837 3116 2897 QQ g ò òγ qq Ωp Dp οy g ΩŽ Db Op Dp Ω Ω qq ôγ Óγ δý Ωy οy ò ò qq ٥y δ qq ÓΥ QY Dp δλ g δ qq δ g

	3017   TGGCTGCGGTGCGTCTGCGTGGTGCTGCTTTTGGTGCTGC	5 Db 4376	Oy 4157	Db 4436	Qy	qq	oy oy		g do	Qy	DD 4676	Qy 4457 Db 4736	RESULT 5	sn	; Patent No ; GENERAL ; APPLIC			CITY STAI	Ϋ́.	no .	PF			APPL STILL STICK TOWN	REGI REFE : TELECOI TE	TELE	LENG
1; # 1; # 1; # 1; # 1; P 10 P		TGCTGCGGTGCTCCTAGGTGGGCCCGGGCATCCAGGTTGCTCTTCCAGAGGCTCCTGT	GGGATGTGGGGATCTCCCATCAGCTTCTTTGAGCGGACACCCATTGATCATCACTTGCTAA	ACAGCATCCTGCGGTCACCCATGAGCTTCTTGAGCGGACCCCCAGTGGGGAACCTGGTGA	ACCGCTTCTCCAAGGACACAGACAGGTGGACGTGGGACATTCCAGACAAACTCCGGTCCC	ACCECTTCTCCAAGGAGCTGGACACAGTGGACTCCATGATCCCGGAGGTCATCAAGATGT	TGCTGATGTACGCCTTTGGACTCCTGGAGGTCAGCCTGGTGGTGGCAGTGGCTACCCAC	TCATGGGCTCCCTGTTCAACGTCATTGGTGCCTGCATCGTTATCCTGGTGGCCACGCCCA	TGGCCACTGTGGCCATCCTGCCACTGTTCTCTCTACGCTGGGTTTCAGAGCCTGTATG	TGGTTAGCTCATGCCAGCTGAGACGCTTGGAGTCAGCCAGC	TGGCTTCCTCCCGGCAGCTGAAGCGCCTCGAGTCGGTCAGCCGCTCCCCGGTCTATTCCC	ACATGGCTGAGACGTTCCAGGCAGCACAGTGGTCCGGGCATTCCGAACCCAGGCCCCCT	TTGTGGCTCAGAACAATGCTCGCGTAGAAGCCAGAGGATCAGTTTCCCGCGCGACTCG	TCATCCACCAGATGACCTGAAGGTGGACGAGAAGCCAGAAGGCCTATTACCCCAGCATGG	TGGCTGACAGGTGGGCCAATGTGGAGCTCCTGGGGAATGGCCTGGTGTTTGCAG	CCGCCACGTGTGCTGTGCTGAGCAAAGCCCACCTCAGTGCTGGCCTCGTGGGCTTCTCTG	TOTACH GOTTO TO THE CONTROL OF THE C		TAGAGAACAGCATCGTCTCAGTGGAGCGGATGCAGGACTATGCCTGGACGCCCAAGGAGG	CTCCCTGGAGGCTGCCCACATGTGCAGCTCAGCCCCCTGGCCTCAGGGCGGGC	AGTICCGGGACTITGGGCTAAGAIGCCGACCTGAGCTCCGCTGGCTGTGCAGGGCGTGT	AATTCCGGAACTACTGCCTGCGCTACCGAGAGGACCTGGACTTCGTTCTCAGGCACATCA	CCITCAGGATCCACGCAGGAGAAGGTGGGCATCGTTGGCAGGACGGGGCAGGAAGT	CCTCCCTGGCCAGTGGGCTGCTGCGGCAGCAGCTGAGGGTGGGATCTGGATCGGTIIIIIIIIII	ACGGGTCCCCATTGCCCACGTGGGCTGCACACACTGCGCTCCAGGATCAGCATCATCC	CCCAGGACCCCATCCTGTTCCTGGGGATGAACCTCGACTGCTGCAGGAGC	

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AGAAACAGCTCCTGTGTCTGGCACGTGCCCTTCTCCGGAAGACCCAGATCCTCATCCTGG 4276
GCCTGCCCGGCCAGCTGCAGTACAAGTGTGTGCTGACCGAGGCGAGGACCTGAGCGTGGGCC 4216
                                                                                   ACGAGGCTACTGCTGCCGTGGACCCTGGCACGGAGCTGCAGATGCAGGCCATGCTCGGGA 4336
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LICANT: Cole, Susan P.C.
LICANT: Cole, Susan P.C.
LICANT: Deeley, Roger G.
ER OF INTENTION: MULTIDRUG RESISTANCE PROTEINS
ER OF SEQUENCES: 10
ESPONDENCE ADDRESS:
BREST: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
REET: Uneen's University at Kingston
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COUNTRY: CANADA
ZIP: K7L 3NG
MEDTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
DERRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
RRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,384B
FILING DATE: 05-JUN-95
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CR APPLICATION DATA:
CR APPLICATION NUMBER: 07/966,923
TILING DATE: 27-071-992
APPLICATION NUMBER: 08/029,340
TILING DATE: 8-MAR-1993
APPLICATION NUMBER: 08/11,1893
TILING DATE: 26-071-1993
APPLICATION NUMBER: 08/407,207
TILING DATE: 20-MAR-1995
APPLICATION NUMBER: 08/407,207
TILING DATE: 20-MAR-1995
APPLICATION NUMBER: 39,539
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ERENCE/DOCKET NUMBER: Q1547
OMMUNICATION INFORMATION:
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EFAX: (613) 545-6853
TION FOR SEQ ID NO: 3:
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LENGTH: 5011 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                Length 5011,
                                                                                                      Indels
                                                                               Score 1227.6; DB 3;
Pred. No. 4e-281;
0; Mismatches 1934;
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                                                                                           Best_Local Similarity 55.8
Matches 2538; Conservative
                                  CDS
196..4788
 TOPOLOGY: linear MOLECULE TYPE: CDNA
linear
                                   NAME/KEY:
                                             ; LOCATION:
US-08-461-384B-3
                                                                                Query Match
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1199 TAAGGTGTTATACAAGACCTTTGGGCCCCTACTTCCTCATGAGCTTCTTCTTCAAGGCCAT 1196 1976 CAGTGATGTCTTCAGGTTCACTGTCCCCAAGCTGCTCAGCCTTTTCCTGGAGTTTATTGG GACCGAGAGCGTCCTCTACCTCAACGGGCTGTGGCTGCCTCTCGTCTGGATCGTGGTCTG CTTCGTCTATCTCTGGCAGCTCCTGGGGCCCTCCGCCCTCACTGCCTGTTTCCT GAGCCTCCTCCTCTGAATTTCTTCATCTCCAAGAAAGGAACCACCATCAGGAGGAGCA CCTCATGGTGCCCGTCAATGCTGTGATGGCGATGAAGACCAAGACGTATCAGGTGGCCCA CATCAAGTTCCATGGCTGGGAGGGAGCCTTTCTGGACAGAGTCCTGGGCATCCGAGGCCA GGCCCAGGCTTTCCTGCCCTTCTCCACTCCTCGTCCAGGCCCGGGTGTCCTTTGA CTGCCTGCAAACGCTGTTTGAGCAGCAGAACATGTACAGGCTCAAGGTGCCGCAGATGAG GTTGCGGTCGGCCATCACTGGCCTGGTGTACAGAAAGGTCCTGGCTCTGTCCAGCGGCTC CAGAAAGGCCAGTGCGGTGATGTGGTCAATCTGGTGTCCGTGGACGTGCAGCGGCT AATGAGGCAGAAGGACTCACGGCCACGCCTCACCAGCTCTATCCTCAGGAACTCGAAGAC GGAGCTGGGCCCTTGCGGACCTCCGGCCTCTTCTCTGTGTGCGCTGGTGTCCTTCCA 1620 AGTGTCTACATTTCTGGTCGCACTGGTGTTTGCTGTCCACACTCTGGTGGCCGAGAA CTGCACGCCCTTCTGGTGGCCTTGTGCCACATTGCCGTCTACGTGACGAGAA CCGTCTGGTCACCTTCCTCGCTGGAAGAGTTGACCCTGGTGTCGTAGACTTCAAGTTC 2097 TGTCAAAGACGGCGGGGCACGAACACATCACCGTGAGGAATGCCACATTCACCTGGGC 2217 GGCCGTGGTGGGCCAGGTGGGCTGCGAAGTCGTCCCTGCTCTCAGCCCTCTTGGCTGA TGATCCCAAGCCTCCAGCCTGGAAGGGCTACCTCCTCGCCGTGCTGATGTTCCTCTCAGC CTCTGGAAGCGCTGCCGGGAAGGATTGCATCACCATACACAGTGCCACCTTCGCCTGGTC CCAGGAAAGCCCTCCCTGCCTCCACAGAATAAACCTCACGGTGCCCCAGGGCTGTCTGCT GGCTGTTGTCGGTCCAGTGGGGGGAAGTCCTCCCTGCTGTCCGCCCTCCTTGGGGA 1137 1020 1257 1080 1140 1260 1320 1617 1440 1677 1857 1680 1917 1197 1380 1737 1560 1797 1737 2157 1977 960 1200 1500 1797 1857 1917 qq g Qγ ōλ g δ QQ ò pp δ Qγ QQ ò Db Óγ g οy Dp οy g oγ g οy QQ δ q Ω qq ٥y g QΥ q ŏ qq Ω g

Thu Dec

3376 3655 3436 3715 3496 3775 3556 3616 3895 3676 4075 3736 4015 3796 4036 4315 4096 4375 4156 ACAGCATCCTGCGGTCACCCATGACTTCTTTGAGCGGACCCCCAGTGGGAACCTGGTGA ACCGCTTCTCCAAGGAGACACGGTTGACGTGGACATTCCAGACAAACTCCGGTCCC TGGCTGACAGGTGGCCTTGCGGCCAATGTGGAGCTCCTGGGGAATGGCCTGGTGTTTGCAG GGGATGTGGTGCGATCTCCCATCAGCTTCTTTGAGCGGACACCCCATTGGTCACCTGCTAA TGCTGATGTACGCCTTTGGACTCCTGGAGGTCAGCCTGGTGGTGGCAGTGGCTACCCCAC TTGTGGCTCAGAACAATGCTCGCGTAGATGAAAGCCAGAGGATCAGTTTCCCGGGACTGG TGGCCAACAGGTGGCTGGCGCTGGAGTGTGTGGGCAACTGCATCGTTCTTTG CCGCCACGTGTGCTGTGCTGAGCAAAGCCCACCTCAGTGCTGGCCTCGTGGGCTTCTCTG TAGAGAACAGCATCGTGTCAGTGGAGCGGATGCAGGACTATGCCTGGACGCCCAAGGAGG TGGCCACTGTGGCCATCCTGCCACTGTTTCTCCTCTACGCTGGGTTTCAGAGCCTGTATG ACATGGCTGAGACGTTCCAGGGCAGCACAGTGGTCCGGGCATTCCGAACCCAGGCCCCCT TCTCTGCTGCCCTCCAGGTGACCCAGACACTGCAGTGGGTTGTTCGCAACTGGACAGACC AGTICCGGGACTITGGGCTAAGAIGCCGACCIGAGCTICCGGCTGTGCAGGGCGTGT AATTCCGGAACTACTGCCTGCGCTACCGAGAGGACCTGGACTTCGTTCTCAGGCACATCA CCTTCAAGATCCACGCAGGAGAAGGTGGGCATCGTTGGCAGGACCGGGGCAGGAAGT CCTCCCTGGCCAGTGGGCTGCTGCGGCTCCAGGAGGCAGCTGAGGGTGGGATCTGGATCG ACGGGGTCCCCATTGCCCACGTGGGGCTGCACACACTGCGCTCCAGGATCAGCATCATCC CCCAGGACCCCATCCTGTTCCCTGGCTCTCTGCGGATGAACCTCGACCTGCTGCAGGAGC GCCTGCCCGGCCAGCTGCAGTACAAGTGTGCTGACCGAGGCGAGGACCTGAGCGTGGGCC 3197 3536 3077 3356 3137 3416 3476 3257 3596 3377 3656 3716 3776 3836 3617 3677 3956 4016 4076 4136 3317 3437 3497 3557 3896 3737 3797 3857 3917 4196 3977 4256 4037 4097 4376 4157 4316 οp δ q Ωý qq QΥ Db Qy Ω g ΟY g QΥ Dp òγ g ò Ω g ΟŻ QΩ QQ g QQ οy Ω Ω δ δλ Dp qq qq δλ οy ò g δy

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                                                                                                                                                  GCTGGTTTGCACAGTGCACTGTGCTGCCCATTGCCCACCGCCTGCGCTCCGTGATGGACT 4396
AGAAACAGCTCCTGTGTCTGGCACGTGCCCTTCTCCGGAAGACCCCAGATCCTCATCCTGG
                                                                                            4277 ACGAGGCTACTGCTGCCGTGGACCCTGGCACGAGCTGCAGATGCAGGCCATGCTCGGGA
                                                                                                                                                                   4616 CACAGTTCGAGGACTGCACCGTCACCATCGCCCACCGGCTCAACACCATCATGAGGCT
                                                                                                                                                                                                     4397 GTGCCCGGGTTCTGGTCATGGACAAGGGGCAGGTGGCAGAGAGGGGCAGCCGGCCCAGC
                                                                                                                                                                                                                                                          TGCTGGCCCAGAAGGCCCTGTTTACAGACTGGCCCAGGAGTCAGGCCTGGT 4508
                                                                                                                                                                                                                                                                        APPLICANT: COle, Susan P.C.
APPLICANT: Deeley, Roger G.
TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEIN
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/966,923; 08/029,340
FLING DATE: 27-0CT-1992; 8-MAR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, SUITE 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/141,893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: DeConti, Giulio A. Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PQI-002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08141893
Patent No. 5489519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5149
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 501 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: MASSACHUSETTS
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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196..4788
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                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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1; Length 5011;

Score 1222.8; DB 1 Pred. No. 5.5e-280;

27.1%;

Query Match Best Local Similarity

1017 GGTTGTACTCCTCCAAGGATCCTGCCCAGCCGAAGAGAGTTCCAAGGTGGGATGCGAA 1076 | GAGAACAGCAGGGTCTGGGTACCCCCCATGTACTCTGGGTCCTTGGTCCCATCTACCT 155 237 GCTCTGGGACTGGAATGTCACGTGGAATACCAGCAACCCGACTTCACCAAGTGCTTTCA 296 356 417 AACTGCCTTGGGATTTTTGCTGTGGATCGTGGGCCAGACCTCTTCTACTCTTCTG 476 395 396 ATCIGGAGIGCIGITIGGITACIGCITCICIGCITIGICIIGCCAGCIACCAACGCIGC 455 506 266 746 802 CACCACGATGAGCTTCGCAGTGTTCCTGATTCACACCGAGAGAAAAAGGGAGTCCAGTC 456 CCAGCAG------GCCTCCGGAGCGGGCTTCCAGAGCGACCCTGTCCGCCACCTGTC GGTCTGGAACCAGACAGAGCCTGAACCTGCCGCCACCAGCCTGCTGAGCCTGTGCTTCCT 297 GAACACGGICCICGIGIGGGIGCCIIGITITIACCICIGGGCCIGITICCCCTICIACII CCTCTTCATCCACCACCATGGCCGGGCTACCTCCGGATGTCCCCACTCTTCAAAGCCAA GATGGTGCTTGGATTCGCCCTCATAGTCCTGTGTACCTCCAGCGTGGCTGTCGCTCTTTG GCCACTGAGACCAAAAGACCTCTGGTCGCTTGGGAGAAAAACTCCTCAGAAGAACTTGT 747 TTCCCGGCTTGAAAAGGAĞTGGATGAGGAACCGC----AGTGCAGCCCGGAGGCACAACA CTTCCCCTCCAAAGCCACGTTCTGGTGGTTTTCTGGCCTGGTCTGGAGGGGATACAGGAG 1077 TGAGGAGGTGGAGGCTTTGATCGTCAAGTCCCCACAGAAGGAGTGGAACCCCTCTCTGTT 1137 TAAGGTGTTATACAAGACCTTTGGGCCCTACTTCCTCATGAGCTTCTTCTAGGCCAT CAGTGATGTCTTCAGGTTCACTGTCCCCAAGCTGCTCAGCCTTTTCCTGGAGTTTATTGG CCACGACCTGATGATGTTTTCCGGGCCGCAGATCTTAAAGTTGCTCATCAAGTTCGTGAA 567 ACCCCCTTCTTCCTGAAGACCCCCAGCAGTCTAACCCCTGTCCAGAGACTGGGGCAGC ------GAGACCGAGCCCTTCCTACGGCAAGAAGGGAGCCAGTGGCGCCCACTGCT 900 GAAGGCCATCTGGCAGGTGTTCCATTCTACCTTCCTCGGGGACCCTCAGCCTCATCAT 1020 TGATCCCAAGCCTCCAGCCTGGAAGGGCTACCTCCTCGCCGTGCTGATGTTCCTCTCAGC 80; Indels 803 AGGCAATAGCATTTAAAAGGAAAGGCGCCAGTGCCATGAAGGCTCCA Mismatches 1937; 0; Matches 2535; Conservative 357 216 477 336 36 96 156 276 627 687 897 850 1197 096 δ

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oy Dp	1080 CTGCC        1317 CTGCC	CTGCCTGCAACGCTGTTTGAGCAGCAGAACATGTACAGGCTCAAGGTGCCGCAGATGAG 1139 
Qy	1140 GTTGC   1 1377 GATCA	GTIGCGGTCGGCCATCACTGGCTGGTGTACAGAAGGTCCTGGCTCTGTCCAGGGCTC 1199 
Oy Dp	1200 CAGAA               1437 CAGAA	CAGAAAGGCCAGTGCGGTGGGTGATGTGGTGAATCTGGTGTCCGTGGACGTGCAGCGGCT 1259 
QY	1260 GACCG   1 1497 CATGG	GACCGAGAGCGTCCTCTACCTCAACGGGCTGTGGCTCTCTCT
QY	1320 CTTCG    1557 TCTCT	CTTCGTCTATCTCTGGGGCCTCCGGCCTCCGCCTCGCCATCGCTGTCTTCCT 1379
Qy	1380 GAGCC   1617 CCTCA	GAGCCTCCTCCTGAATTTCTTCATCTCCAAGAAAGGAACCACCATCAGGAGGAGCA 1439 
Qy	1440 AATGA      1677 CATGA	AATGAGGCAGAAAGACTCACGGCACGGCTCACCTGTATCCTCAGGAACTCGAAGAC 1499 
Qy Dp	1500 CATCA 	CATCAAGTICCATGGCTGGGAGGCTTTCTGGACAGAGTCCTGGGCATCCGAGGCCA 1559 
QY Db	1560 GGAGC             1797 GGAGC	GGAGCTGGGCCCTTGCGGACCTCCGGCCTCCTTCTGTGTCGCTGGTGTCCTTCCA 1619 
Qy	1620 AGTGT	AGTGTCTACATTTCTGGTCGCACTGGTGTGTTTGCTGTCCACACTCTGGTGGCCGAGAA 1679 
O.Y D.b	1680 TGCTA   1917 CAACA	TGCTATGAATGCAGAGAAAGCCTTTGTGACTCTCACAGTTCTCAACATCCTCAACAA 1736 
Oy Db	1737 GGCCC       1977 TCCCC	GGCCCAGGCTTTCTGCATCCACTCCTCGTCCAGGCCCGGGTGTCCTTTGA 1796 
Qy Db	1797 CCGTC       2037 ACGCC	CCGTCTGGTCACCTTCCTCTGCTGGAAGTTGACCTGGTGTCGTAGACTCAAGTTC 1856 
Qy Db	1857 CTCTGC 2097 TGTCA	CTCTGGAAGCGCTGCCGGAAGGATTGCATCACAGTGCCACCTTCGCCTGGTC 1916 
O.y D.b	1917 CCAGG	CCAGGAAAGCCTCCCTGCCTCCACAGAATAAACCTCACGGTGCCCCAGGGCTGTCTGCT 1976 
Qy	1977 GGCTG'         2217 GGCCG'	GGCTGTTGTCGGTCCAGTGGGGAGGGAAGTCCTCCCTGCTGTCCGCCCTCCTTGGGGA 2036 
QY Db	2037 GCTGTO   11 2277 GATGG	GCTGTCAAAGGTGGAGGGTTCGTGAGCATCGAGGGTGCTGTGGCCTACGTGCCCCAGGA 2096 
QY Dp	2097 GGCCT 	GGCCTGGGTGCAGAACACCTCTGTGGTAGAGAATGTGTGCTTCGGGCAGGAGCTGGACCC 2156 

2456 2276 2516 2336 2576 2456 2696 2935 2716 2995 3016 GCTTCTGCAGAGGAAGGGGGCCCTCGTGTCTTCTGGATCAAGCCAGACAGCCAGGAGA 2576 2691 2776 3055 2836 3175 2956 3076 3137 ACCGCTTCTCCAAGGACACAGACACGGTTGACGTGGACATTCCAGACAACTCCGGTCCC 3196
1111111111111111111 | 11111 | 111 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 3415 GGGATGTGGTGCGATCTCCCATCAGCTTCTTTGAGCGGACACCCATTGGTCACCTGCTAA 3136 3197 TGCTGATGTACGCCTTTGGACTCCTGGAGGTCAGCCTGGTGGTGGCTAGCCTACCCCAC 3256 ACCCTGGCTGGAGAGAGTACTAGAAGCCTGTGCAGCAGCAGATGTGGACAGCTTCCC GCGCCTGAGCCTGGCCCGGGCTGTATACAGAAAGGCAGCTGTGTACCTGCTGGATGACCC TAGAGGAGAAGGAGAAACAGAACCTGGGACCAGGCACCAAAGGACCCCAGAGGCACCTCTGC ----GACCGTACCACTTCAGAAGCCCAGA--TGAGGGAATCCACACTTCAATTGGGGAGCAGGGCATGAATCTCTCCGGAGGCCAGAAGCA 2936 TCAGCAGCTCCTCCTCTATAGTGGGGACATCAGCAGGACACCACAACAACAACAACAAAAC ACAGCATCCTGCGGTCACCCATGAGCTTCTTTGAGCGGACCCCCAGTGGGAACCTGGTGA CAGAGGTTCCTCTGGATGACCCTGACAGGGCAGGATGGCCAGCAGGAAAGGACAGCATCC AATACGGCAGGGTGAAGGCCACAGGTGCACCTGGCCTACCTGCGTGCCGTGGGCACCCCCC TCTGCCTCTACGCACTCTTCCTCTTCCTCTGCCAGCAAGTGGCCTCCTTCTGCCGGGGCT TGCGTGGCGGGATCTTCGGGCTCCTCGGCTGTCCCAAGCCATTGGGCTGTTTGCCTCCA 3017 TGGCTGCGGTGCTCCTAGGTGGGGCCCGGGCATCCAGGTTGCTCTTCCAGAGGCTCCTGT CCATGGCCGTGTCCATCGGGGGGATCTTGGCTTCCCGCTGTCGACGTGGACCTGCTGC 2996 TGCAGAAAGCTGAGGCCAAGAAGGAGGAGCCTGGAAGCTGATGGAGGCTGACAAGGCGC 2157 2217 2517 2637 2757 2577 2876 3056 2397 2577 2697 2717 3116 2457 2277 2337 2397 2457 2517 2637 2692 2897 3077 3356 2837 2957 3236 3296 δ qq Ω qq QΥ g δ QQ οy qq δλ Dp qq δy qq g ò οy g qq δý QY pp δ ΩŸ g ò ΩĐ δy qq δy g Dp δ qq ŏ ŏ

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08463092B Patent No. 5766880 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: Q1546
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 545-2342
TELEFAX: (613) 545-6853
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/966,923
FILING DATE: 27-02T-1992
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/029,340 FILING DATE: 8-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/141,893
FILING DATE: 26-0CT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/407,207
FILING DATE: 20-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Steeg, Carol Miernicki
REGISTRATION NUMBER: 39,539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 5011 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: Queen's
CITY: Kingston
STATE: Ontario
COUNTRY: CANADA
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ZIP: K7L 3N6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 8-1 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 26
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
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                                                                                                                                                                                                                                                         RESULT 7
US-08-463-092B-1
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3596 TGGCTTCCTCCGGCAGCTGAAGCGCCTCGAGTCAGCCGCTCAGCCGGTCTATTCCC 3655
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                                                                                                                                                                                    ACATGGCTGAGACGTTCCAGGGCAGCACAGTGGTCCGGGCATTCCGAACCCAGGCCCCCT 3436
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                                                 3257 TGGCCACTGTGGCCATCCTGCCACTGTTTCTCCTCTACGCTGGGTTTCAGAGCCTGTATG
                                                                    TTGTGGCTCAGAACAATGCTCGCGTAGATGAAAGCCAGAGGATCAGTTTCCCGCGACTGG
                                                                                                                                                                                                                                                                                                                     TGGCTGACAGGTGGCTTGCGGCCAATGTGGAGCTCCTGGGGAATGGCCTGGTGTTTGCAG
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                                             4337 GCTGGTTTGCACAGTGCACTGTGCTGCCCATTGCCCACCGCCTGCGCTCCGTGATGGACT
                                                                                                                                                                                                                            4457 TGCTGGCCCAGAAGGGCCTGTTTTACAGACTGGCCCAGGAGTCAGGCCTGGT 4508
                                                                                                                                                                                                                                                   APPLICANT: Cole, Susan P.C.
APPLICANT: Deeley, Roger G.
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING
TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
Queen's University at Kingston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,092B
FILING DATE: 05-JUN-1995
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1197 ΩD Qγ ò QQ οy QQ οχ Db ò g δ q op Ωp Qγ Qγ ò qq δy q δy g ò qq ŏ g δ qq Ω q δ g g δy ò ; 1019 476 215 275 356 335 395 596 455 959 GCTCTGGGACTGGAATGTCACGTGGAATACCAGCAACCCCGACTTCACCAAGTGCTTTCA 296 506 716 776 626 836 989 746 926 899 GAGAACAGCAGGGGTCTGGGTACCCCCCATGTACCTCTGGGTCCTTGGTCCCATCTACCT GGTCTGGAACCAGACAGAGCCTGAACCTGCCGCCACCAGCCTGAGCCTGTGCTTCCT CCTCTTCATCCACCACCATGGCCGGGGTACCTCCGGATGTCCCCCACTCTTCAAAGCCAA GATGGTGCTTGGATTCGCCCTCATAGTCCTGTGTACCTCCAGCGTGGCTGTCGCTTTTG CACCACGATGAGCTTCGCAGTGTTCCTGATTCACACCGAGAGAAAAAGGGAGTCCAGTC 396 ATCIGGAGIGCIGITIGGTTACIGGCTICICIGCITIGICITGCCAGCIACCAACGCIGC 597 Trcadedarcarecretrerederegradeceraerereceraecearecereae CCAGCAG-------GCCTCCGGAGCGGGCTTCCAGAGCGACCCTGTCCGCCACCTGTC ATCCAAAATTATGACAGCCTTAAAAGAGGATGCCCAGGTGGACCTGTTTCGTGACATCAC CTTCCCCTCCAAAGCCACGTTCTGGTGGGTTTCTGGCCTGGTCTGGAGGGGGATACAGGAG GCCACTGAGACCAAAAGACCTCTGGTCGCTTGGGAGAGAAAACTCCTCAGAAGAACTTGT 1077 TGAGGAGGTGGAGGCTTTGATCGTCAAGTCCCCACAGAAGGAGTGGAACCCCTCTGTT CAGTGATGTCTTCAGGTTCACTGTCCCCAAGCTGCTCAGCCTTTTCCTGGAGTTTATGG ACCCCCCTTCTTCCCTGAAGACCCCCAGCAGTCTAACCCCTGTCCAGAGACTGGGGCAGC TTCCCGGCTTGAAAAGGAGTGGATGAGGAACCGC----AGTGCAGCCCGGAGGCACAACA 1137 TAAGGTGTTATACAAGACCTTTGGGCCCTACTTCCTCATGAGCTTCTTCTTCAAGGCCAT GGTTGTGTACTCCTCCAAGGATCCTGCCCAGCCGAAAGAGAGTTCCAAGGTGGATGCGAA -----GAGACCGAGCCCTTCCTACGGCAAGGAGGCAGCCAGTGGCGCCCACTGCT GAAGGCCATCTGGCAGGTGTTCCATTCTACCTTCCTCGGGGACCCTCAGCCTCATCAT Length Indels **AGGCAATAGCATTTAAAAGGAAAGGCGGCAGTGGCATGAAGGCTCCA** 0; Mismatches 1937; 1222.8; DB 1 No. 5.5e-280; Score Pred. 27.1%; 55.7%; Conservative 196..4788 Similarity LOCATION: Matches 2535; ; LOCATION: US-08-463-092B-1 Query Match Best Local 36 237 357 477 96 297 156 216 276 336 1017 456 267 111 957 657 507 717 627 837 687 897 747 803 006 960 ò g g ρp ò δ ò g Qγ D ò g ò 셤 ò q οy 셤 οy q à Op a qq g ò ŏ à g ò 9 g δ

1436 AATGAGGCAGAAGGACTCACGGGCACGGCTCACCAGCTCTATCCTCAGGAACTCGAAGAC 1499 TGCTA---TGAATGCAGAGAAAGCCTTTGTGACTCTCACAGTTCTCAACATCCTCAACAA 1736 CCAGGAAAGCCCTCCCTGCCTCCACAAAACCTCACGGTGCCCAGGGCTGTCTGCT 1976 CTCTGGAAGCGCTGCCGGGAAGGATTGCATCACCATACACAGTGCCACCTTCGCCTGGTC 1916 CCACGACCTGATGATGTTTTCCGGGCCGCAGATCTTAAAGTTGCTCATCAAGTTCGTGAA TGACACGAAGGCCCCAGACTGGCAACTTCTACACCGTGCTGCTGTTGTCACTGC CTGCCTGCAAACGCTGTTTGAGCAGCAGAACATGTACAGGCTCAAGGTGCCGCAGATGAG TGATCCCAAGCCTCCAGCCTGGAAGGGCTACCTCCTCGCCGTGCTGATGTTCCTCTCAGC GTTGCGGTCGGCCATCACTGGCCTGGTGTACAGAAAGGTCCTGGCTCTGTCCAGCGGCTC CATGGACTTGGCCACGTACATTAACATGATCTGGTCAGCCCCCCTGCAAGTCATCCTTGC CTTCGTCTATCTCTGGCAGCTCCTGGGGCCCTCCGCCCTCACTGCCATCGCTGTCTTCCT GAGCCTCCTCTCTGAATTTCTTCATCTCCAAGAAAAGGAACCACCATCAGGAGGAGCA TCCCCTGAACATTCTCCCCATGGTCATCAGCAGCCAGGCGAGTGTCTCCCTCAA CCGTCTGGTCACCTTCCTCTGCCTGGAAGAAGTTGACCCTGGTGTCGTAGACTCAAGTTC GACCGAGAGCGTCCTCTACCTCAACGGGCTGTGGCTGCCTCTCGTCTGGATCGTGGTCTG CATCAAGTTCCATGGCTGGGAGGGAGCCTTTCTGGACAGAGTCCTGGGCATCCGAGGCCA GGAGCTGGGCGCTTGCGGACCTCCGGCCTCTTCTCTGTGTCGCTGGTGTCCTTCCA CAGAAAGGCCAGTGCGGTGATGTGGTCAATCTGGTGTCCGTGGACGTGCAGCGGCT 1620 AGTGTCTACATTTCTGGTCGCACTGGTGGTGTTTGCTGTCCACACTCTGGTGGCCGAGAA GGCCCAGGCTTTCCTGCCCTTCTCCATCCACTCCTTCGTCCAGGCCCGGGTGTCCTTTGA GGCTGTTGTCGGTCCAGTGGGGGAAGTCCTCCCTGCTGTCCGCCCTCCTTGGGGA 1317 1020 1257 1080 1140 1200 1260 1377 1437 1320 1677 1497 1557 1500 1737 1560 1797 1857 1680 1977 2037 1797 2097 1857 1917 2157 1977 2217 2037 2277 gg

4195 3475 3316 3376 3655 3436 3715 3496 3775 3556 3616 3895 3676 3736 4015 3796 4135 3916 3976 4255 4036 4315 4096 4075 4375 4156 4216 4217 AGAAACAGCTCCTGTGTCTGGCACGTGCCCTTCTCCGGAAGACCCAGATCCTCATCCTGG 4276 TGCTGATGTACGCCTTTGGACTCCTGGAGGTCAGCCTGGTGGTGGCGTGGCTACCCCAC 3596 TGGCTTCCTCCGGCAGCTGAAGCGCCTCGAGTCAGCCGCTCAGTCCC TGGCTGACAGGTGGCTTGCGGCCAATGTGGAGCTCCTGGGGAATGGCCTGGTGTTTGCAG CCGCCACGTGTGCTGTGCTGAGCAAAGCCCACCTCAGTGCTGGCCTCGTGGGCTTCTCTCT TCTCTGCTGCCCTCCAGGTGACCCAGACACTGCAGTGGGTTGTTCGCAACTGGACAGACC 3536 redecederearcarecedecerragecerearcaretrecreargagerrerace TTGTGGCTCAGAACAATGCTCGCGTAGATGAAAGCCAGAGGATCAGTTTCCCGCGACTGG CTCCCTGGAGGCTGCCCACATGTGCAGCTCAGCCCCCCTGGCCTCAGGGCGGCGGCAGATCG ACTCGGACGACGACGTATCTGGGCAGCCCTGGAGACGGTGCAGCTCAAAGCCTTGGTGGCCA CCCTTCCTGACAAGCTAGACCATGAATGTGCAGAAGGCGGGGGAGAACCTCAGTGTCGGGC ACATGGCTGAGACGTTCCAGGGCAGCACAGTGGTCCGGGCCATTCCGAACCCAGGCCCCCT ATTTCAACGAGACCTTGCTGGGGGTCAGCGTCATTCGAGCCTTCGAGGAGCAGGAGCGCT TAGAGAACAGCATCGTGTGAGGGGGATGCAGGACTATGCCTGGACGCCCAAGGAGG CCTCCCTGGCCAGTGGGCTGCTGCGGCTCCAGGAGGCAGCTGAGGGTGGGATCTGGATCG ACGGGGTCCCCATTGCCCACGTGGGGCTGCACACACTGCGCTCCAGGATCAGCATCATCC CCCAGGACCCCATCCTGTTCCCTGGCTCTCTGCGGATGAACCTCGACCTGCTGCAGGAGC GCCTGCCCGGCCAGCTGCAGTACAAGTGTGCTGACCGAGGCGAGGACCTGAGCGTGGGCC 3416 3137 3197 3476 3257 3317 3377 3656 3437 3716 3497 3776 3557 3836 3617 3896 3677 3956 3737 4016 3797 4076 3857 4136 3917 4196 3977 4256 4037 4316 4097 4376 4157 4436 qq δy Ω δ qq δλ QQ δ QQ δý qq Qγ qq ŏ g qq QQ οχ QQ ōλ QQ q qq ò Οy οy δy Óλ ò g g qq qq δ Q ò

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4337 GCTGGTTTGCACAGTGCACTGTGCTGCCCATTGCCCACCGCCTGCGCTCCGTGATGGACT
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                                                               ACGAGGCTACTGCTGCCGTGGACCCTGGCACGGAGCTGCAGATGCAGGCCATGCTCGGGA
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APPLICANT: Deeley, Roger G.
TITLE OF INVENTION: METHODS FOR IDENTIFYING
TITLE OF INVENTION: MULTIDRUG RESISTANT TUMOR CELLS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: LAHYVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: DeConti, Giulio A. Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PQI-002CP4
TELECOMUNICATION INPORMATION:
TELEPRONE: (617) 227-7400
TELEPRONE: (617) 227-7401
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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60 State Street, suite 510
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,109A
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/966,923
FILING DATE: 27-0CT-1992
APPLICATION NUMBER: 08/029,340
FILING DATE: 8-MAR-1993
APPLICATION NUMBER: 08/11,893
ATTORNEY,AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08462109A
Patent No. 5882875
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TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 02109
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US-08-462-109A-1
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                                                                                      237 GCTCTGGGACTGGAATGTCACGTGGAATACCAGCAACCCCGACTTCACCAAGTGCTTTCA 296
                                                                                                                     GAGAACAGCAGGGTCTGGGTACCCCCCATGTACCTCTGGGTCCTTGGTCCCATCTACCT 155
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   Length 5011;
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    DB 2;
Score 1222.8; DB 2;
Pred. No. 5.5e-280;
0; Mismatches 1937;
Query Match 27.1%;
Best Local Similarity 55.7%;
Matches 2535; Conservative
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Qy Dp	1020	TGATCCCAAGCCTCCAGCTGGAAGGGCTACCTCCTCGCCGTGCTGATGTTCCTCTCAGC 1079
o y	1080	CTGCCTGCAAACGCTGTTTGAGCAGCAGAACATGTACAGGCTCAAGGTGCCGCAGATGAG 1139 
7 Y	1140	GTTGCGGTCGCCCATCACTGGCCTGTACAGAAAGGTCCTGGCTCTGTCCAGCGGCTC 119 GTTGCGGTCGCCCACCAGCGCTCTGTACAGAAAGGTCCTGGCTCTGTCCAGCGGCTC 119 GTTGCGGTCGCTGTACAGAAAGGTCCTGGCTCTGTACACAAAGAAAG
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qa	1437	CAGAAAATCCTCCACGGTGGGGAGATTGTCAACTCTCTGTGGGACGCTCAGAGGTT 1496
Oy Db	1260	GACCGACAGCGTCCTCTACCTCAACGGCTGTGGCTCTCGTCTGGATCGTGGTCTG 1319
Qy Db	1320	CTTCGTCTATCTCTGGCAGCTCCTGGGGCCCTCGCCTCATCGCATCGCTGTTCCT 1379
Qy	1380	
QQ	1617	
O O O	1440	AATGAGGCAGAAGGACTCACGGCTCACCAGCTCTATCCTCAGGAACTCGAAGAC 1499 
λo. i	1500	CATCAAGTICCAIGGGTGGGAGGCGTTCTGGACAGAGTCCTGGGCAICCGAGGCA 155
Q D	1737	
Oy Dp	1560	GGAGCTGGGCGCTTGCGGACCTCCGGCGCTCTCTCTGTGTCGCTGGTGTCCTTCCA 1619 
λo.	1620	AGTGTCTACATTTCTGGTCCCACTGGTGTTTGCTCTCCACACTCTGGTGGCCGAGAA 167
qq	1857	CIGCACGCCCTITCIGGIGGCCTIGIGCACAITIGCCGTCTACGIGACCAITGACGAGAA 1916
9. O.y	1680 1917	TGCTATGAATGCAGAGAAGCCTTGTGACTCTCACAGTTCTCAACATCCTCAACAA 1736
QY	1737	GGCCCAGGCTTTCCTGCCCTTCTCCACTCCTCGTCCAGGCCCGGGTGTCCTTTGA 1796
γ̈́	1797	185
o qq	2037	
δλ	1857	CTCTGGAAGCGCTGCCGGGAAGGATTGCATCACCATACACAGTGCCACCTTCGCCTGGTC 1916
Ор	2097	TGTCAAAGACGGCGGGGCACGAACAGCATCACCGTGAGGAATGCCACATTCACCTGGGC 2156
Qy Dp	1917	CCAGGAAAGCCTCCTGCCTCCACAGAATAAACCTCACGGTGCCCCAGGGCTGTCTGCT 1976
څ	1077	,
g Z	2217	GGCCGTGGTGGCCAGGTGGGCTGCGAAAGTTGTCCTCTCTCAGCCCTCTTGGGGA 2030 GGCCGTGGTGGGCCAGGTGGGCTGCGGAAAGTTGTCCCTGCTCTCAGCCCTCTTGGCTGA 2276
οy	2037	GCTGTCAAAGGTGGAGGGTTCGTGAGCATCGAGGGTGCTGTGGCCTACGTGCCCCAGGA 2096
Db	2277	GATGGACAAAGTGGAGGGCACGTGGCTATCAAGGCCTCCGTGGCCTATGTGCCACAGCA 2336
ý	2097	GGCCTGGGTGCAGAACACCTCTGTGGTAGAAATGTGTGCTTCGGGCAGGAGCTGGACCC 2156

2216 2276 2516 2336 2576 2396 2456 2696 2516 2756 2576 2815 2636 2636 2691 2935 2716 2995 2776 3055 2836 2896 3175 3235 3016 3076 AGACAGGCAGGTCAAGCTTTCCGTGTACTGGGACTACATGAAGGCCATCGGACTCTTCA 3115 3355 GGGATGTGGTGCGATCTCCCATCAGCTTCTTTGAGCGGACACCCATTGGTCACCTGCTAA 3136 ACCGCTTCTCCAAGGAGACAGACACGTTGACGTGGACATTCCAGACAAACTCCGGTCCC 3196 CAGTGGGGATCGGACAGAGATTGGCGAGAAGGCGTGAACCTGTCTGGGGGGACAGAAGCA GCTTCTGCAGAGGGGGGCCCTCGTGTGTCTTCTGGATCAAGCCAGACAGCCAGGAGA 2577 TAGAGGAGAAGGAGAAACAGAACCTGGGACCAGCACCAAGGACCCCAGAGGCACCTCTGC 2936 TCAGCAGCTCCTCCTCTATAGTGGGGACATCAGCAGGCACCACAACAGCACCGCAGAAC TGCGTGGCGGGATCTTCGGGCTCCTCGGCTGTCTCCAAGCCATTGGGCTGTTTGCCTCCA 2157 ACCCTGGCTGGAGAGAAGTACTAGAAGCCTGTGCCCTGCAGCCAGATGTGGACAGCTTCCC 2217 TGAGGGAATCCACACTTCAATTGGGGAGCAGGCATGAATCTCTCCGGAGGCCAGAAGCA GGCTGATTGGATCATAGTGCTGGCAAATGGGGCCCATCGCAGAGATGGGTTCCTACCAGGA 2876 AGCAAATGGAGAATGCTGGTGACGACAGTGCAGGGAACTGCAGAGACAGC 2717 CAGAGGTTCCTCTGGATGACCCTGACAGGCCAGGATGGCCAGCAGGAAAGGACAGCATCC 2996 TGCAGAAAGCTGAGGCCAAGAAGGAGAGACCTGGAAGCTGATGGAGGCTGACAAGGCGC 2837 TCTGCCTCTACGCACTCTTCCTCTCTCCCAGCAAGTGGCCTCCTTCTGCCGGGGCT TCCGGCTGAGCGTCTATGGAGCCCTGGGCATTTCACAAGGGATCGCCGTGTTTGGCTACT ACAGCATCCTGCGGTCACCCATGAGCTTCTTTGAGCGGACCCCCAGTGGGAACCTGGTGA 3017 TGGCTGCGGTGCTCCTAGGTGGGCCCGGGCATCCAGGTTGCTTTCCAGAGGCTCCTGT 2337 2457 2397 2697 2517 2757 2637 2777 3056 3116 2897 2957 3296 3077 2457 2692 3176 3236 3356 3137 QQ g qq δ Qγ ΩÝ Db Qγ qq g δλ Op Qγ qq Ω Dp Ob QΥ Q δy δ g ò g ÓΥ Db Ωÿ g Óγ qq Q D ογ a Q

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                                                                            3197 TGCTGATGTACGCCTTTGGACTCCTGGAGGTCAGCCTGGTGGTGGCAGTGGCTACCCCAC
                                          3476 TCATGGGCTCCCTGTTCAACGTCATTGGTGCCTGCATCGTTATCCTGCTGGCCACGCCCA
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                                                                 TGGCCACTGTGGCCATCCTGCCACTGTTTCTCCTCTACGCTGGGTTTCAGAGCCTGTATG
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4277 ACGAGGCTACTGCTGCCGTGGACCCTGGCACGGAGCTGCAGATGCAGGCCATGCTCGGGA
                         4616 CACAGTTCGAGGACTGCACCGTCCACCATCGCCCACCGGCTCAACACCCATCATGGACT
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                                                                                                                                                                                                                                                                    APPLICANT: Deeley, Roger G.
APPLICANT: Cole, Susan P.C.
TITLE OF INVENTION: METHODS FOR CONFERRING MULTIDRUG
TITLE OF INVENTION: RESISTANCE ON A CELL
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESS: RAKTEQ RESEARCH & DEVELOPMENT INNOVATIONS
STREET: Queen's University at Kingston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,907B
FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08460907B Patent No. 5891724 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/029,340
FILING DATE: 8-MAR-1993
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/141,893
FILING DATE: 26-0CT-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/966,923
FILING DATE: 27.0CT-1992
CLASSIFICATION: 424
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REGISTRATION NUMBER: 39,539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION
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TELEFRAX: (613) 545-6853
INFORMATION FOR SEO ID NO: 1.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/4(FILING DATE: 20-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 5011 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: CRANDA
21P: K7L 3N6
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Kingston STATE: Ontario
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                                                                        80;
                                                      Length
                                                                       0; Mismatches 1937; Indels
                                                     Score 1222.8; DB 2;
Pred. No. 5.5e-280;
                                                     27:1%;
55.7%;
                                                                        Matches 2535; Conservative
                 CDS
196..4788
                                                               Similarity
MOLECULE TYPE:
               NAME/KEY:

LOCATION:

US-08-460-907B-1
                                                      Query Match
                                                                Best Local
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Qy Db	2037	' GCTGTCAAAGGTGGAGGGGTTCGTGAGCATCGAGGGTGCTGGCCTACGTGCCCCAGGA 2096 	
Oy Dp	2097	' GGCCTGGGTGCAGAACACCTCTGTGGTAGAGAATGTGGTGCTTCGGCAGGAGCTGGACCC 2156 	
Oy	2157	ACCCTGGCTGGAGAGAGTACTAGAGCCTGTGCCCTGCAGCCAGTGTGGACAGCTTCCC 2216 	
δ. O.	2217	TGAGGAATCCACACTTCAATTGGGGAGCAGGCATGAATCTCTCCGGAGGCCAGAAGCA 2276	
δγ	2277	GCGGCTGAGCCTGGCCCGGGCTGTATACAGAAAGGCAGCTGTGTATACCTGCTGGATGACCC 233	
da .	2337	CCTGGCGGCCTGGATGCCCACGTTGGCCACGATGTCTTCAACCAGGTCATGGGCCTGG 239	
O _Y	2397		
Oy Og	2457 2697	GGCTGATTGGATCATAGTGCTGGCAAATGGGGCCATCGCAGAGATGGGTTCCTACCAGGA 2516 	
Oy Dp	2517 2757	GCTTCTGCAGAGGAGGCCCTCGTGTGTCTTCTGGATCAAGCCAGACAGCCAGGAGA 2576	
Oy Db	2577 2816		
Oy Db	2637 2876	AGGCAGGAGGCCCGAGCTTAGACGCGAGAGGTCCATCAAGTCAGTC	
Q P	2692		
Oy Db	2717	CAGAGGTTCCTCTGGATGACCTGACAGGGATGCCAGCAGGAAAGGACAGCATCC 2776	
Oy Db	2777 3056	AATACGGCAGGGTGAAGGCCACAGTGCACCTGCCTGCGTGCG	
Qy Db	2837 3116	TCTGCCTCTACGCACTCTTCCTCTTGCCAGCAAGTGGCCTCCTTCTGCCGGGGCT 2896	
Qy	2897 3176	ACTGGCTGAGCCTGTGGGCGGACCTGCAGTAGGTGGGCAGCAGCAGCGAGCCC 2956	
Qy Db	2957 3236	TGCGTGGCGGGATCTTCGGGCTCCTCGGCTGTCTCCAAGCCATTGGGCTGTTTGCCTCCA 3016	
QY	3017	TGGCTGCGGTGCTCCTAGGTGGGCCCGGGCATCCAGGTTGCTCTTCCAGAGGCTCCTGT 3076	
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ACAGCATCCTGCGGTCACCCATGAGCTTCTTTGAGCGGACCCCCAGTGGGAACCTGGTGA 3415 3316 3835 ACCGCTTCTCCAAGGAGACAGACACGGTTGACGTGGACATTCCAGACAAACTCCGGTCCC 3196 3595 3376 3775 3556 3655 3436 3715 3496 3616 3895 3676 3736 4015 4075 3856 4135 3916 3976 4255 3796 4195 4036 4096 4375 4315 GCCTGCCCGGCCAGCTGCAGTACAAGTGTGCTGACCGAGGCCAGAGCACCTGAGCGTGGCCC 4216 TGCTGATGTACGCCTTTGGACTCCTGGAGGTCAGCCTGGTGGTGGCAGTGGCTACCCCAC 3476 reargegerecergricaacgrearriggecergearcgraarcgraecrigeceacgecea TGGCCACTGTGGCCATCCTGCCACTGTTTCTCCTCTACGCTGGGTTTCAGAGCCTGTATG TTGTGGCTCAGAACAATGCTCGCGTAGATGAAAGCCAGAGGATCAGTTTCCCGCGACTGG TGGCTGACAGGTGGCTTGCGGCCAATGTGGAGCTCCTGGGGAATGGCCTGGTGTTTGCAG CCGCCACGIGIGCTGTGCTGAGCAAAGCCCACCTCAGTGCTGGCCTCGTGGCTTCTCTG TCTCTGCTGCCCTCCAGGTGACCCAGACACTGCAGTGGGTTGTTCGCAACTGGACAGACC ACATGGCTGAGACGTTCCAGGGCAGCACAGTGGTCCGGGCATTCCGAACCCAGGCCCCCT AGTICCGGGACITIGGGCTAAGAIGCCGACCTGAGCTCCCGCTGGCTGTGCAGGGCGTGI CCTCCCTGGCCAGTGGGCTGCTGCGGCTCCAGGAGGCAGCTGAGGGTGGGATCTGGATCG **ACTCGGACGAGGCTATCTGGGCAGCCCTGGAGACGGTGCAGCTCAAAGCCTTGGTGGCCA** TAGAGAACAGCATCGTGTCAGTGGAGCGGATGCAGGACTATGCCTGGACGCCCAAGGAGG CCTTCAAGATCCACGCAGGAGAAGGTGGGCATCGTTGGCAGGACCGGGGCAGGAAGT CCCAGGACCCCATCCTGTTCCCTGGCTCTCTGCGGATGAACCTCGACCTGCTGCAGGAGC 3356 3137 3416 3197 3536 3317 3257 3596 3377 3656 3776 3437 3716 3497 3836 3896 3557 3617 3677 3956 3737 4016 3797 4076 4136 3977 4256 4316 3857 3917 4196 4037 4097 4376 4157 g ò qq δŻ Op Qγ Dp δy qq οy qq Ω qq δy Ωp ΩŸ QQ QY Q ΩÝ Dp οŽ qq δ qq οy Ωp δ g g ò δλ qq qq δ ò

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; LOCATION:
JS-08-463-179A-1
                                                   Query Match
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4436 CCCTTCCTGACAAGCTAGACCATGAATGTGCAGAAGGCGGGGAGAACCTCAGTGTCGGGC 4495
                              4217 AGAAACAGCTCCTGTGTCTGGCACGTGCCCTTCTCCGGAAGACCCCAGATCCTCATCCTGG 4276
                                                                                                           4676 ACACAAGGGTGATCGTCTTGGACAAAGGAGAAATCCAGGAGTACGGCGCCCCATCGGACC 4735
                                                4496 AGCGCCAGCTTGTGTGTCCTAGCCCGGCCCTGCTGCAGGAAGACGATCCTTGTGTTGG
                                                                                                                                                     4277 ACGAGGCTACTGCTGCCGTGGACCCTGGCACGGAGCTGCAGATGCAGGCCATGCTCGGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Cole, Susan P.C.
APPLICANT: Deeley, Roger G.
TITLE OF INVENTION: METHODS FOR IDENTIFYING CHEMOSENSITIZERS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,179A
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/966,923
FILING DATE: 27-0CT-1992
APPLICATION NUMBER: 08/029,340
FILING DATE: 8-MAR-1993
APPLICATION NUMBER: 08/141,893
FILING DATE: 26-0CT-1993
APPLICATION NUMBER: 08/407,207
FILING DATE: 20-MAR-1995
ATTORNEY AGENT INFORMATION:
NAME: DECONTI, GIULIO A Jr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08463179A Patent No. 6001563 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DeConti, Giulio A. Jr. RATION NUMBER: 31,503
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REFERENCE/DOCKET NUMBER: PO
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TYPE: nucleic acid
STRANDEDNESS: double
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CITY: Boston
STATE: Massachusetts
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                                                                                                                                                                                                                                                                                                                                                       CCTCTTCATCCACCATGGCCGGGGCTACCTCCGGATGTCCCCCACTCTTCAAAGCCAA
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                                                                    Length 5011;
                                                                  Score 1222.8; DB 3; Length
Pred. No. 5.5e-280;
0; Mismatches 1937; Indels
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                                                                    27.1%;
55.7%;
                                                                                                                   Conservative
196..4788
                                                                                        Best Local Similarity
Matches 2535; Conserv
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1256	1079	1139	1199	1259	1319	37	1439	1499	1559 1796	1619 1856	1679	1736 1976	1796 2036	1856	1916 2156	1976 2216	2036	2096 2336
. CCACGACCTGATGATGTTTTCCGGGCCGCAGATCTTAAAGTTGCTCATCAAGTTCGTGAA	TGATCCCAAGCCTCCAGCCTGGAAGGCTACCTCCTCGCCGTGCTGGTGTTCCTCTCAGC	CTGCCTGCAAACGCTGTTTGAGCAGCAGAACATGTACAGGCTCAAGGTGCCGCAGATGAG		CAGAAAGGCCAGTGCGGTGATGTGGTCAATCTGGTGTCGTGGACGTGCAGCGGCTT			GAGCCTCCTCCTCTGAATTTCTTCATCTCCAAGAAAAGGAACCACCATCAGGAGGAGACA 	AATGAGGCAGAAGGACTCACCAGCTCTATCCTCAGGAACTCGAAGAC	CATCAAGTTCCATGGCTGGGAGCCTTTCTGGACAGAGTCCTGGGCATCCGAGGCCA   111   111   111   1   1   1   1   1	GGAGCTGGGCGCTTGCGGACCTCCGCTCTCTCTGTGTCGCTGGTGTCCTTCCA	AGTGTCTACATTTCTGGTCGCACTGGTGGTGTTTGCTGTCCACACTCTGGTGGCCGAGAA	TGCTATGAATGCAGAGAAAGCCTTTGTGACTCTCACAGTTCTCAACATCCTCAACAA 	GGCCCAGGCTTTCCTGCCCTTCTCCATCCATCCTCGTCCAGGCCCGGGTGTCCTTTGA	CCGTCTGGTCACCTTCCTCTGCCTGGAAGAAGTTGACCCTGGTGTCGTAGACTCAAGTTC	CTCTGGAAGCGCTGCCGGGAAGGATTGCATCACCATACACAGTGCCACCTTGGCCTGGTC	CCAGGAAAGCCCTCCCTGCCTCCACAATAAACCTCACGGTGCCCCAGGGCTGTCTGCT	GGCTGTTGTCGGTCCAGTGGGGCAGGGAAGTCCTCCCTGCTGTCCGCCCTCCTTGGGAAGTCCTCCTGCTGTCGCCTCTTTGGGAAGTCCCTGCTGCTCAGCCTCTTGGCTGAAGTTGTCCCTGCTCTCAGCCTCTTGGCTGA	GCTGTCAAAGGTGGAGGGGTTCGTGAGCATCGAGGGTGCTGTGGCCTACGTGCCCCAGGA 
1197	1020 1257	1080	1140	1200	1260	1320 1557	1380 1617	1440	1500	1560 1797	1620 1857	1680 1917	1737 1977	1797 2037	1857 2097	1917 2157	1977	2037 2277
QQ	Qy Db	da.	Óy	Oy Dp	Qy Db	Qy	Oy Db	Qy Dp	Oy Op	oy Db	Oy Dp	Qy Db	Oy Db	Q _Y	OY Dp	Oy Op	Oy Dp	QY

2396 2216 2456 2276 2516 2456 2516 2756 2815 2875 2396 GCTTCTGCAGAGGAAGGGGGCCCTCGTGTGTCTTCTGGATCAAGCCAGACAGCCAGGAGA 2576 TAGAGGAGAAGGAGAAACAGGAACCTGGGACCAGCACCAAGGACCCCCAGAGGCACCTCTGC 2636 2691 2776 3055 2896 3016 3295 3076 2935 2337 GGCCTGGATTCAGAATGATTCTCTCCGAGAAAACATCCTTTTTGGATGTCAGCTGGAGGA GCTGCTGGCTCGAGACGGCGCCTTCG-CTGAGTTCCTGCGTACCTATGCCAGCACAGAGC TCTGCCTCTACGCACTCTTCCTCTTGCCAGCAAGTGGCCTCCTTCTGCCGGGGCT GCGCGTGAGCCTGGCCCGGGCCGTGTACCTCTACCTCTTCGATCC GGCTGATTGGATCATAGTGCTGGCAAATGGGGCCCATCGCAGAGATGGGTTCCTACCAGGA 2876 AGCAAATGGAGAATGGCATGCTGGTGACGACAGTGCAGGGAAGCAACTGCAGAGACAGC 2717 CAGAGGTTCCTCTGGATGACCCTGACAGGGCAGGATGGCCAGCAGGAAAGGACAGCATCC TGCAGAAAGCTGAGGCCCAAGAAGGAGGAGGCTGGAAGCTGATGGAGGCTGACAAGGCGC CCATGGCCGTGTCCATCGGGGGGATCTTGGCTTCCCGCTGTCTGCACGTGGACCTGCTGC GCGGCTGAGCCTGGCCCGGGCTGTATACAGAAAGGCAGCTGTGTACCTGCTGGATGACCC CCTGGCGGCCCTGGATGCCCACGTTGGCCAGGATGTCTTCAACCAGGTCATTGGGCCTGG TGCGTGGCGGGATCTTCGGCTCCTCGGCTGTCTCCAAGCCATTGGGCTGTTTGCCTCCA TGGCTGCGGTGCTCCTAGGTGGGGCCCGGGCATCCAGGTTGCTCTTCCAGAGGCTCCTGT 2397 2157 2217 2457 2337 2577 2397 2757 2577 2637 2692 2996 2897 3236 3296 2097 2277 2517 2637 2457 2697 2517 3026 2837 3116 3176 2957 3017 δy qq Q qq òγ Dp Qγ Dρ Q qq Qγ Op δλ g ò qq δy qq QQ рp q qq Qγ ò οy δy QQ δy ò qq qq q ò ò δy

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Score 1222.8;
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APPLICATION NUMBER: 07/966
FILING DATE: 27-0CT-1992
APPLICATION NUMBER: 08/029
FILING DATE: 8-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (613) 545-2342
TELEFAX: (613) 545-6853
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: double
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196..4788
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FILING DATE: 26-0CT
APPLICATION NUMBER:
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SOFTWARE: ASCII t
                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Ontario
COUNTRY: CANADA
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US-08-461-384B-1
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             TGCTGATGTACGCCTTTGGACTCCTGGAGGTCAGCCTGGTGGTGGCAGTGGCTACCCCAC
                                                                   TCATGGGCTCCCTGTTCAACGTCATTGGTGCTGCATCGTTATCCTGCTGGCCACGCCCA
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4556 ATGAGGCCACGCAGCCGTGGACGGACGACCTCATCCACCACCACCGGA
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                                                                 ACGAGGCTACTGCTGCCGTGGACCCTGGCACGGAGCTGCAGATGCAGGCCATGCTCGGGA
                                                                                                                                                        GCTGGTTTGCACAGTGCACTGTGCTGCCCATTGCCCACCGCCTGCGCTCCGTGATGGACT
                                                                                                                                                                                                                                                                                                                                      TGCTGGCCCAGAAGGGCCTGTTTTACAGACTGGCCCAGGAGTCAGGCCTGGT 4508
                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS STREET: Queen's University at Kingston CITY: Kingston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Cole, Susan P.C.
APPLICANT: Deeley, Roger G.
APPLICANT: Deeley, Roger G.
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,384B
FILING DATE: 05-JUN-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08461384B Patent No. 6025473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UMBER: 08/141,893
26-0CT-1993
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FILING DATE: 20-MAR-1995
THORNEY AGENT INFORMATION:
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REGISTRATION NUMBER: 39,539
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Length 5011;

DB 3;

7;																		
Gaps	r 95 A 296	r 155     356	A 215 A 416	275	335	395	455	506	566	626	968 1	746	802	849	899	959 1196	1019	1079
7%; Pred. No. 5.5e-280; 0; Mismatches 1937; Indels 80;	GGTCTGGAACCAGACCAGAACCTGCCGCCACCAGCGTGCTGGGCTTCCT	GAGAACAGCAGGGGTCTGGGTACCCCCATGTACCTCTGGGTCCTTGGTCCCATCTACCT	CCTCTTCATCCACCACCATGCCGGGGCTACCTCCGGATGTCCCCACTCTTCAAAGCCAA	GATGGTGCTTGGATTCGCCCTCATAGTCCTGTGTACCTCCAGCGTGGCTGTGCCTCTTTG	GAAAATCCAACAGGGAACGCCTGAGGCCCCAGAATTCCTCATTCAT	CACCACGATGAGCTTCGCAGTGTTCCTGATTCACACCGAGGGGAAAAAGGAGTCCAGTC	ATCTGGAGTGCTGTTTGGTTACTGGCTTCTGTCTTGCCAGCTACCAAGGCTGC	CCAGCAGGCCTCCGGAGCGGGCTTCCAGAGCGACCCTGTCCGCCACTGTC	CACCTACCTATGCCTGTCTCTGGTGGTGGCACAGTTTGTGCTGCTGCCTGGCGGATCA	ACCCCCTTCTTCCCTGAAGACCCCCAGCAGTCTAACCCCTGTCCAGAGACTGGGGCAGC	CTICCCCTCCAAAGCCACGTICTGGGGTTTCTGGCCTGGTCTGGAGGGGATACAGGAG 	GCCACTGAGACCAAAAGACCTCTGGTCGCTTGGGAGAGAAAACTCCTCAGAAGAACTTGT 	TTCCCGGCTTGAAAAGGAGTGGATGGAACCGCAGTGCAGCCGGAGGCACAACA 	AGCAATAGCATTTAAAAGGAAAGCGGCAGTGGCTGAGGCTCCA	GAGACCGAGCCCTTCCTACGGCAAGAAGGGAGCCAGTGGCGCCCACTGCT	GAAGGCCATCTGGCAGGTGTTCCATTCTACCTTCCTGGGGACCCTCAGCCTCATCATATITIT	CAGIGAIGICTICAGGITCACIGICCCCAAGCIGCICAGCCITITCCIGGAGITIAITIGG	TGATCCCAAGCCTCCAGCCTGGAAGGCTACCTCCTCGCCGTGCTGATGTTCCTCTCAGC
Local Similarity 55. Hes 2535; Conservative							ATCTGGAGTGCTGTTTG                    TTCAGGGATCATGCTC	CCAGCAG   ATCCAAAATTAT	CACCTACCTATGCCTG1                   TTTCTACGTCTACTTT	ACCCCCTTCTTCCCTG	CTTCCCCTCCAAAGCCA	GCCACTGAGACCAAAAG	TTCCCGGCTTGAAAGG	AGGCAATAGCATTTAAA 	GAGACCG	GAAGGCCATCTGGCAGG 	CAGTGATGTCTTCAGGT	TGATCCCAGCCTCCAG
Best Loc Matches	36	96	156 357	216	276	336	396	456	507	567	627	687	747	803	850	900	960	1020
- <b>-</b>	Qy Db	QY Db	Oy Dp	Oy Dp	QY	Oy Dp	Qy Db	Qy Dp	Qy Dp	Oy Dp	Qy Db	δy do	Oy Dp	Qy	Oy Db	Qy Dp	Qy Db	ΟY

1139 1376 1436 1259 1496 1616 1439 1796 1856 TGACACGAAGGCCCCCAGACTGGCAGGGCTACTTCTACACCGTGCTGCTGTTTGTCACTGC 1316 GACCGAGAGCGTCCTCTACCTCAACGGGCTGTGGCTGCCTCTCGTCTGGATCGTGGTCTG 1319 1379 AATGAGGCAGAAGGACTCACGGCACGGCTCACCAGCTCTATCCTCAGGAACTCGAAGAC 1499 CATCAAGITCCATGGCTGGGAGGGAGCCITTCTGGACAGAGICCTGGGCATCCGAGGCCA 1559 GGAGCIGGGCGCTTGCGGACCTCCGGCCTCTTCTCTGTGTCGCTGGTGTCCTTCCA 1619 1679 CTGCACGCCCTTTCTGGTGGCCTTGTGCACATTGCCGTCTACGTGACCATGACGAGAA 1916 1736 2036 1856 2096 CTCTGGAAGCGCTGCCGGGAAGGATTGCATCACCATACACAGTGCCACCTTCGCCTGGTC 1916 2156 1976 2216 2036 2276 GGCCCAGGCTTTCCTGCCTTCTCCATCCACTCCTCGTCCAGGCCCGGGTGTCCTTTGA 1796 2336 CTGCCTGCAAACGCTGTTTGAGCAGCAGAACATGTACAGGCTCAAAGGTGCCGCAGATGAG GTTGCGGTCGGCCATCACTGGCCTGGTGTACAGAAAGGTCCTGGCTCTGTCCAGCGGCTC CTTCGTCTATCTCTGGCAGCTCCTGGGGCCCTCCGCCCTCACTGCCATCGCTGTTCCT 1380 GAGCCTCCTCCTCTGAATTTCTTCATCTCCAAGAAAAGGAACCACCATCAGGAGGAGCA 1620 AGTGTCTACATTTCTGGTCGCACTGGTGTTTGCTGTCCACACTCTGGTGGCCGAGAA 1680 IGCIA---TGAATGCAGAGAAGCCTTTGTGACTCTCACAGTTCTCAACATCCTCAACAA TCCCCTGAACATTCTCCCCATGGTCATCAGCAGCAGCGCGAGTGTCTCCCTCAA CCGTCTGGTCACCTTCCTCTGCAAGAAGTTGACCCTGGTGTCGTAGACTCAAGTTC CAGAAAGGCCAGTGCGTGGTGATGTGGTCAATCTGGTGTCCGTGGACGTGCAGCGGCT CCAGGAAAGCCCTCCCTGCCTCCACAGAATAAACCTCACGGTGCCCCAGGGCTGTCTGCT GCTGTCAAAGGTGGAGGGGTTCGTGAGCATCGAGGGTGCTGTGGCCCTACGTGCCCCAGGA GGCCTGGGTGCAGAACACCTCTGTGGTAGAGAATGTGTGTTCCGGGCAGGAGCTGGACCC 1257 1140 1200 1260 1497 1320 1440 1500 1080 1560 1857 1737 2037 1977 1797 1857 2157 1977 2217 2037 2277 2337 1917 2097 ŏλ PP Qγ Db οy QQ οy g ογ QQ οy qq ·δ qq qq ά 셤 Ωp òγ ò οχ qq δy qq ò Q δ g g δy δy 셤 Q ò qq ò

2576 2935 3175 3475 2756 GGTGGACGTCATCATCGTCATGAGTGGCGGCAAGATCTCTGAGATGGGCTCCTACCAGGA GCTCTGGAGGAGGAGGCCCTCGTGTGTCTTCTGGATCAAGCCAGACAGCCAGGAGA ---GACCGTACCACTTCAGAAGCCCAGA--TCTGCCTCTACGCACTCTTCCTCTTCCTCTGCCAGCAAGTGGCCTCCTTCTGCCGGGCT TCCGGCTGAGGGTCTATGGAGCCCTGGGCATTTCACAAGGGATCGCCGTGTTTGGCTACT CCATGGCCGTGTCCATCGGGGGGATCTTGCCTCCTGCTGCACGTGGACCTGCTGC GCGCCTGAGCCTGCCCCGGCCTGTATACAGAAAGGCAGCTGTGTACCTGCTGGATGACCC GCGCGTGAGCCTGGCCCGGGCCGTGTACTCCAACGCTGACATTTACCTCTTCGATGATCC CCTGGCGCCCTGGATGCCCACGTTGGCCAGCATGTCTTCAACCAGGTCATTGGGCCTGG GGCTGATTGGATCATAGTGCTGGCAAATGGGGCCCATCGCAGAGATGGGTTCCTACCAGGA GCTGCTGGCTCGAGACGCGCCTTCG-CTGAGTTCCTGCGTACCTATGCCAGCACAGAGC AGCAAATGGAGAATGGCATGCTGGTGACGGACAGTGCAGGGAAGCAACTGCAGAGACAGC 2936 TCAGCAGCTCCTCCTCTATAGTGGGGACATCAGCAGGCACCACAACAGCACCGCAGAAC CAGAGGTTCCTCTGGATGACCCTGACAGGGCAGGATGGCCCAGCAGGAAAGGACAGCATCC 2996 TGCAGAAAAGCTGAGGCCAAGAAGGAGGAGCCTGGAAGCTGATGGAGGCTGACAAGGCGC TGCGTGGCGGGATCTTCGGGCTCCTCGGCTGTCTCCAAGCCATTGGGCTGTTTGCCTCCA GGGATGTGGTGCGATCTCCCATCAGCTTCTTTGAGCGGACACCCATTGGTCACCTGAA ACAGCATCCTGCGGTCACCCATGAGCTTTTTAAGCGGACCCCCAGTGGGAACCTGGTGA **ACCCTGGCTGGAGAGAGTACTAGAAGCCTGTGCCCTGCAGCCAGATGTGGACAGCTTCCC** TAGAGGAGAAAGGAGAAACAGAACCTGGGACCAGCACCAAGGACCCCAGAGGCACCTCTGC TGGCTGCGGTGCTCCTAGGTGGGGCCCCGGGCATCCAGGTTGCTTCCAGAGGCTCCTGT ACCGCTTCTCCAAGGAGACAGACACGCTTGACGTGGACATTCCAGACAAACTCCGGTCCC TGAGGGAATCCACACTTCAATTGGGGAGCAGGGCATGAATCTCTCCGGAGGCCAGAAGCA 2397 3116 3236 3296 3416 2157 2876 3056 3326 2217 2457 2637 2517 2692 2717 2837 2897 3176 2957 3017 3077 3137 2277 2517 2337 2577 2397 2457 2697 2757 2577 2637 2777 qq g q Q οy Dp Ω qq g ŏ q οy g q δ g Q Dp οy g ογ g ò g ογ QQ ò ò οy οy ŏ δ φ õ Ω

3616 3676 3655 4096 3496 3556 4015 4075 3916 4375 4156 4216 4336 3856 4435 4495 TGCTGATGTACGCCTTTGGACTCCTGGAGGTCAGCCTGGTGGTGGCAGTGGCTACCCCAC 3256 TCATGGGCTCCCTGTTCAACGTCATTGTGTGCCTGCATCGTTATCCTGCTGGCCACGCCCA ACGAGGCTACTGCTGCTGGACCCTGGCACGGAGCTGCAGATGCAGGCCATGCTCGGGA TGGCCACTGTGGCCATCCTGCCACTGTTTCTCCTCTACGCTGGGTTTCAGAGCCTGTATG ACATGGCTGAGACGTTCCAGGGCAGCACAGTGGTCCGGGCATTCCGAACCCAGGCCCCCT TGGCTGACAGGTGGCTTGCGGCCAATGTGGAGCTCCTGGGGAATGGCCTGGTGTTTGCAG CCGCCACGTGTGCTGTGCTGAGCAAAGCCCACCTCAGTGCTGGCCTCGTGGGCTTCTCTG TCTCTGCTGCCCTCCAGGTGACCCAGACACTGCAGTGGGTTGTTCGCAACTGGACAGACC TAGAGAACAGCATCGTGTCAGTGGAGCGGATGCAGGACTATGCCTGGACGCCCAAGGAGG TGGAAACCAACATCGTGGCCGTGGAGAGGCTCAAGGAGTATTCAGAGACTGAGAAGGAGG CCTCCCTGGCCAGTGGGCTGCTGCGGCTCCAGGAGGCAGCTGAGGGTGGGATCTGGATCG ACGGGGTCCCCATTGCCCACGTGGGGCTGCACACACTGCGCTCCAGGATCAGCATCATCC CCCAGGACCCCATCCTGTTCCCTGGCTCTCTGCGGATGAACCTCGACCTGCTGCAGGAGC ACTCGGACGCTATCTGGGCAGCCCTGGAGACGGTGCAGCTCAAAGCCTTGGTGGCGAA ACTCGGATGAAGAAGTCTGGACGTCCCTGGAGCTGGCCCACCTGAAGGACTTCGTGTCAG AGAAACAGCTCCTGTGTCTGGCACGTCCCTTCTCCGGAAGACCCAGATCCTCGG AGCGCCAGCTTGTGTGCCTAGCCCGGGCCCTGCTGAGGAGGACGAAGATCCTTGTGTTGG ATTTCAACGAGACCTTGCTGGGGGTCAGCGTCATTCGAGCCTTCGAGGAGCAGGAGCGCT TTGTGGCTCAGAACAATGCTCGCGTAGATGAAAGCCAGAGGATCAGTTTCCCGCGACTGG CCTTCAAGATCCACGCAGGAGAAGGTGGGCATCGTTGGCAGGACCGGGGCAGGGAAGT GCCTGCCCGGCCAGCTGCAGTACAAGTGTGCTGACCGAGGCGAGGACCTGAGCGTGGGCC CCCTTCCTGACAAGCTAGACCATGAATGTGCAGAAGGCGGGGAGAACCTCAGTGTCGGGC 3476 3257 3536 3596 3656 3716 3776 3836 3896 3956 4016 4076 3857 3917 3977 3197 3317 3377 3437 3497 3557 3617 3677 3797 4136 4196 4256 4037 4316 4097 4436 4496 4277 3737 4376 4217 4157 Db Ω d ά Db Ω Dp οy QQ οy Db οy qq Q g οy g δy g Óγ P Ω dd . οy g οy Ω ò Db ò qq ò qq δy qq δ

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GCTGGTTTGCACAGTGCACTGTGCTGCCCATTGCCCACCGCCTGCGCTCCGTGATGGACT
                                                                                             1397 GTGCCCGGGTTCTGGTCATGGACAAGGGGCAGGTGGCAGAGGGGGCGGCCCGGCCCAGC
                                                                                                                    4676 ACACAAGGGTGATCGTCTTGGACAAAGGAGAAATCCAGGAGTACGGCGCCCCATCGGACC
                                                                                                                                                                                                                                                                              APPLICANT: Deeley, Roger G.
APPLICANT: Cole, Susan P.C.
TILLE OF INVENTION: ANTIBODIES TO A MULTIDRUG RESISTANCE PROTEIN NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
STREET: Queen's University at Kingston
                                                                                                                                              DB 3; Length 5011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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Pred. No. 5.5e-280;
0; Mismatches 1937;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/407,207A
FILING DATE: 20-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA.
APPLICATION DATA.
APPLICATION NUMBER: 07/966,923
FILING DATE: 27-0CT-1992
APPLICATION NUMBER: 08/029,340
FILING DATE: 8-MAR-1993
APPLICATION NUMBER: 08/141,893
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: K7L 3N6
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                         Sequence 1, Application US/08407207A Patent No. 6063621 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Steeg, Carol Miernicki
REGISTRATION NUMBER: 39,539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: Q1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (613) 545-2342
TELEFAX: (613) 545-6853
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 5011 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
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196..4788
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                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: CANADA ZIP: K7L 3N6
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Best Local Similarity
Matches 2535; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 20 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                          CITY: Kingston
STATE: Ontario
                                                                                                                                                                                                                              US-08-407-207A-1
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36 GGTCTGGAACCAGACAGAGCCTGAACCTGCCGCCACCAGCCTGCTGAGCCTGTGCTTCCT 95

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657 ATCCAAAATTATGACAGCCTTAAAAGAGGATGCCCAGGTGGACCTGTTTCGTGACATCAC 716
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        747 TTCCCGGCTTGAAAAGAGTGGATGAGAACCGC----AGTGCAGCCCGGAGGCACAACA 802
                                                                                                                                   CCTCTTCATCCACCACCACCAGGGGGTACCTCCGGATGTCCCCACTCTTCAAAGCCAA
                                                                                                                                                                                                                                                                                                                                             417 AACTGCCTTGGGATTTTTGCTGTGGATCGTCTGGGCAGACCTCTTCTACTCTTTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             567 ACCCCCTTCTTCCCTGAAGACCCCCAGCAGTCTAACCCCTGTCCAGAGACTGGGGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 197 GAACACGGTCCTCGTGTGGGTGCCTTGTTTTACCTCTGGGCCTGTTTCCCCCTTTACTT
                                                                                                                                                                               CCTCTATCTCTCCCGACATGACCGAGGCTACATTCAGATGACACCTCTCAACAAAACCAA
                                                                                                                                                                                                                          216 GATGGTGCTTGGATTCGCCCTCATAGTCCTGTGTACCTCCAGCGTGGCTGTCGTCTTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      396 ATCTGGAGTGCTGTTTGGTTACTGGCTTCTCTGCTTTGTCTTGCCAGCTACCAACGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCAGCAG------GCCTCCGGAGCGGGCTTCCAGAGCGACCCTGTCCGCCACCTGTC
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                                            GAGAACAGCAGGGGTCTGGGTACCCCCCATGTACCTCTGGGTCCTTGGTCCCATCTACCT
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Qy	1140	GTTGCGGTCGGCCATCACTGGCCTGTACAGAAAGGTCCTGGCTCTGTCCAGCGGCTC 119
g	1377	GATCAAGACCGCTGTCATTGGGGCTGTCTATCGGAAGGC
δ	1200	12
g	1437	CAGAAAATCCTCCACGGTCGGGGAGATTGTCAACCTCATGTCTGTGGACGCTCAGAGGTT 1496
δ	1260	131
g	1497	CATGGACTTGGCCACGTACATTAACATGATCTGGTCAGCCCCCCTGCAAGTCATCCTTGC 1556
oy Oy	1320	CTTCGTCTATCTCTGGCAGCTCCTGGGGCCCTCCCCTCATGCTGTCTTCCT 1379
οy	1380	TTCTTCATCTCCAAGAAAAGGAACCACC
οp	1617	CCTCATGGTGCCCGTCAATGCTGTGTGCGATGAAGACCAAGACGTATCAGGTGGCCCA 1676
δy	1440	AATGAGGCAGAAGGACTCACGGCTCACCAGCTCTATCCTCAGGAACTCGAAGAC 1499
Dp	1677	CATGAAGAAGCAAAGACAATCGGATCAAGCTGAACGAAATTCTCAATGGGATCAAAGT 1736
οy	1500	CATCAAGTICCAIGGCIGGGGGGGGGGGGCTITCIGGACAGCAGCCAGGCCA 1559
g	1737	cciegeaecrescaticaassacaassis
γ	1560	GGAGCTGGGCCCTTGCGGACCTCCGCCTCCTTGTGTGCCTGGTGTCCTTCCA 1619
QQ	1797	GGAGCTGAAGGTGCTGAAGAAGTCTGCCTACCTGTCACCTGTGGCACCTTCACCTGGGT 1856
οy	1620	AGTGTCTACATTTCTGGTGGTGGTGTGTTTGCTGTCCACACTCTGGTGGCCGAGAA 1679
qq	1857	CTGCACGCCCTTTCTGGTGGCCTTGTGCCACTTTGCCGTCTACGTGACCATTGACGAGAA 1916
οy	1680	TGCTATGAATGCAGAGAAAGCCTTTGTGACTCTCACAGTTCTCAACATCTCAACAA 1736
g	1917	GATGCCCAGACAGCCTTCGTGTTTGGCCTTGT
οy	1737	GGCCCAGGCTTTCCTGCCTTCTCCACTCCTCGTCCAGGCCCGGGTGTCCTTTGA 1796
qq	1977	cccarggrcarcagcarcgrgcaggrgra
Οy	1797	CCGICIGGICACCITCCICIGGAAGAAGIIGACCCIGGIGGICGIAGACICAAGIIC 1856
g	2037	aggarctrictccargagagcrggaa
οy	1857	CTCTGGAAGCGCTGCCGGGAAGGATTGCATCACCATACACAGGCCACCTTGGCTGGTC 1916
qq	2097	ccercacaraccaracacca
0y 0p	1917	CCAGGAAAGCCTCCCTGCCTCCACAATAAACCTCACGGTGCCCCAGGGCTGTCTGCT 1976
δ	1977	GGCTGTTGTCGGTCCAGTGGGGGGGGAAGTCCTCCCTGCTGTCGGCCCTCCTTGGGGA 2036
qq	2217	
ογ	2037	GCTGTCAAAAGGTGGAGGGTTCGTGAGCATCGAGGGTGCTGTGGCCCTACGTGCCCCAGGA 2096
qq	2277	GATGGACAAGTGGAGGGCACGTGGCTATCAAGGCTCCGTGGCTATGTGCCACAGCA 2336
QY Db	2097	GCCCTGGGTGCAGACCTCTGTGGTAGAGAATGTGTGCTTCGGCAGGAGCTGGACCC 2156
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g ,	739/	ACCATATTACAGGTCCGTGATACAGGCCTGTGCCCTCCTCCCAGACCTGGAAATCCTGCC 2456

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CLASSIFICATION: 435
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MEDIUM TYPE: Floppy
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MOLECULE TYPE: CDNA
FEATURE:
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; LOCATION:
US-08-463-092B-5
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US-08-463-092B-5
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APPLICANT: Cole, Susan P.C.
APPLICANT: Deeley, Roger G.
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING
TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: PATEQ RESEARCH & DEVELOPMENT INNOVATIONS
STREET: Queen's University at Kingston
CITY: Kingston
STRATE: Ontario
COUNTRY: CANADA
ZIP: K7L 316
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,092B
FILING DATE: 05-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                            Sequence 5, Application US/08463092B Patent No. 5766880
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APPLICATION NUMBER: 08/029,340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/141,893 FILING DATE: 26-0CT-1993 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/407,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNBER: 07/966,923
FILING DATE: 27.0CT-1992
CLASSIFICATION: 435
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NAME: Steeg, Carol Miernicki
REGISTRATION NUMBER: 39,539
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TELEPHONE: (613) 545-2342:
TELEFAX: (613) 545-6853
INFORMATION FOR SEQ. ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 589 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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CLASSIFICATION: 435
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ATGACAGGGAGGCTCCCGACTGGCAGGGCTACTTTTACACAGCACTGCTGTTTGTCAGCG 1128
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                                                                                  AAATGAGGCAGGACTCACGGCACGCTCACCAGCTCTATCCTCAGGAACTCGAAGA
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Qy	OY 2216 CIGAGGGAATCCACACTTCAATIGGGGAGCAGGGCATGAATCTCTCCGGAGGCCAGAAG	() — ()	2275 2325
Oy Dp	OY 2276 AGCGGCTGAGCCCGGGCTGTATACAGAAAGGCAGCTGTGTACCTGCTGGATGACC III		2335 2385
Oy Dp	QY 2336 CCCTGGCGGCCCTGGATGCCCACGTTGGCCAGGATGTCTTCAACCAGGTCATTGGGCCTG		2395 2445
oy Ob	QY 2396 GTGGGCTACTCCAGGAAACAACACGGATTCTCGTGACGCACGC		
Qy Db	QY 2456 AGGCTGATTGGATCATAGTGCTGGCAAAATGGGGCCATCGCAGAGATGGGTTCC 	CTACCAGG             TATCAGG	2515 2565
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oy Ob	QY 2618 ACCCCAGAGGCACCTCTGCAGGCGGGGGCCCGAGCTTAGACGCGAGAGGTCCATAGAGGAGAGAGGTCCATAGAGAGAG	CAAGT	2677
Qy Db	QY .2678 CAGTCCCTGAGAAGGACCGTACCACTTCAGAAGCCCAGACAGA	כז כי	2737 2805
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Qy	QY 3086 TGCGATCTCCCATCAGCTTCTTGAGCGGACACCCCATTGGTCACCTGCTAAACCGCTTCT 	CACCTGCTAAACCGCTTCT 3	1145
Qy Db	OY 3146 CCAAGGAGACAGACAGGTTGACGTGGACATTCCAGACAAACTCCGGTCCCTGCTGATGT	CTCCGGTCCCTGCTGATGT 3	1205

3265 3325 3405 3385 3465 3445 3505 3645 GGTGGCTTGCGCCAATGTGGAGCTCCTGGGGAATGGCCTGGTGTTTGCAGCCGCCACGT 3565 3566 GIGCIGIGCIGAGCAAAGCCCACCICAGIGCIGGCCICGIGGGCITCICICICTGCIG 3625 3626 CCCTCCAGGTGACCCAGACACTGCAGTGGGTTGTTCGCAACTGGACAGACCTAGAGAACA 3685 4065 4105 4165 3686 GCATCGTGTCAGTGGAGCGGATGCAGGACTATGCCTGGACGCCCAAGGAGGCTCCCTGGA 3745 3746 GGCIGCCCACATGIGCAGCICAGCCCCCTGGCCTCAGGGCGGGGAGAICGAGTICCGGG 3805 3806 ACTITGGGCTAAGATGCCGACCTGAGCTCCCGCTGGCTGTGCAGGCGTGTCCTTCAAGA 3865 3886 ATTACTGCCTGAGGTATCGAGAAGACTTGGACTTGGTTCTCAAGCACATAAATGTCACA 3945 4245 3946 TIGAGGGTGGAGAAAAGGTGGGTATTGTAGGTCGTACGGGAGCTGGGAATCATCTCTCA 4005 CCAGTGGGCTGCTGCGGCTCCAGGAGGCAGCTGAGGGTGGGATCTGGATCGACGGGTTCC 3985 4225 4305 4285 4365 3866 TCCACGCAGGAGAGAAGGTGGCCATCGTTGGCAGGACCGGGGCAGGGAAGTCCTCCCTGG 3925 ACGCCTTTGGACTCCTGGAGGTCAGCCTGGTGGTGGCAGTGGCTACCCCACTGGCCACTG AGACGTTCCAGGGCAGCACAGTGGTCCGGGCATTCCGAACCCAGGCCCCCTTTGTGGCTC TGGCCATCCTGCCACTGTTTCTCCTCTACGCTGGGTTTCAGAGCCTGTATGTGGTTAGCT AGAACAATGCTCGCGTAGATGAAAGCCAGAGGATCAGTTTCCCGGGGACTGGTGGCTGACA 3586 GATGGCTTGCTGTGGCCTTGAGTGTGTGGGCAACTGCATTGTGCTGCTGCTCT CCATCCTGTTCCCTGGCTCTCTGCGGATGAACCTCGACCTGCTGCAGGAGCACTCGGACG 4106 AGCTATCTGGGCAGCCCTGGAGACGGTGCAGCTCAAAGCCTTGGTGGCCAGCCTGCCCG 4226 TCCTGTGTCTGGCACGTGCCCTTCTCCGGAAGACCCAGATCCTCATCCTGGACGAGGCTA GCCAGCTGCAGTACAAGTGTGCTGACCGAGGCGAGGACCTGAGCGTGGGCCCAGAAACAGC 3206 3286 3266 3346 3326 3406 3386 3446 3506 3926 4046 4166 4286 δy 8 δ Db Db 92 92 93 qq QY Db QQ qq oy Oy Ω QΫ qq δy Qy Db Oy Oy Dp a QQ Qγ Qy δý gg QΥ qq QΥ

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                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Cole, Susan P.C.
APPLICANT: Deeley, Roger G.
TITLE OF INVENTION: METHODS FOR IDENTIFYING
TITLE OF INVENTION: MULTIDRUG RESISTANT TUMOR CELLS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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60 State Street, suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,109A
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APPLICATION NUMBER: 07/966,923
FILING DATE: 27-0cm-1992
APPLICATION NUMBER: 08/029,340
FILING DATE: 8-MAR-1993
APPLICATION NUMBER: 08/141,893
FILING DATE: 26-0cm-1993
APPLICATION NUMBER: 08/407,207
FILING DATE: 20-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/08462109A Patent No. 5882875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: DeConti, Giulio A. Jr. REGISTRATION NUMBER: 31,503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (617) 227-5941 INFORMATION FOR SEQ ID NO:
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Best Local Similarity 55.4
Matches 2516; Conservative
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Boston
STATE: Massachusetts
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CLASSIFICATION: 435
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US-08-462-109A-5
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                                                                                                                          98 GAACAGGGGTCTGGGTACCCCCATGTACCTCTGGGTCCTTGGTCCCATCTACCTCC
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                                        49 TCTGGGACTGGAATGTCACATGGCACACCAGCACTTACCAAGTGCTTTCAGA
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38 TCTGGAACCAGACAGAGCCTGAACCTGCCGCCACCAGCCTGAGCCTGTGTGCTTCCTGA
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1138	1198	1258 1308	1318	1368	1378	1438	49	1548	1558	61	1668	1675		1788	79		1855 1908	91	9	1975 2025	2035	2095	14	2155	2205	2215
9 CCTGCCTGCAAAGGCTGTTTGAGCAGCAGAACATGTACAGGCTCAAGGTGCCGCAGATGA	9 GGTIGCGGTCGCCATCACTGGCCTGGTACAGAAAGGTCCTGGCTCTGTCCAGCGGCT 	9 CCAGAAAGGCCAGTGCGGTGGGTGGGTCAATCTGGTGTCCGTGGACGTGCAGGCGCC	9 TGACCGAGAGCGTCCTCTACCTCAACGGGCTGTGGCTGCCTCTCGTCTGGATCGTGTCT	o.	9 GCTTCGTCTATCTCTGGCAGCTCCTGGGGCCCTCCGCCTCACTGCCATCGCTGTCTTCC	9 TGAGCCTCCTCCTCTGAATTTCTTCATCTCCAAGAAAAGGAACCACCATCAGGAGGAGC 1			9 CCATCAAGTICCAIGGCAGGGAGCCTTICTGGACAGAGTCCTGGGCATCCGAGGCC	AGGAGCTGGGCGCCTTGCGGACCTCCGCCTCTTCTCTGTGTCGCTGTGTCCTTTCC		AAGTGTCTACATTTCTGGTCGCACTGGTGGTGTTTGCTGTCCACACTCTGGTGGCCG		GAAATATCCTAGATGCAAAGAAGCCTTTGTGTCCTAGCCTGTTCAATATCTTGCACG	* AGGCCCAGGCTTTCCTGCCTTCTCCATCCATCCTCGTCCAGGCCGGGTGTCTTG		ACCGTCTGGTCACCTTCCTCTGCAGGAGAGAGTTGACCCTGGTGTCGTAGACTCAAGTT	CCTCTGGAAGGGCTGCCGGGAAGGATTGCATCACCATACACAGTGCCACCTTCGCCTGGT		CCCAGGAAAGCCTCCCTGCCTCCAGAATAAACCTCAGGTGCCCCAGGGCTGTCTGC	TGGCTGTTGTCGGTCCAGTGGGGCAGGGAAGTCCTCCCTGCTGTCGCCCCTCCTTGGGG			AGGCCTGGGTGCAGAACACCTCTGTGGTAGAATGTGTGTG		CACCCTGGCTGGAGAGAGTACTAGAAGCCTGTGCCCTGCAGCCAGATGTGGACAGCTTCC
107	1139	1199	1259		1319	1379	1439	1489	1499	1559	1609	1619		1729	1736	0 0	1796	1856	, ,	1916 1966	1976 2026	2036	2086	2096	2146	2156
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2275 2325 2335 2385 2445 2455 2515 2565 2625 2685 2745 CCCTGGCGGCCCTGGATGCCCACGTTGGCCAGCATGTCTTCAACCAGGTCATTGGGCCTG 2395 2505 2617 2677 2737 2908 2985 3045 ----GATC 2557 2805 2788 2865 2848 2962 ACGCCTTTGGACTCCTGGAGGTCAGCTGGTGGCAGTGGCTACCCCACTGGCCACTG 3265 3205 CAGTGGGGACCGCACAGAGATCGGTGAGAGGGTGTGAGACCTGTCAGGGGGCCAGAAGC CACTCTTCCTCTTCCTCTGCCAGCAGGCGTCCTTCTGCCGGGGGTACTGGCTGAGCC AAGCCAGACAGCCAGGAGATAGAGGAGAAAGGAGAACCTGGGACCAGCACCAAGG 2618 ACCCCAGAGGCACCTCTGCAGGCGAGGCCCGAGCTTAGACGCGAGAGGTCCATCAAGT CT-----GACAGGCAGGATGGCCAGGAAAGGACAGCATCCAATACGGCAGGG CTGGAGCTAAGGAGGAGGCGGAGGCTAATGGAAGCAGACAAGGCCCAGACACGGCAGG 2926 GTATCTTCCTTTTCCTGTGCAACCATGTATCTGCACTGGCCTCTAACTATTGGCTGAGCC CTGAGGGAATCCACACTTCAATTGGGGAGCAGGGCATGAATCTCTCCGGAGGCCAGAAGC AGCGGCTGAGCCTGGCCCGGGCTGTATACAGAAAGGCAGCTGTGTACCTGCTGGATGACC AGGCTGATTGGATCATAGTGCTGGCAAATGGGGCCATCGCAGAGATGGGTTCCTACCAGG 2686 AAAATGGGATGCTGGTGACAGACACGTAGGAAAGCACCTGCAGAGGCATCTCAGCAACT TGAAGGCCACAGTGCACCTGGCCTACCTGCGTGCCGTGGGCACCCCCCTCTGCCTCTACG TGTGGGCGGACGACCCTGCAGTAGG---TGGGCAGCAGAGCGAGGCAGCCCTGCGTGGCG TGCTCCTAGGTGGGGCCCCGGGCATCCAGGTTGCTCTTCCAGAGGCTCCTGTGGGATGTGG GGATCTTCGGGCTCCTCGGCTGTCTCCAAGCCATTGGGCTGTTTGCCTCCATGGCTGCGG TGCGATCTCCCATCAGCTTCTTTGAGCGGACACCCATTGGTCACCTGCTAAACCGCTTCT CCAAGGAGACAGACACGGTTGACGTGGACATTCCAGACAAACTCCGGTCCCTGCTGATGT AGCTTCTGCAGAGGGGGCCCTCGTGTGTCTTCTG-------2326 2396 2506 2206 2216 2266 2276 2336 2386 2456 2516 2558 2806 2789 2849 2966 2678 2746 2738 2866 2909 2986 3046 3026 3106 3166 3146 3206 3086 3226 δ g οy qq Óγ Dp οy QQ οy g òγ qq Qy QQ qq ŏ δ Q δ Dβ QQ QQ ŏ δ Oγ g Qγ g Q qq δ g Qγ g ά

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3286 CACTCTTCAGTGTCATTGGAGCTGTCATCATCATCCTACTGGCCACGCCCATTGCCGCAG 3345
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                                                                                  GGTGGCTTGCGGCCCAATGTGGAGCTCCTGGGGAATGGCCTGGTGTTTGCAGCCGCCACGT
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                                                                       AGACGTTCCAGGGCAGCACAGTGGTCCGGGCATTCCGAACCCAGGCCCCCTTTGTGGCGTC
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                      TGGCCATCCTGCCACTGTTTCTCCTCTACGCTGGGTTTCAGAGCCTGTATGTGGTTAGCT
                                             3346 TCATCATCCCACCCTTGGGTCTGGTTTACTTCTTTGTGCAGAGGTTCTATGTGGCTTCCT
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                      4426 AAGACTGTACTGTGCTCACGATTGCTCATCGCCTTAACACCATAATGGACTACACACGGG
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4346 CACAGTGCACTGTGCTGCCCCATTGCCCACCGCCTGCGCTCCGTGATGGACTGTGCCCGGG
                                                                                      TTCTGGTCATGGACAAGGGGCAGGTGGCAGAGAGCGGCAGCCCGGCCCAGCTGCCTGGCCC
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                                                                                                                                                                           4466 AGAAGGGCCTGTTTTACAGACTGGCCCAGGAGTCAGGCCTGGT 4508
                                                                                                                                                                                               TITLE OF INVENTION: METHODS FOR CONFERRING MULTIDRUG
TITLE OF INVENTION: RESISTANCE ON A CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/460,907B
FILING DATE: 05-JUN-1995
CLASSIFICAMION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/966,923
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 545-6853
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 5889 base pairs
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N: 424
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/08460907B
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APPLICATION NUMBER: 08/029,340
FILING DATE: 8-MAR-1993
CLASSIFICATION: 424
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PREIGHTON NUMBER: 08/141,893
FILING DATE: 26-0CT-1993
CLASSIFICATION: 424
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FILING DATE: 20-MAR-1995
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NAME: Steeg, Carol Miernicki
REGISTRATION NUMBER: 39,539
                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Deeley, Roger G.
APPLICANT: Cole, Susan P.C.
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
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STATE: Ontario
COUNTRY: CANADA
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Thu Dec

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2155 2275 2325 2335 2395 2515 2625 2865 2557 2685 2805 2965 3145 2677 2925 3085 3205 2206 AAAATTACTACAAGGCAGTTATGGAAGCCTGTGCCCTTCTTCCAGATTTGGAAATCCTGC CCCTGGCGCCCTGGATGCCCACGTTGGCCAGCATGTCTTCAACCAGGTCATTGGGCCTG TGGGCCTACTGAAGAACAAGACACGGATCCTGGTCACCCATGGTATCAGCTACCTGCCCC -----GATC AGCTGCTAGACCGGGATGGGGCCTTCGCTGAGTTCCTGCGCACCTATGCCAACGCTGAGC CACTCTTCCTCTCTCTCGCCAGCAAGTGGCCTCCTTCTGCCGGGGCTACTGGCTGAGCC CACCCTGGCTGGAGAGAGTACTAGAAGCCTGTGCCCTGCAGCCAGATGTGGACAGCTTCC CTGAGGGAATCCACACTTCAATTGGGGAGCAGGGCATGAATCTCTCCGGAGGCCCAGAAGC AGCGGCTGAGCCTGGCCCGGGCTGTATACAGAAAGGCAGCTGTGTACCTGCTGGATGACC AGGCTGATTGGATCATAGTGCTGGCAAATGGGGCCCATCGCAGAGATGGGTTCCTACCAGG **AAGCCAGACAGCCAGGAGATAGAGGAGAAGGAGAAACAGAACCTGGGACCAGCACCAAGG** AGGACCTGGCCTCGGAGGATGACAGTGTCAGTGGTTCAGGGAAGGAGTCAAAGCCGGTGG CT-----GACAGGCAGGATGGCCAGGAAAGGACAGCATCCAATACGGCAGGG TGAAGGCCACAGTGCACCTGGCCTACCTGCGTGCCGTGGGCACCCCCCTCTGCCTCTACG GTATCTTCCTTTTCCTGTGCAACCATGTATCTGCACTGGCCTCTAACTATTGGCTGAGCC GEGETATEGGGCCTTGGCATCTTGCAAGGTGCAGCAATATTTGGCTACTCCATGGCTG 3026 recretaggegeccegecarccaggreererrecagaegerecretagg TGTCCATCGGGGGCATCTTTGCCTCCGTCGCTTGCACCTGGACCTGCTATACAATGTTC CCAAGGAGACACACGCTTGACGTGGACATTCCAGACAAACTCCGGTCCCTGCTGATGT ACCCCAGAGGCACCTCTGCAGGCAGGAGGCCCGAGCTTAGACGCGAGAGGTCCATCAAGT AAAATGGGATGCTGGTGACAGACCCGTAGGAAAGCACCTGCAGAGGCATCTCAGCAACT TGTGGGCGGACGACCCTGCAGTAGG - - - TGGGCAGCAGCCAGGCAGCCCTGCGTGGCG GGATCTTCGGGCTCCTCGGCTGTCTCCAAGCCATTGGGCTGTTTGCCTCCATGGCTGCGG TTCGATCACCCATGAGTTTCTTCGAGCGTACACCCAGTGGGAACCTAGTGAACCGATTCT AGCTTCTGCAGAGGGGGGCCCTCGTGTGTCTCTG----2146 2156 2216 2266 2276 2326 2336 2386 2396 2446 2456 2506 2516 2566 2558 2626 2618 2686 2678 2806 2789 2866 2926 2986 3146 2746 2738 3106 2096 2849 3046 3086 3166 2909 2966 음 ò QQ Qγ g ò g δ g ò g ŏ Q Ω a οy g δ g οý 셤 õ g ò g δ g g g qq g ő õ ò õ õ

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Human ATP-binding Human ATP-binding Rat sequence diffe Mouse ATP-binding Human ATP binding

Prostate cancer-as Human MRP variant Human multidrug re Human MDR variant

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Multidrug resistan Human MRP variant

Multidrug resistan cDNA encoding mult

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ALIGNMENTS

RESULT 1

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cDNA encoding a human MPR-related ABC transporter designated MOAT-E.
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                                                                                                               Human; MPR-related ABC transporter; MOAT protein; MOAT-E;
MOAT mediated transport; anticancer drug sensitivity;
transporter mediated cellular efflux; anticancer; ss.
                                                                                                                                                                                    Location/Qualifiers
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            BP:
          AAZ30081 standard; cDNA; 4509
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                                                               (first entry)
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                                                              26-JAN-2000
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                                    AAZ30081;
AAZ30081
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Human ATP-binding

AAD16231 AAD16256 AAD16257 AAD16258 AAD16260 AAD16261 AAD16262

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The present sequence encodes a human MPR-related ABC transporter (MOAT) protein, designated MOAT-E. The protein comprises a multi-domain structure including a tandem repeat of nucleotide binding folds appended C-terminal to a hydrophobic domain, having Walker A and B ATP binding sites and several potential membrane spanning domains. The MOAT nucleic acids are useful for screening a test compound for inhibition of MOAT mediated transport, indicated by restoration of anticancer drug sensitivity, which in turn causes a reduction of transporter mediated cellular efflux of anticancer agents. MOAT DNA or RNA may be used as probes to detect the presence or expression of genes encoding MOAT proteins. Anti-MOAT antibodies are useful for detecting and quantitating
                                                                                                                                                                                                          for anti-cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4509 BP; 833 A; 1385 C; 1353 G; 938 T; 0 other;
                                                                                                                                                                                                          New transporter gene useful for screening
                                                                                                                                                                                                                                                Claim 34; Page 143-144; 153pp; English
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                 98US-0079759.
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03-AUG-1998;
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 DB 20; Length 4509;
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                Indels
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         Pred. No. 0;
0; Mismatches
100.0%; Score 4509; 100.0%; Pred. No. 0;
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Screening presence of Pseudoxanthoma elasticum mutation useful for identifying homozygotes, compound heterozygotes or carriers involves determining presence of mutation in MRP6 (ABCC6) nucleic acid

Example 2; Page 130-137; 163pp; English.

treating Pseudoxanthoma elasticum (PKE) and PKE associated physiological dysfunctions. The invention is useful for screening for the presence of a PKE mutation. Mutations associated with PKE maps to the ArP-binding cassette transporter ABCC6 (MRP6) with PKE maps to the ArP-binding cassette transporter ABCC6 (MRP6) and presence of protein 6) gene locus on chromosome 16. ABCC6 (MRP6) gene encodes a 165 protein 10 forated in the plasma membrane containing 17 membrane. Spanning helices grouped into three transmembrane domains. PKE is inherited as an autosomal recessive phenotype or appears as a sporadic clastic fibers is a heritable disorder characterised by mineralisation of elastic fibers in skin, arteries and the retina, that result in dermal lesions with associated laxity and loss of elasticity, arterial macular degeneration. The method is useful for screening a population of individuals in order to identify individuals with one or more PKE individuals in order to identify individuals with appropriate genetic counselling in view of the PKE status. The methods are useful for identifying homozygotes, compound heterozygotes or carriers and thus are useful in the area of genetic testing, carrier detection and prenatal dagnanosis. The present CDNA sequence encodes human ATP-binding cassette (ABC) transporter, ABCC6 (MRP6) protein belonging to sub-family "C". Since ABCC6 protein is involved in drug-resistance it is also called Multidrug Resistance associated protein 6 (MRP6). The invention relates to methods and compositions for diagnosing and

Sequence 4512 BP; 835 A; 1380 C; 1354 G; 943 T; 0 other;

CCTGCCGCCACCAGCCTGCTGAGCCTGTGCTTCCTGAGAACAGCAGGGTCTGGGTACCC 120 360 480 480 240 300 420 420 540 540 CCCATGTACCTCTGGGTCCTTGGTCCCATCTACCTCCTCTTCATCCACCACCATGGCCGG 180 GCCCCAGAATTCCTCATTCATCCTACTGTGTGGCTCACCACGATGAGCTTCGCAGTGTTC 360 009 009 099 999 720 780 Gaps 9 GTCCTGTGTACCTCCAGCGTGGCTGTCGTTTTGGAAAATCCAACAGGGAACGCCTGAG GGCTACCTCCGGATGTCCCCCACTCTTCAAAGCCAAGATGGTGCTTGGATTCGCCCTCATA CTGATTCACACCGAGAGAAAAAGGGAGTCCAGTCATCTGGAGTGCTGTTTGGTTACTGG CAGAGCGACCCTGTCCGCCACCTGTCCACCTATGCCTGTCTCTGGTGGTGGCACAG AGAGAAAACTCCTCAGAAGAACTTGTTTCCCGGCTTGAAAAGGAGTGGATGAGGAACCGC TITGTGCTGTCCTGCCTGGCGGATCAACCCCCTTCTTCCCTGAAGACCCCCAGCAGTCT 601 AACCCCTGTCCAGAGACTGGGGCAGCCTTCCCCTCCAAAGCCACGTTCTGGTGGGTTTCT GCCCTGGTCTGGAGGGGATACAGGAGGCCACTGAGACCAAAAGACCTCTGGTCGCTTGGG AAGGCCATCTGGCAGGTGTTCCATTCTACCTTCCTCGGGACCCTCAGCCTCATCATC Length 4512; ; 0 6; Indels DB 22; Score 4499.4; 0; Mismatches Pred. No. 99.88; 99.98; Query Match 99.8 Best Local Similarity 99.9 Matches 4503; Conservative 181 241 121 121 181 241 361 481 541 601 661 301 301 361 181 541 661 721 721 781 841 901 961 781 841 901 196 qq ò a Qγ ōλ g Dp qq ò δ ò g δλ g Qγ qq g g 셤 Óγ Ω ò ŏ g ò a δ a δ Db ò Dp ò 셤

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Human, prenatal diagnosis, dermal lesion, cardiovascular disease, MRP6, whilidorg Resistance-associated protein 6; macular degeneration, ABCC6; ATP-binding cassette transporter; arterial insufficiency; chromosome 16; Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage.
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                          CAGGCCATGCTCGGGAGCTGGTTTGCACAGTGCACTGTGCTGCCCATTGCCCACCGCCTG
                                                                                                                                                                                                            GGCAGCCCGGCCCAGCTGCCCAGAAGGGCCTGTTTTACAGACTGGCCCAGGAGTCA
                                                                                                      CGCTCCGTGATGGACTGTGCCCGGGTTCTGGTCATGGACAAGGGGCCAGGTGGCAGAGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human ATP-binding cassette transporter ABCC6 (MRP6) mutant cDNA
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comming helices grouped into three transmembrane domains. PXE is inherited as an autosomal recessive phenotype or appears as a sporadic phenotype. PXE is a heritable disorder characterised by mineralisation of elastic fibers in skin, arteries and the retina, that result in dermal lesions with associated laxity and loss of elasticity, arterial lemant adsequention. The method is useful for screening a population of macular degeneration. The method is useful for screening a population of individuals in order to identify individuals with one or more PXE associated MRPG allels who are then provided with appropriate genetic counselling in view of the PXE status. The methods are useful for identifying homozygotes, compound heterozygotes or carriers and thus are useful in the area of genetic testing, carrier detection and prenatal diagnosis. The present sequence is human ATP-binding cassette (ABC) transporter, ABCC6 (MRP6) mutant cDNA. This mutant cDNA results in an amino acid change from Arg to Pro at position 1114 of MRP6 protein.

Note: The present sequence is not shown in the specification but is derived from human ATP-binding cassette transporter ABCC6 (MRP6) cDNA (SED ID NO: 2) shown in page 130-137 of the specification (AAD16231). 55555555555555555555558888

Sequence 4512 BP; 835 A; 1381 C; 1353 G; 943 T; 0 other;

; 360 360 61 CCTGCCGCCACCAGCCTGCTGAGCCTGTTCCTGAGAACAGCAGGGGTCTGGGTACCC 120 180 180 420 420 480 540 540 900 960 9 120 GGCTACCTCCGGATGTCCCCACTCTTCAAAGCCAAGATGGTGCTTGGATTCGCCCTCATA 240 GTCCTGTGTACCTCCAGCGTGGCTGTCGCTTTTGGAAAATCCAACAGGGAACGCCTGAG 300 480 900 GGCCTGGTCTGGAGGGGATACAGGAGGCCACTGAGACCAAAAGACCTCTGGTCGCTTGGG 720 0; Gaps 121 CCCATGIACCTCTGGGTCCTTGGTCCATGTACCTCTTTATCATCCACCACCATGGCCGG GCCCCAGAATTCCTCATTCATCCTACTGTGTGGCTCACCACGATGAGCTTCGCAGTGTTC GCCCCAGAATTCCTCATTCATCCTACTGTGTGGCTCACCACGATGAGCTTCGCAGTGTTC CITCICIGCTITGTCITGCCAGCTACCAACGCTGCCCAGCAGGCCTCCGGAGCGGCCTTC CCTGCCGCCACCAGCCTGCTGAGCCTGTGCTTCCTGAGAACAGCAGGGGTCTGGGTACCC CCCATGTACCTCTGGGTCCTTGGTCCCATCTACCTCCTTCTTCATCCACCACCATGGCCGG CTGATTCACACCGAGAGAAAAAGGGAGTCCAGTCATCTGGAGTGCTGTTTGGTTACTGG CTGATTCACACCGAGAGAAAAAGGGAGTCCAGTCATCTGGAGTGCTGTTTGGTTACTGG CTTCTCTGCTTTGTCTTGCCAGCTACCAACGCTGCCCAGCAGGCCTCCGGAGCGGGCTTC CAGAGCGACCCTGTCCGCCACCTGTCCACCTACCTATGCCTGTCTCTGGTGGTGGCACAG TITGIGCTGTCCTGCCTGCGGGATCAACCCCCCTTCTTCCCTGAAGACCCCCAGCAGTCT AACCCCTGTCCAGAGACTGGGGCAGCCTTCCCCTCCAAAGCCACGTTCTGGTGGGTTTCT Score 4497.8; DB 22; Length 4512; Pred. No. 0; 0; Mismatches 7; Indels 0; 99.8%; Best Local Similarity 99.8 Matches 4502; Conservative Query Match 121 181 181 241 301 361 421 181 481 541 541 601 601 661 661 241 301 361 421 g qq ŏ ò g qq g g ò qq qq δ δ à g Qγ ò g ò ò Q Ω g

AACCGC 780	CATG 84        CATG 84	GCTG 90  -	ATCATC 960         ATCATC 960	ATTGGT 1020         ATTGGT 1020	AGCC 108	GAGG 11       GAGG 11	CTCC 120       CTCC 120	GCTG 126       GCTG 126	crec 1	CCTG 138	3CAA 14       3CAA 14	GACC 150        GACC 150	CCAG 156       CCAG 156	CCAA 16	3AAT 168      3AAT 168	AAGGCC 1740           AAGGCC 1740	CCGT 180	TCCTCT 1860
BAGTGGATGAGG	AAAGGCGGCAGTIIIIIIIIIIIIIIIIIIIIIIIIIIII	AGTGGCGCCCA 	ACCTCAGCCTC 	FTCCFGGAGTTT 	TGATGTTCCTC 	AAGGTGCCGCAGA           AAGGTGCTGCAGA	SCTCTGTCCAGO	stgacgtgcag 	STCTGGATCGTG	SCCATCGCTGTCT' 	DACCATCAGGAGG 	CTCAGGAACTCG 	TEGGCATCCGA 	rcecrestercc 	ACTCTGGTGGCC	ACATCCTCAACAACAACAACAACAACAACAACAACAACAA	SGGTGTCCTTT 	STAGACTCAAGT'
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	SCCCGAGGCACI	CAGAGACCGAGG	ATCTGGCAGGTGT 	STCTTCAGGTTCAGGTTCAGGTTCAGGTTCA	TCCCAAGCCTCCAGCCTGGAAGGCTACCTCCTCGCCGTGCTGATGTTCCTCTCTCT	AAACGCTGTTTC	CGGCCATCACTC	SCCAGTGCGGTG	AGCGTCCTCTACO	ATCTCTGGCAGG	TCCCTCTGAAT	AGAAGGACTCAC 	TCCATGGCTGG	GCGCCTTGCGGA 	CATTTCTGGTCC	atgcagagaaa 	TCCTGCCCTTCT 	ACCTTCCTCTGC
AGAGAAP	AGTGCAG            AGTGCAG	AAGGCTC            AAGGCTC	AAGGCCP             AAGGCCP	AGTGATG 	GATCCCP          GATCCCP	TGCCTGC         TGCCTGC	TTGCGGT          TTGCGGT	AGAAAGG 	ACCGAGA 	TTCGTCT	AGCCTCC 	ATGAGGC 	ATCAAGI         ATCAAGI	GAGCTGG         GAGCTGG	GTGTCTA           GTGTCTA	GCTATGA 	a a	CTGGTCA
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2881 rccrcccessc	2941 CAGACGCAGGCAGCC 	3001 GGGCTGTTTGCCTCC 	3061 TTCCAGAGGCTCCTG 	3121	3181	3241	3301	3361	3421 CGAACCCAGGCCCCC 	3481	3541	3601	3661	3721	3781	3841		3961 GGTGGGATCTGGATCT 
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	1861 GGAAGCGCTGCCGGGAAGGATTGCATCACCATACACAGTGCCACCTTCGCCTGGTCCCAG 19	1921 GAAAGCCTCCCTGCTCCACAGAATAAACCTCACGGTGCCCCAGGGCTGTCTGCTGGCT 19	1981 GTGTCGGTCCAGTGGGGGCAGGAAGTCCTCCTGCTGTCCGCCCTCCTTGGGGAGCTG 20	Y 2041 TCAAAGGTGGAGGGTTCGTGAGCATCGAGGGTGCTGTGGCCTACGTGCCCCCAGGAGGC 2100	y 2101 TGGGTGCAGAACACCTCTGTGGTAGAGAATGTGTGCTTCGGGCAGGAGCTGGACCCACCC	y 2161 TGGCTGGAGAGAGTACTAGAAGCCTGTGCCGGCCAGACGGACTGGACAGCTTCCCTGAG 2220	# 2221 GGAATCCACACTICAATIGGGGAGCAGGCATGAATCTCTCCGGAGGCCAGAAGCAGCGG 2280	y 2281 CTGAGCCTGGCCCGGCTGTATACAGAAAGGCAGCTGTGTACCTGCTGGATGACCCCTG 2340	y         2341         GCGCCCTGGATGCCCACGTTGGCCACGTGTCTTCAACCAGGTCATTGGCCTGGTGGG         2400           3341         GCGCCCTGGATGCCCACGTTGGCCAGGTTTCAACCAGGTCATTGGCCTGGTGGG         2400	2401 CTACTCCAGGGAACAACACGGATTCTCGTGACGCACGCAC	/ 2461 GATTGGATCATAGTGCTGGCAAATGGGGCCATCGCAGAGATGGGTTCCTACCAGGAGCTT 2520	7 2521 CTGCAGAGGAAGGGGCCCTCGTGTGTCTTCTGGATCAAGCCAGACAGCCAGGAGATAGA 2580 111111111111111111111111111111111111	7 2581 GGAGAAGGAGAAACAGAACCTGGGACCAGCACCAAGGACCCCAGAGGCACCTCTGCAGGC 2640	7 2641 AGGAGCCCGAGCTTAGACGCGAGAGGTCCATCAAGTCAGTC	7 2701 ACTTCAGAAGCCCAGACAGAGGTTCCTCTGGATGACCCTGACAGGGCAGGATGGCCAGCA 2760	y 2761 GGAAAGGACAGCATACAGCAGGGTGAAGGCCACAGTGCACCTGGCCTACCTGCGT 2820 	y 2821 GCCGTGGGCACCCCCTCTGCCTCTACCTCTTCCTCTGCCAGCAAGTGGCC 2880	Y 2881 TCCTTCTGCCGGGCCTACTGGCTGAGCCTGTGGGCGGACGACCTGCAGTAGGTGGGCAG 2940
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CTACTGGCTGAGCCTGTGGGCGGACGACCTGCAGTAGGTGGGCAG 2940 GTCCTTCAAGATCCACGCAGGAGAGAAGGTGGGCATCGTTGGCAGG GTCCTCCCTGGCCAGTGGGCTGCTGCGCCTCCAGGAGGCAGCTGAG CGACGGGTCCCCATTGCCCACGTGGGGCTGCACACACACTGCGCTCC CATGGCTGCGGTGCTCCTAGGTGGGGCCCGGGCCATCCAGGTTGCTC GTGGGATGTGGTGCGATCTCCCATCAGCTTCTTTGAGCGGACACCC **AAACCGCTTCTCCAAGGAGACAGACACGGTTGACGTGGACATTCCA** CCTGCTGATGTACGCCTTTGGACTCCTGGAGGTCAGCCTGGTGGTG ACTGGCCACTGTGGCCATCCTGCCACTGTTTCTCCTCTACGCTGGG CTTTGTGGCTCAGAACAATGCTCGCGTAGATGAAAGCCAGAGGATC GGTGGCTGACAGGTGGCTTGCGGCCCAATGTGGAGCTCCTGGGGAAT CGAGTICCGGGACTITGGGCTAAGATGCCGACCTGAGCTCCCGCTG STCCTTCAAGATCCACGCAGGAGAGAAGGTGGGCATCGTTGGCAGG GTCCTCCCTGGCCAGTGGGCTGCTGCGGCTCCAGGAGGCAGCTGAG CGACGGGGTCCCCATTGCCCACGTGGGGCTGCACACACTGCGCTCC CCTGCGTGGCGGATCTTCGGGCTCTCGGCTGTCTCCAAGCCATT AGCCGCCACGTGTGCTGTGTGAAAGCCCACCTCAGTGCTGGC GGCTCCCTGGAGGCTGCCCACATGTGCAGCTCAGCCCCCCTGGCCT

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                                                                                                                                                       4380
                                                                                                                                                                                                                Human ATP-binding cassette transporter ABCC6 (MRP6) mutant cDNA #2.

      4381
      CGCTCCGTGATGGACTGTGCCCGGGTTCTGGTCATGGACAAGGGGCAGGTGGCAGAGAGC

      4381
      CGCTCCGTGATGGACTGTGCCCGGGTTCTGGTCATGGACAAGGGGCAGGTGGCAGAGAGC

             4141 AAAGCCTTGGTGGCCAGCCTGCCCGGCCAGCTGCAGTGTGTGCTGACCGAGGCGAG
                                                                                             GACCTGAGCGTGGGCCAGAAACAGCTCCTGTGTCTGGCACGTGCCCTTCTCCGGAAGACC
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treating Pseudoxanthoma elasticum (PXE) and PXE associated physiological dysfunctions. The invention is useful for screening for the presence of a PXE mutation. Mutations associated with PXE maps to the APP-binding cassette transporter ABCC6 (MRP6) with PXE maps to the APP-binding cassette transporter ABCC6 (MRP6) with PXE maps to the APP-binding cassette transporter ABCC6 (MRP6) gene encodes a 165 protein 6) gene locus on chromosome 16. ABCC6 (MRP6) gene encodes a 165 concerned in the plasma membrane containing 17 membrane. Spanning helices grouped into three transmembrane domains. PXE is inherited as an autosomal recessive phenotype or appears as a sporadic characterised by mineralisation of elastic fibers in skin, arteries and the retina, that result in dermal consular degeneration. The method is of elasticity, arterial consular degeneration. The method is useful for screening a population of individuals in order to identify individuals with one or more PXE individuals. In order to identify individuals with appropriate genetic counselling in view of the PXE status. The methods are useful for deartifying homozygotes, compound heterozygotes or carriers and thus are cuseful in the area of genetic testing, carrier detection and prenatal classporter. ABCC6 (MRP6) mutant colm. This mutant colm assette (ABC) cransporter. ABCC6 (MRP6) mutant colm the specification but is amino acid change from Ary to Gln at position 1138 of MRP6 protein. Note: The present sequence is not shown in the specification but is derived from human ATP-binding cassette transporter ABCC6 (MRP6) such and present sequence is not shown in the specification but is contracted from human ATP-binding cassette transporter ABCC6 (MRP6) contained to the present sequence is not shown in the specification but is sequence.
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Pred. No. 0;
                                                                                                                                                                                       presence of Pseudoxanthoma elasticum mutation useful
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Matches 4502; Conservative
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Human, prenatal diagnosis, dermal lesion, cardiovascular disease; MRP6. Multidrug Resistance-associated protein 6; macular degeneration, ABCC6, ATP-binding cassette transporter; arterial insufficiency; chromosome 16; Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage;
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The invention relates to methods and compositions for diagnosing and treating Pseudoxanthoma elasticum (PXE) and PXE associated physiological dysfunctions. The invention is useful for screening for the presence of a PXE mutation. Mutations associated with PXE maps to the ATP-binding cassette transporter ABCC6 (MRP6-Multidrug Resistance associated cassette transporter ABCC6 (MRP6-Multidrug Resistance associated cassette transporter ABCC6 (MRP6-Multidrug Resistance associated codes a 165 cassette transporter ABCC6 (MRP6-Multidrug Resistance associated codes a 165 cassenting helices grouped into three transmembrane domains. PXE is therited as an autosomal recessive phenotype or appears as a sporadic phenotype. PXE is a heritable disorder characterised by mineralisation of elastic fibers in skin, arteries and the retina, that result in dermal cassociated laxity and loss of elasticity, arterial insulficiency, cardiovascular disease and retinal haemorrhages leading to macular degeneration. The method is useful for screening a population of individuals in order to identify individuals with one or more PXE associated MRP6 alleles who are then provided with appropriate genetic counselling in view of the PXE status. The methods are useful for counselling in view of the PXE status. The methods are useful for custing the area of genetic testing, carrier detection and prenatal diagnosis. The present sequence is human APP-binding cassette (ABC) transportar, ABCC6 (MRP6) mutant cDNA. This mutant cDNA results in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cassette transporter ABCC6 (MRP6) cDNA 30-137 of the specification
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Pred. No. 0;
0; Mismatches 7; Indels 0:
                                                                                                                                                                                             truncated
                                                                                                                                     (MRP6) mutant protein"
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(SED ID NO: 2] shown in page 130-137 of the specification
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treating Pseudoxanthoma elasticum (PXE) and PXE associated physiological dysfunctions. The invention is useful for screening for the presence of a PXE mutation. Mutation is useful for screening for the presence of associated transporter ABCC6 (MRP6-Multidrug Resistance associated physiological cassette transporter ABCC6 (MRP6-Multidrug Resistance associated protein-6) gene locus on chromosome 16. ABCC6 (MRP6) gene encodes a 165 protein-6) gene locus on chromosome 16. ABCC6 (MRP6) gene encodes a 165 protein located in the plasma membrane containing 17 membrane-spanning helices grouped into three transmembrane domains. PXE is therrited as an autosomal recessive phenotype or appears as a sporadic phenotype. PXE is a heritable disorder characterised by mineralisation of clastic fibers in skin, arterises and the retina, that result in dermal lesions with associated laxity and loss of elasticity, arterial lesions with associated laxity and loss of elasticity, arterial concluded acqueration. The method is useful for screening a population of individuals in order to identify individuals with one or more PXE associated MRP6 alleles who are then provided with appropriate genetic counselling in view of the PXE status. The methods are useful for lefentifying homozygotes, compound heterozygotes or carriers and thus are
                                                                                                                                                                                                                                                                                                               Human, prenatal diagnosis, dermal lesion; cardiovascular disease, MRP6, Multidrug Resistance-associated protein 6; macular degeneration; ABCC6, ATP-binding cassette transporter; arterial insufficiency; chromosome 16, Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage;
4441 GGCAGCCCGGCCCAGCTGCTGGCCCAAAGGCCCTGTTTTACAGACTGGCCCAGGAGTCA 4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      identifying homozygotes, compound heterozygotes or carriers involves determining presence of mutation in MRP6 (ABCC6) nucleic acid
                                                                                                                                                                                                                                                                              Human ATP-binding cassette transporter ABCC6 (MRP6) mutant cDNA #5.
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useful in the area of genetic testing, carrier detection and prenatal diagnosis. The present sequence is human ATP-binding cassette (ABC) transporter, ABCC6 (MRP6) mutant cDNA. This mutant cDNA results in an amino acid change from Val to Phe at position 1298 of MRP6 protein. Note: The present sequence is not shown in the specification but is derived from human ATP-binding cassette transporter ABCC6 (MRP6) cDNA (SED ID NO: 2] shown in page 130-137 of the specification (AAD16231). 8

ö Gaps Length 4512; ; Indels other; 22; 0 7; Ë DB 944 Score 4497.8; Pred. No. 0; 0; Mismatches .; Ö 835 A; 1380 C; 1353 ; 99.8%; ilarity 99.8%; Conservative Best Local Similarity Matches 4502; Conserv BP; Sequence 4512 Match Query

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TTGTCGGTCCAGTGGGGCAGGGAAGTCCTCCCTGCTGCCCCCTCTTGGGGAGCTG 2040 	GGAGGGGTTCGTGAGCATCGAGGGTGCTGGCCTACGTGCCCCAGGAGGCC 2100	TGCAGAACACCTCTGTGGTAGAGAATGTGTGCTTCGGGCAGGAGCTGGACCCACCC	GGAGAGAGTACTAGAAGCCTGTGCCCTGCAGCCAGATGTGGACAGCTTCCCTGAG 2220	CCACACTTCAATTGGGGAGCAGGGCATGATCTCCGGAGGCCAGAAGCAGCGG 2280	GGCCCGGGCTGTATACAGAAAGCAGCTGTGTACCTGCTGGATGACCCCCTG 2340 	GGATGCCCACGTTGGCCAGCATGTCTTCAACCAGGTCATTGGGCCTGGTGGG 2400 	GGGAACAACAGGATTCTCGTGACGCACTCCACATCCTGCCCCAGGCT 2460 	CATAGTGCTGGCAAATGGGGCCATCGCAGAGTTCCTACCAGGAGCTT 2520	CTGCAGAGGAAGGGGCCCTCGTGTGTTCTTCTGGATCAAGCCAGACAGCCAGGAGATAGA 2580 	GAGAAGGAGAAACAGAACCTGGGACCAAGGACCCCAGAGGCACCTCTGCAGGC 2640 	GAGGCCCGAGCTTAGACGCGAGAGGTCCATCAAGTCCCTGAGAAGGACCGTACC 2700 	CAGAAGCCCAGACAGAGGTTCCTGTGGATGACCCTGACAGGCGGGGTGGCCAGGA 2760 	GAAAGGACAGCATCCAATACGGCAGGGGAAGGCCACAGTGCACCTGGCCTACCGT 2820 	AACCCCCTCTGCCTCTACGCACTCTTCCTCTCTCTGCCAGCAAGTGGCC 2880	COGGGCTACTGGCTGAGCCTGTGGGCGGACGACCCTGCAGTAGGTGGGCAG 2940	SGCAGCCCTGCGTGGCGGATCTTCGGCTCCTCGCTGTCTCCAAGCCATT 3000	GCCTCCATGGCTGCGGTCCTAGGTGGGGCCCGGCATCCAGGTTGCTC 3060	SCTCCTGTGGGATGTGGCGATCTCCCATCAGCTTCTTTGAGCGGACACCC 3120
GTTGTCGGTCCAGTG 	TCAAAGGTGGAGGGG 	TGGGTGCAGAACACC	TGGCTGGAGAGAGTA 	GGAATCCACACTTCA	CTGAGCCTGGCCCGG	GCGCCCTGGATGCC	CTACTCCAGGGAACA 	GATTGGATCATAGTGC 	CTGCAGAGGAAGGGG 	GGAGAAGGAGAAACA( 	AGGAGGCCCGAGCTT/	ACTTCAGAAGCCCAGI	GGAAAGGACAGCATCC	GCCGTGGGCACCCCCCCCCCCCCCCCCCCCCCCCCCCCC	TCCTTCTGCCGGGGCTACTG	CAGACGCAGGCAGCCC	GGGCTGTTTGCCTCCA 	TTCCAGAGGCTCCTGTGG
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GACAAACTCCGGTCCCTGCTGATGTACGCCTTTGGACTCCTGGAGGTCAGCCTGGTGGTG GCAGTGGCTACCCCACTGGCCACTGTGGCCATCCTGCCACTGTTTCTCCTCTACGCTGGG GGCCTGGTGTTTGCAGCCGCCACGTGTGCTGTGCTGAGCAAAGCCCACCTCAGTGCTGGC GCTGTGCAGGGCGTGTCCTTCAAGATCCACGCAGGAGAAGGTGGGCATCGTTGGCAGG AAAGCCTTGGTGGCCAGCCTGCCGGCCAGCTGCAGTACAAGTGTGCTGACCGAGGCGAG CGCAACTGGACAGACCTAGAGAACAGCATCGTGTCAGTGGAGCGGATGCAGGACTATGCC TGGACGCCCAAGGAGGCTCCCTGGAGGCTGCCCACATGTGCAGCTCAGCCCCCCTGGCCT ACCEGEGCAGGGAAGTCCTCCCTGGCCAGTGGGCTGCTGCGGCTCCAGGAGGCAGCTGAG GACCTGCTGCAGGAGGACGAGGCTATCTGGGCAGCCCTGGAGACGGTGCAGCTC GGTGGGATCTGGATCGACGGGGTCCCCATTGCCCCACGTGGGGCTGCACACACTGCGCTCC ŏ g QY g δý qq Qγ QQ qq Óγ d ŏ Óγ . <del>Q</del> ολ Dβ Óγ qq δ qq qq QQ dd οy ò Óλ qq q g ò δ Q g δý ó

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Page -; 163pp; English
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                                                                                                                                                                                       identifying homozygotes, compound heterozygotes or carriers involves determining presence of mutation in MRP6 (ABCC6) nucleic acid
                                                                                                                                                                                                                                                                                                                                               Human ATP-binding cassette transporter ABCC6 (MRP6) mutant cDNA #6.
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4141 AAAGCCTTGGTGGCCAGCCTGCCCGGCCAGCTGCAGTACAAGTGTGTGACCGAGGCGAG
                                                                             CAGATCCTCATCCTGGACGACGAGGCTACTGCTGCCGTGGACCCTGGCACGCGGAGCTGCAGATG
                                                                                                                  CAGGCCATGCTCGGGAGCTGGTTTGCACAGTGCACTGTGCTGCTCATTGCCCACCGCCTG
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                  GACCTGAGCGTGGGCCAGAAACAGCTCCTGTGTCTGGCACGTGCCCTTCTCCGGAAGACC
                                      4201 GACCTGAGGGTGGGCCAGAAACAGCTCCTGTGTCTGGCAGGGGCCCTTCTCCGGGAAGACC
                                                         CAGATCCTCATCCTGGACGAGGCTACTGCTGCCGTGGACCCTGGCACGGAGCTGCAGATG
                                                                                               CAGGCCATGCTCGGGAGCTGGTTTGCACAGTGCACTGTGCTGCCCCATTGCCCACCGCCTG
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                                                                   "Human ABCC6 (MRP6) mutant protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99.8%; Score 4497.8; DB 22; Length 4512; 99.8%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4512 BP; 836 A; 1380 C; 1353 G; 943 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 99.8
Matches 4502; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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TCT 660      TCT 660	GGG 720       GG 720	CGC 780           	ATG 840      ATG 840	CTG 900     CTG 900	CATC 960   11   CATC 960	GGT 1020       GGT 1020	cc 1080 	(GG 1140 	cc 1200 	CTG 1260      CTG 1260	GC 1320     CC 1320	CTG 1380     . CTG 1380	AA 1440 	cc 1500 	CAG 1560      CAG 1560	CAA 1620       CAA 1620	AAT 1680       AAT 1680
CCTCCAAAGCCACGTTCTGGTGGGT 	CTGAGACCAAAAGACCTCTGGTCGCTT 	GGCTTGAAAAGGAGTGGATGAGGAAC 	CATTTAAAAGGAAAGGCGGCAGTGGC 	CAAGAAGGAGCCAGTGGCGCCCACTG 	CCTCCTGGGGACCCTCAGCCTCAT	SCTCAGCCTTTTCCTGGAGTTTATT 	TCCTCGCCGTGCTGATGTTCCTCTCAGCC 	TGTACAGGCTCAAGGTGCCGCAGATGAGG 	PACAGAAAGGTCCTGGCTCTGTCCAGCGGCT 	CAATCTGGTGTCCGTGGACGTGCAGCGGC 	GGCTGCCTCTCGTCTGGATCGTGGTCT 	CCCCCCCACCCATCCCTGTCTTC	AAGAAAAGGAACCACCATCAGGAGGAGGAGCIIIIIIIIII	SCAGCTCTATCCTCAGGAACTCGAAGAC 	GGACAGAGTCCTGGGCATCCGAGGC 	CTTCTCTGTGCCTGGTGTCCTTC	TTGCTGTCCACACTCTGGTGGCCGAGP 
AACCCCTGTCCAGAGACTGGGGCAGCCTTCC 	GCCTGGTCTGGAGGGATACAGGAGGCA 	GAGAAAACTCCTCAGAAGAACTTGTTTCCC 	AGTGCAGCCCGGAGGCACAACAAGGCAATAG 	AAGGCTCCAGAGACCGAGCCTTCCTACGGC 	AAGGCCATCTGGCAGGTGTTCCATTCTACCTT 	AGTGATGTCTTCAGGTTCACTGTCCCCAAGCTC 	GATCCCAAGCCTCCAGCTGGAAGGGCTACC; 	GCCTGCAAACGCTGTTTGACAGCAGAGAACATGTA 	TTGCGGTCGGCCATCACTGGCCTGGTGTACA 	GAAAGGCCAGTGCGGTGGGTGATGTGGTCA 	CCGAGAGCGTCCTCACCTCAACGGGCTGTC 	TTGGTCTATCTGTGGCAGCTCCTGGGGCCCT( 	GCCTCCTCCCTGAATTTCTTCATCTCCA 	TGAGGCAGAAGGACTCACGGGCACGGCTCACCAGCTV 	TCAAGTTCCATGGCTGGGAGGAGCCTTTCTC 	AGCIGGGCCCTTGCGGACCTCCGGCCTCCTC 	STCTACATTTCTGGTCGCACTGGTGGTGT 
601 7	661 G         G61 G	721 A 1 721 A	781 A 1 781 A	841 A 841 A	901 A       901 A	961 A 1 961 A	1021 G	1081 T	1141 T       1141 T	1201 A         1201 A	1261 A      1261 A	1321 T       1321 T	1381 A	1441 ATC     441 ATC	1501 A   1501 A	1561 G   1561 G	1621 GT       1621 GT
Oy Dp	Qy	Qy Db	Qy Dp	Oy Dp	Oy Dp	Oy Dp	Oy Dp	Oy Dp	oy Dp	O.Y.	Oy Dp	Oy . Db	O _Y	Qy Db	Qy Db	Oy Db	Qy

Oy .	1681	GCTATGAATGCAGAGAAGCCTTTGTGACTCTCACAGTTCTCAACATCCTCAACAAGGCC 	1740
Qy Db	1741	CAGGCTTTCCTGCCCTTCTCCATCCACCCTCGTCCAGGCCCGGGTGTCCTTTGACCGT	
Qy Db	1801	CIGGICACCITCCTCTGCCTGGAAGATGACCTGGTGTCGTAGACTCAAGITCCTCT 	9
QY	1861	GGAAGCSCTGCCGGGAAGGATTGCATCACCATACACAGTGCCACCTTCGCCTGGTCCCAG 	1920 1920
Qy Db	1921	GAAAGCCCTCCCTGCCTCCACAGAATAAACCTCACGGGCCCCAGGGCTGTCTGCTGGCT 	ထာ ထ
Qy Db	1981 1981	GTTGTCGGTCCAGTGGGGGCAGGAAGTCCTCCTGCTGTCCGCCCTCCTTGGGGAGCTG	2040
Qy Db	2041	TCAAAGGTGGAGGGGTTCGTGAGCATCGAGGGTGCTGTGGCCTACGTGCCCCAGGAGGCC	0
QY	2101	TGGGTGCAGAACACCTCTGTGGTAGAAATGTGTGCTTCGGCAGGAGCTGGACCCACCC	2160
O.y D.b	2161	TGGCTGGAGAGAGTACTAGAAGCCTGTGCCCTGCAGCCAGATGTGGACAGCTTCCCTGAG	2220
Qy	2221	GGAATCCACACTTCAATTGGGGAGCAGGCATGAATCTCTCCGGAGGCCAGAAGCAGGG 	2280
Oy Db	2281	CTGACCTGGCCCGGCTGTATACAGAAAGGCAGCTGTGTACCTGCTGGTGATGACCCCTG :	2340
Qy	2341	GCGGCCCTGGATGCCCACGTTGGCCAGCATGTCTTCAACCAGGTCATTGGGCCTGGTGGG :	
QY	2401	CTACTCCAGGGAACAACGGGTTCTCGTGACGCACGCACTCCACATCTGCCCCGGGCT :	2460
Qy	2461	GATGGGTTCCTACCAGGAGCTT	2520 2520
oy da	2521 2521	ATCAAGCCAGACAGCCAGGAGATAGA 	2580
Oy Op	2581	GGAGAAGGAGAAACAGAACCTGGGACCAGCACCAAGGACCCCAGAGGCACCTCTGCAGGC ;	2640
Q Dp	2641	AGGAGCCCCAGCTTAGACCCGAGAGGTCCATCAAGTCAGTC	2700
Q Q	2701	ACTICAGAAGCCCAGACAGAGGTICCTCIGGAIGACCCIGACAGGGCAGGAIGGCCAGCA ;	2760
QY	2761	GGAAAGGACAGCATCCAATACGGCAGGGTGAAGGCCACAGTGCACCTGGCCTACCTGCGT 2	2820

Db	Db 3961 GGTGGGATCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	QY         4081         GACCTGCTGCAGGAGCACTCGGAGGCTATCTGGGCAGCCTGGAGACGTCAGCTC         4140           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Db 4141 AAAGCCTTGGTGGCCAGCCTGCCGGCCAGCTGCAGTACAAGTGTGCTGACCGAGGCGAG 4200  Qy 4201 GACCTGAGCGTGGGCCAGAAACAGCTCCTGTGTCTGGCACGTGCCCTTCTCCGGAAGAC 4260	Qy         4261         CAGATCCTCATCCTGGACGAGGCTACTGCTGCTGGACGGCACGGAGGTGCAGATG         4320           L111111111111111111111111111111111111	4321 CAGGCCATGCTCGGGAGCTGGTTTGCACAGTGCACTGTGCTGCTGCTATGCCCACCGCCTG 4	4381 CGCTCCGTGATGGACTGTGCCCGGGTTCTGGTCATGGACAAGGGGCAGGTGCAGAGAGAG	4441 GGCAGCCGGCCCAGTGCCCAGAAGGGCCTGTTTACAGACTGCCCAGAGTCA 45	501 GCCTGGTC	RESULT 8 AAD16262 ID AAD16262 standard; CDNA; 4512 BP.	AC AAD16262; XX DT 19-NOV-2001 (first entry)	Human ATP-binding cassette transporter ABCC6 (MRP6) mutant cDNA #7.  Human; prenatal diagnosis; dermal lesion; cardiovascular disease; MRP6  Multidan Desistant and American American American American American American	NW MILLIALUNG CASSELLE TRANSPORTER; ARTERIAL INSULFACE TO SECONDING ARP-binding cassette transporter; arterial insulficiency; chromosome 16; KW Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage; KW mutant; mutein; ss.	Homo sapiens. Synthetic.	FT CDS 1.4512 FT CDS 7*tag- a FT /*tag- a FT /product= "Human ABCC6 (MRP6) mutant protein"	mutation
	2981 TCCTTCTGCGGGGCTACTGGGTGGGGGGGGGGGGGGGGG	3001 GGGCTGTTTGCCTCCATGGCTGCGGTGCTCCTAGGTGGGGCCCGGGCATCCAGGTTGCTC	11111111111111111111111111111111111111	3181 GACAAACTCCGGTCCCTGCTGATGTACGCCTTTGGACTCCTGGAGGTCAGCCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	Qy       3241       GCAGTGGCTACCCACTGGCCATCCTGCCACTGTTTCTCCTCTACGCTGGG       3300         Db       3241       GCAGTGGCTACCCCACTGGCCATCCTGCCACTGTTTCTCCTCTACGCTGGG       3300	Qy     3301     TTTCAGAGCCTGFATGTGGTTAGCTCATGCCAGCTGAGACGCTTGGAGTCAGCCAGC	Oy 3361 TCGTCTGTCTCCTCCCACATGGCTGAGACGTTCCAGGGCAGCACAGTGGTCCGGGCATTC 3420	Oy     3421     CGAACCCAGGCCCCTTTGTGGCTCAGAATGCTCGCGTAGATGAAAGCCAGAGGATC     3480       Db     3421     CGAACCCAGGCCCCCTTTGTGGCTCAGAACAATGCTCGCGTAGATGAAGAAGGATC     3480	Qy 3481 AGTTTCCCGCGACTGGTGGTGACAGGTGGCTTGCGGCCAATGTGGAGCTCCTGGGGAAT 3540	Qy 3541 GGCCTGGTGTTTGCAGCCCCACGTGTGCTGAGCAAGCCCACCTCAGTGCTGGC 3600	Qy 3601 CTCGTGGGCTTCTCTGTGCTGCCCTCCAGGTGACCCAGACACTGCAGTGGGTTGTT 3660	OY 3661 CGCAACTGGACAGACCTAGAGAACAGCGTGTGTGTGGGGGGGG	Qy       3721       TGGACGCCCAAGGAGGCTCCCTGGAGGCTGCCCACATGTGCAGCTCAGCCCCCTGGCCT       3780         Db       3721       TGGACGCCCAAGGAGGCTCCCTGGAGGCTGCCCACATGTGCAGCTCAGCCCCTGGCCT       3780	Qy 3781 CAGGCGGGCAGATCGAGTTCCGGGACTTTGGGCTAAGATGCCGACCTGAGCTCCCGCTG 3840	Oy 3841 GCTGTGCAGGCGTGTCCTTCAAGATCCACGCAGGAGAAGGTGGGCATCGTTGGCAGG 3900

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The invention relates to methods and compositions for diagnosing and treating Pseudoxanthoma elasticum (PXE) and PXE associated physiological dysfunctions. The invention is useful for screening for the presence of a PXE mutation. Mutations associated with PXE maps to the ATP-binding cassette transporter ABCC6 (MRD6-MILLIdruy Resistance associated of protein-6) gene locus on chromosome 16. ABCC6 (MRP6) gene encodes a 165 cm protein located in the plasma membrane containing 17 membrane. Spanning helices grouped into three transmembrane domains. PXE is conherited as an autosomal recessive phenotype or appears as a sporadic phenotype. PXE is a heritable disorder relaracterised by mineralisation of elastic fibers in skin, arteries and the retina, that result in dermal insufficiency, cardiovascular disease and retinal haemorrhages leading to macular degeneration. The method is useful for screening a population of individuals in order to identify individuals with one or more PXE associated MRP6 alleles who are then provided with appropriate genetic counselling in view of the PXE status. The methods are useful for cuseful in the area of genetic testing, carriers and thus are useful in the area of genetic testing, carrier detection and prenatal cuseful in the area of genetic testing, carrier detection and prenatal cuseful in the area of genetic testing, carrier detection and prenatal cuseful in the present sequence is human ATP-Dinding cassette (ABC) amino acid change from Ala to Pro at position 1303 of MRP6 protein.

Counselling manner and are provided with appropriate on an animal and prenatal conference from human ATP-Dinding cassette (ABC) (MRP6) mutant cDNA, This mutant cDNA results in an animal and prenate sequence is not shown in the specification but is conference in the present sequence is not shown in the specification but is conference to the present sequence is not shown in the specification but is conference to the present sequence is not shown in the specification but is conference to the present sequence 
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DB 22; Length 4512; ö Sequence 4512 BP; 835 A; 1381 C; 1353 G; 943 T; 0 other; Score 4497.8; Pred. No. 0; 99.88; 99.88;

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CTATGAATGCAGAAAAGCCTTTGT 
CAGGCTTTCCTGCCCTTCTCCATCCATCCCTCGTCCAGGCCCGGGTGTCCTTTGACCGT
GGFCACCTFCCTGGGAGAAGTTGACCCTGGTGTCGTAGACT 
GAAGCGCTGCCGGAAGGATTGCATC 
GAAAGCCTCCCTGCCTCCACAGAATAAACCTCACGGTG 
TGFCGGTCCAGTGGGGGCAGGAAGTCCTCCTGCTGTCCGG 
rcaaaggtggaggggttggtgag 
GGGTGCAGAACACCTCTGTGGTAGAGAATGTGTGCTTCGGGCAGGAGCT. 
GGCTGGAGAGTACTÀGAAGC 
GAAFCCACACTTCAATTGGGGAGCAGGCATGAATCT 
TGAGCCTGGCCCGGGCTGTATACAGAAAGC 
GGCCCTGGATGCCCACGTTGGC 
CTACTCCAGGGAACAACACGGATTCTCGTGACGCACGCAC
TTGGATCATAGTGCTGGCAAAT

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                          CGCAACTGGACAGACCTAGAGAACAGCATCGTGTCAGTGGAGCGGATGCAGGACTATGCC
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AAD16263 standard; cDNA; 4512

AAD16263 ID AAD RESULT

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The invention relates to methods and compositions for diagnosing and treating Pseudoxanthoma elasticum (PXE) and PXE associated physiological dysfunctions. The invention is useful for screening for the presence of a PXE mutation. Mutations associated with PXE maps to the ATP-binding cassette transporter ABCC6 (MRP6-Multidrug Resistance associated protein located in the plasma membrane containing 17 membrane. Spanning helices grouped into three transmembrane domains. PXE is a heritable disorder characterised by mineralisation of elastic fibers is a heritable disorder characterised by mineralisation of elastic fibers in skin, arteries and the retina, that result in dermal lesions with associated laxity and loss of elasticity, arterial insufficiency, cardiovascular disease and retinal hemorrhages leading to macular degeneration. The method is useful for screening a population of individuals in order to identify individuals with appropriate genetic connealing in view of the PXE status. The methods are useful for identifying homozygotes, compound heterozygotes or carriers and thus are useful in the area of genetic testing, carrier detection and prenatal
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                                                               Human; prenatal diagnosis; dermal lesion; cardiovascular disease; MRP6; Multidrug Resistance-associated protein 6; macular degeneration; ABCC6; ATP-binding cassette transporter; arterial insufficiency; chromosome 16; Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transporter, ABCCG (MRP6) mutant cDNA. This mutant cDNA results in an amino acid change from Arg to Trp at position 1314 of MRP6 protein. Note: The present sequence is not shown in the specification but is derived from human ATP-binding cassette transporter ABCCG (MRP6) cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Screening presence of Pseudoxanthoma elasticum mutation useful for identifying homozygotes, compound heterozygotes or carriers involves determining presence of mutation in MRP6 (ABCC6) nucleic acid
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                               ATP-binding cassette transporter ABCC6 (MRP6) mutant cDNA #8
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Best Local Similarity 99.8
Matches 4502; Conservative
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1	Qy 1081 TGCCTGCAACGCTGTTTGAGCAGCAG 	1141	1201	1261	1321	1381	1441	1501	1561	1621	1681	1741	1801	1861	OY 1921 GAAAGCCTCCCTGCCTCCACAGAATA 	1981 (	2041	Oy 2101 TGGGTGCAGAACACCTGTGTGGTAGAG	1017
	1 ATGCCGCGCCTGCTGAGCCCTGCGGGGCAGGGGGTCTGGAACCAGACAGA	61 CCTGCCGCACCAGCTGCTGCTTCCTGAGAACAGCAGGGTCTGGTACCC	121 CCCATGTACCTCTGGGTCCTTGGTCCCATCTACCTCCTCTTCATCCACCACCATGGCCGG	181 GGCTACCTCCGGATGTCCCCACTCTTCAAAGCCAAGATGGTGCTTGGATTCGCCCTCATA	241 GTCCTGTGTACCTCCAGCGTGGCTGTCGCTCTTTGGAAAATCCAACAGGGAACGCCTGAG	301 GCCCCAGAATTCCTCATTCATCCTACTGTGGCTCACCACGATGAGCTTCGCAGTGTTC	361 CTGATTCACACCGAGAGAAAAAGGGAGTCCAGTCATCTGGAGTGCTGTTTGGTTACTGG 42	421 CITCICIGCIIIGECIIGCCAGCIACCAACGCIGCCCAGCAGGCCTCCGGAGGGGGCCTTC 48	481 CAGAGCGACCCTGTCCGCCACCTGTCCACCTACCTATGCCTGTCTCTGGTGGTGGTCGCACAG 54	541 TITGIGCIGCCIGCCGGAICAACCCCCCTTCTTCCCTGAAGACCCCCAGCAGTCT	601 AACCCCTGTCCAGAGACTGGGGCAGCCTTCCCCTCCAAAGCCACGTTCTGGTGGGTTTCT	661 GGCCTGGTCTGGAGGGATACAGGAGGCCACTGAGACCAAAAGACCTCTGGTCGCTTGGG 72	721 AGAGAAAACTCCTCAGAAGAACTTGTTTCCCGGCTTGAAAAGGAGTGGATGAGGAACCGC 780 	781 AGTGCAGCCCGGAGGCACAACAAGGCAATAGCATTTAAAAGGAAAGGCGGCAGTGGCATG 84	841 AAGGCTCCAGAGACCGAGCCCTTCCTACGGCAAGAAGGGAGCCAGTGGCGCCCACTGCTG	901 AAGGCCATCTGGCAGGTGTTCCATTCTACCTTCCTCGGGACCCTCAGCCTCATCATCATCATC	961 AGTGATGTCTTCAGGTTCACTGTCCCCAAGCTGCTCAGCCTTTTCCTGGAGTTTATTGGT 102 	1021 GATCCCAAGCCTCCAGCTGGAAGGGCTACCTCGCCGTGCTGATGTTCCTCTCAGCC   1111111111111111111111111111111111	

2220	1 TGGCTGGAGAGAGTACTAGAAGCCTGTGCCCTGCAGCCAGATGTGGACAGCTTCCCTGAG	2163	Ωy
16		210]	qq
2160	GGGTGCAGAACACCTCTGTGGGTAGAGAATGTGTGTGCTTCGGGGAGGAGGAGGTGCCACC	210]	Qy
2100			qq
2100	TCAAAGGTGGAGGGGTTCGTGAGCATCGAGGGTGCTGTGGCCTACGTC	2041	Qγ
2040		8	qq
2040	GTTGTCGGTCCAGTGGGGGCAGGGAAGTCCTCCCTGCTGTCCGCCT	1981	QY
1980		1921	qq
1980	CCTCCCTGCCTCCACAGAATAAACCTCACGGTGCCCCAGGGCTGTC	1921	δλ
1920		9	qq
1920	SAAGCGCTGCCGGGAAGGATTGCATCACCATACACAGTGCCACCTTCGCCT	1861	δy
1860	1 CTGGTCACCTTCCTCTGCCTGGAAGTTGACCCTGGTGTCGTAGACTCAAGTTCCTCT	1801	QQ
1860	SGTCACCTTCCTCTGGAAGAAGATTGACCCTGGTGTCGTAGACTCAA	1801	Oy
1800	SCITICCIGCCCTTCTCCATCCACTCCCTCGTCCAGGCCCGGGTGTCCTTTGACC	1741	qq
1800	CTTTCCTGCCCTTCTCCATCCACGCCCGGGGCCCGGGTGTCTTTGAC	1743	δλ
1740	CTATGAATGCAGAGAAGCCTTTGTGACTCTCACAGT	1681	QQ
	ATGAATGCAGAGAAAGCCTTTGTGACTCTCACAGTTCTCAACATCCTCAA	1681	QY
168	ACTGGTGTTTGCTGTCCACACTCTGGTGG	1621	qq
168	GTCTACATTTCTGGTCGCACTGGTGGTGTTTGCTGTCCACACTCTGGTGG	1621	QY
16	GCCTTGCGGACCTCCGGCCTCC	1561	qa.
٦	SGGCGCCTTGCGGACCTCCGGCCTCTTTTCTCTGTGTCGCTGGTGT	1561	Qy
	ATCANGITCCATGCTGGGAGGGAGCCTTCTGGACAGAGTCCTGGGCATCCGAGCCCAG	1501	QC
156	ATCAAGTTCCATGGCTGGGAGGGAGCCTTTCTGGACAGAGTCCTGGGCATCC	1501	QY
5	1 ATGAGGCAGAAGGACTCACGGCACGCTCACCAGCTCTATCCTCAGGAACTCGAAGAC	1441	qq
1500	3AGGCAGAAGGACTCACGGGCTCACCAGCTCTATCCTCAGGAACTCGAAG	144]	δλ
1440		1381	QΩ
1440	CTCCCTCTGAATTTCTTCATCTCCAAGAAAAGGAACCACCATCAGGAGGAGC	1381	Qy
3	GCCCTCGCCTCACTGCTTTTTTTTTTTTTTTTTTTTTTT	1321	qq
ñ	CGTCTATCTCTGGCAGCTCCTGGGGCCCTCGCCTCACTGCCATGGCTGTCTTCCT		Qy
1320	GIGGCIGCCICIC	1261	qq
32	SAGAGCGTCCTCTACCTCAACGGGCTGTGGCTGCCTCGTCTGGATCGTGGTCTTG	1261	Qy
1260	AGAAAGGCCAGTGCGGTGGTGATGTGGTCAATCTGGTGTCCGTGGACGTGCACCGCT	0	q _O
56	SCCAGTGCGGTGGTGATGTGGTCAATCTGGTGTCCGTGGACGTGCAGCGGCT	1201	QY
12	TTGCGGTCGGCCATCACTGGCCTGGTGTACAGAAAGGTCCTGGCTCTGTCCAGCGCTCT	4	QQ
120	TTGCGGTCGGCCATCACTGGCCTGTACAGAAAGGTCCTGGCTCTGTCC	4	ÓΣ
11	GCCTGCAAACGCTGTTTGAGCAGCAGAACATGTACAGGCTCAAGGTGCTGCAGATGA		QQ
14	TGCCTGCAAACGCTGTTTGAGCAGCAGAACATGTACAGGCTCAAGGTGCCGCAGAT	1081	Οy

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2220	2280	2340	2400	2460	2520	2580	2640	2700	2760	2820	2880	2940	3000	3060	3120	3180 3180	3240 3240	3300
1 TGCCTGGAGAGAGTACTAGAAGCCTGTGCCTGCAGCCAGATGTGGACAGCTTCCCTGAG	1 GGAATCCACACTTCAATTGGGGAGCAGGCATGAATCTCTCCGGAGGCCAGAAGCAGCGGGTHIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	1 CTGAGCCTGGCCCGGGCTGTATACAGAAAGGCAGCTGTGTACCTGCTGGTGGATGACCCCCTG	1 GCGGCCCTGGATGCCCACGTTGGCCAGCATGTCTTCAACCAGGTCATTGGGCCTGGTGGG	CTACTCCAGGGAACAACACGGATTCTCGTGACGCACGCAC	GATTGGATCATAGTGCTGGCAAATGGGGCCATCGCAGAGATGGTTCCTACCAGGAGCTT 	CTGCAGAGGAAGGGGCCCTCGTGTGTCTTCTGGATCAAGCCAGACAGCCAGGAGTAGA 	GGAGAAQGAGAAACAGAACCTGGGACCAGCACCAAGGACCCAGAGGCACCTCTGCAGGC	AGGAGGCCCGAGCTTAGACGCGAGAGGTCCATCAAGTCAGTC	ACTICAGAAGCCCAGACAGAGGTICCTCTGGATGACCCTGACAGGGCAGGATGGCCAGCA	GGAAAGGACAGCATCCAATACGGCAGGGTGAAGGCCACAGTGCACCTGGCCTACCTGCGCTACCTGCGCTACCTGCGCTACCTGCGCTACCTGCGCTACCTGCGCTACCTGCGCTACCTGCGTTACAAGGAAAGGACAACAAACGAAAGGCCACAGTGCACAGTGCACTGCCTACCTGCGT	1 GCCGTGGGCACCCCCTCTGCGCACTCTTCCTCTTCCTCTGCCAGCAGTGGCC :	1 TCCTTCTGCCGGGGCTACTGGCTGAGCCTGTGGGCGGACGACGTGCAGTAGGTGGGCAG :	1 CAGACGCAGGCAGCCCTGCGTGGCGGGATCTTCGGGCTCCTCGGCTGTCTCCAAGCCATT :	GGGCTGTTTGCCTCCATGGCTGCGTGTTCCTAGGTGGGGCCCGGGCATCCAGGTTGCTC	1 TTCCAGAGGCTCCTGTGGGATGTGCTGCGATCTCCCATCAGCTTCTTTGAGCGGACACCC (	1 ATTGGTCACCTGCTAAACCGCTTCTCCAAGGAACAGACACGGTTGACGTGGACATTCCA (	1 GACAAACTCCGGTCCCTGCTGATGTACGCCTTTGGACTCCTGGAGGTCAGCTGGTGGTG 3	1 GCAGTGGCTACCCCACTGGCCACTGTGGCCATCCTGCCACTGTTTCTCCTCTACGCTGG :
216	222	228	234	2401	2461	2521	2581	2641	2701	2761 2761	282	288	294	3001	306	312	318:	324
qq	Oy Db	QY Dp	QY Up	QY Db	OY Db	QY Db	OY Dp	Qy Db	QY	QY Dp	Qy Dp	OY ob	Oy Db	oy D	Oy Dp	Qy Dp	Oy Db	Οy

3360 3360 3420 3420 3480 3480 3540 3540 3600 3600 3660 3660 3720 3720 3780 3780 3840 3840 3900 4020 4020 4080 4080 4140 4140 GCAGTGGCTACCCCACTGGCCACTGTGGCCATCCTGCCACTGTTTCTCCTCTACGCTGGG 3300 3900 3960 3960 4200 4200 4260 4320 4380 4260 4320 4380 CGAACCCAGGCCCCCTTTGTGGCTCAGAACAATGCTCGCGTAGATGAAAGCCAGAGGATC CGCAACTGGACAGACCTAGAGAACAGCATCGTGTCAGTGGAGCGGATGCAGGACTATGCC AGTITCCCGCGACTGGTGGCTGACAGGTGGCTTGCGGCCAATGTGGAGCTCCTGGGGAAT GGCCTGGTGTTTGCAGCCGCCACGTGTGCTGTGCTGAGCAAAGCCCACCTCAGTGCTGGC CTCGTGGGCTTCTCTCTCTGCTGCCCTCCAGGTGACCCAGACACTGCAGTGGGTTGTT ACCGGGGCAGGGAAGTCCTCCCTGGCCAGTGGGCTGCTGCGGCTCCAGGAGGCAGCTGAG GCTGTGCAGGGCGTGTCCTTCAAGATCCACGCAGGAGAGAAGGTGGGCATCGTTGGCAGG AAAGCCTTGGTGGCCAGCCTGCCGGCCAGCTGCAGTACAAGTGTGCTGACCGAGGCGAG GACCTGAGCGTGGGCCAGAACAGCTCCTGTGTCTGGCACGTGCCCTTCTCCGGAAGACC CAGATCCTCATCCTGGACGAGGCTACTGCTGCCGTGGACCCTGGCACGAGCTGCAGATG CAGGCCATGCTCGGGAGCTGGTTTGCACAGTGCACTGTGCTGCCCCATTGCCCACCGCCTG 3241 3301 3541 3661 3841 3841 3301 3361 3361 3421 3421 3481 3481 3541 3601 3601 3661 3721 3901 3901 3961 3961 4081 4141 3721 3781 3781 4021 4021 4081 4141 4201 4201 4261 4261 4321 4321 g δ q QΥ Db Qγ qq ρý Op Qγ g δλ g Q Op δ QΥ q Ob g Db Op g δ οy δŽ οy δ δý Q QY Qγ g δ Pp Óγ Dp

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treating Pseudoxanthoma elasticum (PXE) and PXE associated physiological dysfunctions. The invention is useful for screening for the presence of a PXE mutation. Mutations associated with PXE maps to the ATP-binding cassette transporter ABCC6 (MRP6-Multidarug Resistance associated protein-6) gene locus on chromosome 16. ABCC6 (MRP6) gene encodes a 165 kDa protein located in the plasma membrane containing 17 membrane. Spanning helices grouped into three transmembrane domains. PXE is inherited as an autosomal recessive phenotype or appears as a sporadic phenotype. PXE is a haritable disorder characterised by mineralisation of elastic fibers in skin, arteries and the retina, that result in dermal
                                                                                                                                                                                                                                                                                                                                              Human; prenatal diagnosis; dermal lesion; cardiovascular disease; MRP6; Multidrug Resistence-associated protein 6; macular degeneration; ABCC6; ATP-binding cassette transporter; arterial insufficiency; chromosome 16; Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage;
                                                                         Screening presence of Pseudoxanthoma elasticum mutation useful for identifying homozygotes, compound heterozygotes or carriers involves determining presence of mutation in MRP6 (ABCC6) nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention relates to methods and compositions for diagnosing and
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 CCTCCGTGATGGACTGTGCCCGGGTTCTGGTCATGGACAAGGGGCAGGTGGCAGAGAGC
                 GGCAGCCCGGCCCAGCTGCTGGCCCAGAAGGGCCTGTTTTACAGACTGGCCCAGGAGTCA
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lesions with associated laxity and loss of elasticity, arterial insufficiency, cardiovascular disease and retinal haemorrhages leading to macular degeneration. The method is useful for screening a population of individuals in order to identify individuals with one or more PXE associated MRP6 alleles who are then provided with appropriate genetic counselling in view of the PXE status. The methods are useful for changelling in view of the PXE status. The methods are useful for useful in the area of genetic testing, carrier detection and prenatal diaptosis. The present sequence is human APP-binding cassette (ABC) transporter. ABCG6 (MRP6) mutant cDNA. This mutant cDNA results in an amino acid change from Gly to Ser at position 131 of MRP6 protein, but it is incorrectly referred as Gly to Ile in page 49 of the specification. Note: The present sequence is not shown in the specification but is derived from human APP-binding cassetter ABCG6 (MRP6) cDNA (SED ID NO: 2] shown in page 130-137 of the specification (AAD16231).
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                                                                                                                                                                                                                                                                               Score 4497.8;
Pred. No. 0;
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of

191   ACTIONACCICCOGGGGCCCAACAACACCAACACCAACACCAACACCACCACC
181   AGTGCAGCCGGAGCCAAACAAGGCAATAGCATTTAAAAGGAAAGGCGGGGGGGG
181   AGTGCAGCCCGGAGCCAAACAAGCCATTACAAAGGAAAGCCGGGGGGGG
781 781 841 841 841 901 901 1021 1021 1021 1141 1141 1141 1150 1150 1150 1150 1150 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1161 1
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Qy Db	1861	GGAAGCGCTGCCGGGAAGATTGCATCACCATACACAGTGCCACCTTCGCCTGGTCCCAG 1920
Qy Db	1921 1921	CCCTGCCTCCACAGAATAAACCTCACGGTGCCCCAGGGCTGTCTGCTGGCT 19
QY	1981 1981	agtegggcagggaagtcc 
QY	2041	TCAAAGGIGGAGGGTTCGFGAGCAFCGAGGGTGCTGFGGCCTACGTGCCCCAGGAGGCC 2100
Qy	2101	TGGGTGCAGAACACCTCTGTGGTAGAATGTGTGCTTCGGGCAGGAGCTGGACCCACC 2160
Qy	2161	TGGCTGGAGAGAGTACTAGAAGCCTGTGCCCTGCAGCAGATGTGGACAGCTTCCCTGAG 2220
QY	2221	GGAATCCACACTICAATTGGGGAGCAGGGCATGAATCTCTCCGGAGGCCAGAAGCAGCGG 2280 
QY	2281	CTGAGCCTGGCCCGGGCTGTATACAGAAAGGCAGCTGTGTACCTGCTGGATGACCCCCTG 2340
QY	2341	ATGTCTTCAACCAGGTCAT 
QY	2401	GGGAACAACAGGAITCICGIGACGCACGCACTCCACAICCIGCCCCAGGCT 246
QY	2461	GATTGGATCATAGTGCTGGCAAATGGGGCCATCGCAGAGATGGGTTCCTACCAGGAGCTT 2520
OY Db	2521 2521	CTGCAGAGGAAGGGGCCCTCGTGTGTCTTCTGGATCAAGCCAGACAGCCAGGAGATAGA 2580 
Qy	2581	GGAGAAGGAGAAACAGAACCTGGGACCAGCACCAAGGACCCCAGAGGCACCTCTGCAGGC 2640 
QY Db	2641	AGGAGGCCCGAGCTTAGACGCGAGAGGTCCATCAAGTCAGTC
QY	2701 2701	CAGACAGAGGTTCCTCTGGATGACCCTGACAGGGCAGGATGGCCAGCA 2
QY	2761 2761	GGAAAGGACAGCATCCAATACGGCAGGGTGAAGGCCACAGTGCACCTGGCCTACCTGCGT 2820 
Qy	2821	GCCGTGGGCACCCCCCTCTGCCTCTACGCACTCTTCCTCTTGCTTG
Qy	2881	CCGGGGCTACTGGCTGAGCCTGTGGGCGGACGACCTTILITITITITITITITITITITITITITITITITIT
ΟY	2941	CAGACGCAGGCAGCCCTGCGTGGCGGGATCTTCGGGCTCCTCGGCTGTCTCCAAGCCATT 3000

Db 4021 AGGATCAGCATCATCCCCCAG	4 4	DD 4081 GACCIGCAGGAGCACTCG OV 4141 AAAGCCTTGGTGGCCAGCAG	414	Oy 4201 GACCTGAGGGTGGCCAGAAA	Qy 4261 CAGATCCTCATCCTGGACGAG	Oy 4321 CAGGCCATGCTCGGGAGCTGG 	4381 CGCTCCGTGATGGAC 	GGCAGCCGGCCC	Oy 4501 GGCCTGGTC 4509 	RESULT 11 AAD16259 ID AAD16259 standard; cDNA; 4	XX AC AAD16259; XX DT 19-NOV-2001 (first entry)		KW Multidrug Resistance-assoc KW ATP-binding cassette trans KW Pseudoxanthoma elasticum; KW mutant; mutein; ss.		WO200162977-A2. 30-AUG-2001.	001; 2001 000; 2000	PA (PXEI-) PXE INT INC. PA (UYHA-) UNIV HAWAII. XX PI BOYd CD, Csiszar K, Lesa	WPI; 2001-536645/59. Screening presence of P	PT identifying homozygotes, c PT determining presence of mu XX
	2941 CAGACGCAGGCACCTGCGTGGCGGGATCTTCGGCCTCCTCGGCTGTCTCCAACCCAT. 3001 GGGCTGTTTGCCTCCATGGCTGCGGTGCTCCTCCTAGGTGGGGCCCGGGCATCCAGGTTGCT	3001 GGGCTGTTTGCCTCCATGGCTGCGGTGCTCCTAGGTGGGGCCCCGGGCATCCAGGTTGCTC 3060	3061 TTCCAGAGGCTCCTGTGGGATGTGGTGGGATCTCCCATCAGCTTCTTTGAGCGGACACCC 3120 1011	3121 ATTGGTCACCTGCTAAACCGCTTCTCCAAGGAGACAGACA	3121 ATTGGTCACCTGCTAAACCGCTTCTCCAAGGAGACACAGGGTTGACGTGGACGTTCCA 318 3181 GACAAACTCCGGTCCTGCTGATGTACGCCTTTGGACTCCTGGAGGTCAGCCTGGTGGTG 324 111111111111111111111111111111111111	3241	3301 TTTCAGAGCCTGTATGTGGTTAGCTCAGCTGAGACGCTTGGAGTCAGCCAGC	3361 TCGTCTGTCTCCCACATGGCTGAGACGTTCCAGGGCAGCACAGTGGTCCGGGCATTC 3420 	3421 CGAACCCAGGCCCCTTTGTGGCTCAGAACAATGCTCGCGTAGATGAAAGCCAGAGGATC 3480 	3481 AGTTTCCCGCGACTGGTGGCTGACAGGTGGCTTGCGGCCAATGTGGAGCTCCTGGGGAAT 3540	3541 GGCCTGGTGTTTGCAGCCGCCACGTGTGCTGAGCAAAGCCCACCTCAGTGCTGGC 3600 	3601 CTCGTGGGCTTCTCTGTGCTGCCCTCCAGGTGACCCAGACACTGCAGGTTGTT 3660	3661	3721 TGGACGCCCAAGGAGGTCCCTGGAGGCTGCCCAATGTGCAGCTCAGCCCCCTGGCCT 3780	3781 CAGGGCGGCAGATCGAGTTCCGGGACTTTGGGCTAAGATGCCGACCTGAGCTCCCGCTG 3840 	3841 GCTGTGCAGGGCGTGTCCTTCAAGATCCAGGAGAGAAGGTGGGCATCGTTGGCAGG 3900 	3901 ACCGGGCAGGAAGTCCTCCCTGGCCAGTGGGCTGCTGCGGCTCCAGGAGCAGCTGAG 3960 	3961 GGTGGGATCTGGATCGACGGGTCCCCATTGCCCACGTGGGGCTGCACACTGCGCTCC 4020 	4021 AGGATCAGCATCATCCCCAGGACCCCATCCTGTTCCCTGGCTCTCTGCGGATGAACCTC 4080
	dy g	qq	Q Q	δλ	a v	a vo a	Qy Dp	9 6	oy da	Oy Dp	<b>&amp;</b> 점.	Oy Pb	QY	Oy Dp	oy B	Qy Dp	6 Pp	Qy Dp	δ,

s; dermal lesion; cardiovascular disease; MRP6; cotated protein 6; macular degeneration; ABCC6; nsporter; ratbrial insufficiency; chromosome 16; PSE; heritable disorder; retinal haemorrhage; AGACCCCATCCTGTTCCCTGGCTCTCTGCGGATGAACCTC 4080 GCCCGGCCAGCTGCAGTACAAGTGTGCTGACCGAGGCGAG 4200 ACAGCTCCTGTGTCTGGCACGTGCCCTTCTCCGGAAGACC 4260 CCGGGTTCTGGTCATGGACAAGGGGCAGGTGGCAGAGAGC 4440 undoxanthoma elasticum mutation useful for compound heterozygotes or carriers involves nutation in MRP6 (ABCC6) nucleic acid e transporter ABCC6 (MRP6) mutant cDNA #4. aux O, Urban Z, Terry S; 4511 BP 41. .69

And plotted in located in the prasma membrane contenting t, membrane spanning helices grouped into three transmambrane domains. PXE is inherited as an autosomal recessive phenotype or appears as a sporadic phenotype. PXE is a heritable disorder characterised by mineralisation of elastic fibers in skin, arteries and the retina, that result in dermal lesions with associated laxity and loss of elasticity, arterial insufficiency, cardiovascular disease and retinal haemorrhages leading to macular degeneration. The method is useful for screening a population of individuals in order to identify individuals with one or more PXE counselling in view of the PXE status. The methods are useful for identifying homozygotes, compound heterozygotes or carriers and thus are treating Pseudoxanthoma elasticum (PXE) and PXE associated physiological dysfunctions. The invention is useful for screening for the presence of a PXE mutation. Mutations associated with PXE maps to the ATP-binding cassette transporter ABCC6 (MRP6-Multidrug Resistance associated protein-6) gene locus on chromosome 16. ABCC6 (MRP6) gene encodes a 165 kDa protein located in the plasma membrane containing 17 membrane useful in the area of genetic testing, carrier detection and prenatal diagnosis. The present sequence is human ATP-binding cassette (ABC) transporter. ABCC6 (MRP6) mutant cDMA. This mutant cDNA is obtained by the deletion of base T at position 3775 of wild-type MRP6 cDNA. Note: The present sequence is not shown in the specification but is derived from human ATP-binding cassette transporter ABCC6 (MRP6) cDNA [SED ID NO: 2] shown in page 130-137 of the specification (AAD16231). invention relates to methods and compositions for diagnosing and Example 2; Page -; 163pp; English.  $\overset{\text{N}}{\times} \overset{\text{N}}{\times} \overset{\text{O}}{\times} \overset{\text{O}}{\times$ 

Sequence 4511 BP; 835 A; 1380 C; 1354 G; 942 T; 0 other;

ä 360 420 CCTGCCGCCACCAGCCTGCTGAGCCTGTGCTTCCTGAGAACAGCAGGGGTCTGGGGTACCC 120 121 CCCATGTACCTCTGGGTCCTTGGTCCCATCTACCTCCTCTTCATCCACCACCATGGCCGG 180 121 CCCATGTACCTCTGGGTCCTTGGTCCCATCTACCTCCTCTTCATCCACCATGGCCGG 180 GGCTACCTCCGGATGTCCCCACTCTTCAAAGCCAAGATGGTGCTTGGATTCGCCCTCATA 240 241 GTCCTGTGTACCTCCAGCGTGGCTGTCGTCTTTGGAAAATCCAACAGGGAACGCCTGAG 300 CAGAGCGACCCTGTCCGCCACCTGTCCACCTATGCCTGTCTCTGGTGGTGGTGCCACAG 540 540 900 CTTCTCTCTGCTTTGTCTTGCCAGCTACCAACGCTGCCCAGCAGGCCTTCGGAGCGGGCTTC 480 Gaps 1 ATGGCCGCCCTGCTGAGCCCTGCGCGGGGCTCTGGAACCAGACCAGAGCCTGAA 60 GCCCCAGAATTCCTCATTCATCCTACTGTGTGGCTCACCACGATGAGCTTCGCAGTGTTC CTGATTCACACCGAGAGGAAAAAGGGAGTCCAGTCATCTGGAGTGCTGTTTGGTTACTGG TITGTGCTGTCCTGCCGGGTCAACCCCCCTTCTTCCCTGAAGACCCCCAGCAGTCT 99.5%; Score 4487.4; DB 22; Length 4511; ilarity 99.8%; Pred. No. 0; Conservative 0; Mismatches 6; Indels 1; ( Similarity Best Local Sim Query Match 61 181 301 301 481 541 361 361 421 421 481 541 g ŏ g g à q δy g δλ ò g οğ g δ qq ŏ g

Qy	601	AACCCCTGTCCAGAGACTGGGCAGCCTTCCCCTCCAAAGCCACGTTCTGGTGGGTTTCT 660
Qy	661	16GAGGGGATACAGGGCCACTGAGACCAAAAGACCTCTGGTCGCTTGGG
QQ	661	GCCTGGTCTGGAGGGGATACAGGAGGCCACTGAGACCAAAAGACCTCTGGTCGTTGGG 720
Qy Gp	721	AAAAGGAGTGGATGAGGAACCGC
Ò	781	AGTGCAGCCCGGAGGCACAACAAGGCAATAGCATTAAAAGGAAAGGCGGCAGTGGCATG 840
qa	781	
Οy	841	AAGGCTCCAGAGACCGAGCCCTTCCTACGGCAAGAAGGGAGCCAGTGGCGCCCACTGCTG 900
qq	841	AAGGCTCCAGAGACCGAGCCCTTCCTACGGCAGAGGGAGCCAGTGGCGCCCCACTGCTG 900
δy	901	AAGGCCATCTGGCAGGTGTTCCATTCTACCTTCCTGGGGACCCTCAGCCTCATCATC 960
qq	901	AAGGCCATCTGGCAGGTGTTCCATTCTACCTTCCTCGGGGACCCTCAGCCTCATCATC 960
δy	961	AGTGATGTCTTCAGGTTCACGTCCCCAAGCTGCTCAGCCTTTTCCTGGAGTTTATTGGT 1020
QQ	961	AGTGATGTCTTCAGGTTCACTGTCCCCAAGCTGCTCAGCCTTTTCCTGGAGTTTATTGGT 1020
Qγ	1021	GATCCCAAGCCTCCAGCCTGGAAGGGCTACCTCGCCGTGCTGATGTTCCTCTCAGCC 1080
QQ	1021	GATCCCAAGCCTCCAGCCTGGAAGGCTACCTCCTCGCCGTGCTGATGTTCCTCTCAGCC 1080
Οy	1081	TGCCTGCAAACGCTGTTTGAGCAGCAGCAGTGTACAGGCTCAAGGTGCCGCAGATGAGG 1140
QQ	1081	TGCCTGCAAACGCTGTTTGAGCAGCAGCAGAACATGTACAGGCTCAAGGTGCTGCAGATGAGG 1140
Qy	1141	TTGCGGTCGGCCATCACTGGCCTGGTGTACAGAAAGGTCCTGGCTCTGTCCAGCGGCTCC 1200
qq	1141	TTGCGGTCGGCCATCACTGGCTCGTGTACAGAAAGGTCCTGGCTCCTGTCCAGCGGCTCC 1200
δy	1201	AGAAAGGCCAGTGCGGTGGTGATGTGGTCAATCTGGTGTCCGTGGACGTGCAGCGGCTG 1260
qq	1201	AGAAAGGCCAGTGCGTGGTGTGTGGTCAATCTGGTGTCCGTGGACGTGCAGCGCCGCTG 1260
Οy	1261	GAGAGCGTCCTCTACCTCAACGGGCTGTGGCTGCCTCGTCGGATCGTGGTCGTCTGC
qq	1261	CTACCTCAACGGGCTGTGTGTGTTTTTTTTTTTTTTTTT
ΟY	1321	CGTCTATCTCTGGCAGCTCCTGGGGCCCTCCGCCCTCACCGCCATCGCTGTCTTG
đ		GTCTATCTCTGGCAGCTCCTGGGGCCCTCCGCCCTCACTGCCATCGCTGTCTTCCTG
QY	1381	CCTCCCTCCGATTTCTTCATCTCCAAGAAAAGGAACCACCATCAGGAGGAAA
q	1381	CTCCTCCTCTGTGTTTCTTCATCTCCAAGAAAGGAACCACCATCAGGAGGAGCAA
QY	1441	GAGGCAGAAGGACTCACGGCTCACCAGCTCTATCCTCAGGAACTCGAAGACC
QQ		AGGCAGAAGGACTCACGGGCACGGCTCACCAGCTCTTTTTTTT
QY	1501	CAAGTTCCATGGCAGGAGCCTTTCTGGACAGTCCTGGCATCCGAGGCCAG
qq	1501	TCAAGTTCCATGGCTGGGAGGGAGCCTTTCTGGACAGAGTCCTGGGCATCCGAGGCCCAG
Qy	1561	GCTGGGCGCCTTGCGGACCTCCGCCTCTTCTCTGTGTCGCGTGGTCCTTCCAA
QQ	1561	AGCTGGCGCCCTTGCGGACCTCCGGCCTCCTCTTTTTTTT
Οy	21	RGGTCGCACTGGTGGTGTTTGCTGTCCACACTCTGGTGGCCGAGAAT
QQ	1621	STCTACATTTCTGGTCGCACTGGTGGTGTTTGCTGTCCACACTCTGGTGGCCGAGAAT 1

TGGACGCCCAAGGAGGCTCCCTGGAGGCTGCCCACATGTGCAGCTCAGCCCCCCCTGGCCT 3780 GCTGTGCAGGGGGTGTCCTTCAAGATCCACGCAGAGAAGAAGATGGGCATCGTTGGCAGG 3900 GCAGTGGCTACCCCACTGGCCACTGTGGCCATCCTGCCACTGTTTCTCCTCTACGCTGGG CTCGTGGGCTTCTCTGTCTCTGCTGCCCTCCAGGTGACCCCAGACACTGCAGTGGGTTGTT CAGGGCGGCCAGATCGAGTTCCGGGACTTTGGGCTAAGATGCCGACCTGAGCTCCCGCTG GACAAACTCCGGTCCCTGCTGATGTACGCCTTTGGACTCCTGGAGGTCAGCCTGGTGGTG CGAACCCAGGCCCCCTTTGTGGCTCAGAACAATGCTCGCGTAGATGAAAGCCAGAGGATC AGTTTCCCGCGACTGGTGGCTGACAGGTGGCTTGCGGCCAATGTGGAGCTCCTGGGGAAT GGCCTGGTGTTTGCAGCCGCCACGTGTGTGTGTGAGAAAACCCCACCTCAGTGCTGGC CGCAACTGGACAGACCTAGAGAACAGCATCGTGTCAGTGGAGCGGATGCAGGACTATGCC GCCGTGGGCACCCCCTCTGCCTCTACGCACTCTTCCTCTTCCTCTGCCAGCAAGTGGCC GGGCTGTTTGCCTCCATGGCTGCGGTGCTCCTAGGTGGGGCCCGGGCATCCAGGTTGCTC TTCCAGAGGCTCCTGTGGGATGTGGTGCGATCTCCCATCAGCTTCTTTGAGCGGACACCC 

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121
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Rat sequence differentially expressed in response to a hepatotoxin #479.
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                                                                                                                                                                                                                                                                                                     3840 GCTGTGCAGGCCGTGTCCTTCAAGATCCACGCAGGAGGAGGTGGGCGATCGTTGGCAGG 3899
                                                                                                                                                   CAGGCCATGCTCGGGAGCTGGTTTGCACAGTGCACTGTGCTGCCCATTGCCCACCGCCTG 4380
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                ACCGGGCAGGGAAGTCCTCCCTGGCCAGTGGGCTGCTGCGGCTCCAGGAGGCAGCTGAG
                                                      ACCGGGGCAGGGAAGTCCTCCCTGGCCAGTGGGCTGCTGCGGCTCCAGGAGGCAGCTGAG
                                              GGTGGGATCTGGATCGACGGGGTCCCCATTGCCCACGTGGGGCTGCACACACTGCGCTCC
                                                                              AGGATCAGCATCACCCCCAGGACCCCATCCTGTTCCCTGGCTCTCTGCGGGATGAACCTC
                                                                                              AGGATCAGCATCATCCCCCAGGACCCCATCCTGTTCCCTGGCTCTCTGCGGATGAACCTC
                                                                                                             GACCTGCTGCAGGAGCACTCGGACGAGGCTATCTGGGCAGCCCTGGAGACGGTGCAGCTC
                                                                                                                     4141 AAAGCCTTGGTGGCCAGCCTGCCCGGCCAGCTGCAGTACAAGTGTGCTGACCGAGGCGAG
                                                                                                                                                                           GACCTGAGCGTGGGCCAGAACAGCTCCTGTGTCTGGCACGTGCCCTTCTCCGGAAGACC
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                                                                                                                                                                                                                                                                        CGCTCCGTGATGGACTGTGCCCGGGTTCTGGTCATGGACAAGGGGGCAGGTGGCAGAGAGC
                                                                                                                                                                                                                                                                                drug screening;
                                                                                       Rat, ss; hepatotoxin; expressed sequence tag; EST; drug sca
differential expression; centrilobular necrosis; steatosis.
                                                                                                                                                                                                                                                                                                                                                                                         ABK62572 standard; cDNA; 5728 BP
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02-NOY-2000; 2000US-244880P.
11-MAY-2001; 2001US-29029P.
12-MAY-2001; 2001US-29045P.
22-MAY-2001; 2001US-292336P.
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                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                             4500 GGCCTGGTC 4508
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                                                                                                                                                                                                                                                                                                                                                                                                          ABK62572;
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The invention relates to methods for predicting toxic effects of compounds or the progression of these toxic effects by determining the compounds or the progression of these toxic effects by determining the compounds or progression in tissues or cells exposed to the toxic colls. Also included are methods of predicting at least one toxic cells. Also included are methods of predicting at least one toxic ceffect of a compound or progression of a toxic effect, preferably the expension in a tissue or cell sample exposed to the compound of two or care genes listed in the specification, where differential expression of the genes is indicative of at least one toxic effect or progression. Compare genes listed in the specification, where differential expression of the method can also be used to identify an agent which modulates the coxic response and predict cellular pathways that a compound modulates in a cell. The method sufflise a set of at least two probes (on a solid support in kit form), where each of the probes comprises a sequence that specifically hybridises to a gene listed in the specification, a computer system comprising at least two genes listed in the specification.

Compared to a set of the probes comprises a sequence of a set of genes comprising at least two genes listed in the specification. The method is useful for elucidating global chartifying the expression level in a tissue or cell of at least one gene listed in the specification. The method is useful for elucidating global charges in gene expression level in a tissue or cell of at least comprises or cell exposed to a known toxin. The genes may be used as toxicity markers in drug screening and toxicity assays. The genes and conservation of the physiological state of tissue or cell sample that has been exposed to a compound or agent. Hepatotoxicity consider the present independent or compound or agent. Hepatotoxicity asserd and a used to compound or agent. Hepatotoxicity asserd and evenuence is an every consider or cell exposed to a compound or agen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'n.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Predicting toxic effects of compounds or the progression of these toxic effects by determining the changes in gene expression in tissues or cells exposed to the toxin and comparing these to gene expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence is an expressed sequence tag (EST) or cDNA derived from a gene which is differentially expressed in response to a hepatotoxic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 CCTGCCGCCACCAGCCTGTGTGCTTCCTGAGAACAGCAGGGGTCTGGGTACCC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 GTCCTGTGTACCTCCAGCGTGGCTGTCGCTTTTGGAAAATCCAACAGGGAACGCCTGAG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                 Castle AL,
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80.3%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Seq ID No 479; 239pp; English.
                                                                                                                                                                                                                                                                                                 Johnson KR,
06-JUN-2001; 2001US-295798P.
13-JUN-2001; 2001US-297457P.
19-JUN-2001; 2001US-298884P.
09-JUL-2001; 2001US-303459P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inexposed tissues or cells
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                                                                                                                                                                                                                                                                                                 Porter MW,
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                                                                                                                                                                                                               (GENE-) GENE LOGIC
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Matches 3629; Conserv
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q	283	CHTCHCHAPACACOTHTCAACCTTCTTTTTTTTTTTTTTTTTTTTTTTT	
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g 6	343	GCCCCAGAGCTTCTCATTCACCCTACCGTGTGGCCTCACCATGAGCTTCGCCACCTTC 40	Ω
Qy Db	361	CTGATTCACACCGAGAGAAAAAGGGAGTCCAGTCATCTGGAGTGCTGTTTGGTTACTGG 420	α Δ.
Oy Dp	421	CTTCTCTGCTTTGTCTTGCCAGCTACCAACGCTGCCCAGCAGCGGGCGCTTC 480	о д
Oy Db	481	CAGAGCGACCCTGTCCGCCACCTGTCCTACCTATGCCTGTCTCTGGTGGTGGCACAG 540	0 0
Qy Db	541	TTGTGCTGTCCTGCCGGGGATCAACCCCCTTCTTCCCTGAAGACCCCCAGCAGTCT 600	ο <u>α</u>
Oy Ob	601	AACCCCTGTCCAGAGACTGGGGCAGCCTTCCCCTCCAAAGCCACGTTCTGGTGGGTTTCT 660	0 0
Qy Db	661	GGCCTGGTCTGGAGGGGATACAGGAGGCCACTGAAAGACCTCTGGTCGCTTGG 720 	
Qy Db	721	AGAGAAAACTCCTCAGAAGATTGTTTCCCGGCTTGAAAAGGAGTGGATGAGGAACGG 780	
Oy Db	781	AGTGCAGCCCGGAGGCACAACAAGGCATTTAAAAGGGAGAAGGCGGCAGTGGCATG 840	φ <u>Δ</u> (
Q.Y	841	AAGGCTCCAGAGACCGAGCCTTCCTACGGCAAGAAGGGAGCCAGTGGCGCCCACTGCTG 900	
Qy Db	901	AAGGCCATCTGGCAGGTGTTCCATTCTACCTTCCTGGGGACCCTCAGCCTCATCATC 960	<b>р</b>
Qy	961	AGTGARGTCTTCAGGTRCACTGTCCCCAAGCTGCTTTTTCCTGGAGTTTATTGGT 1020	
Oy Db	1021	GATCCCAAGCCTCCAGCTGGAAGGGCTACCTCGCCGTGGTGTTCCTCTCAGCC 1080	ם כ
Qy Db	1081	TGCCTGCAAACGCTGTTTGAGCAGCAGCAGAACGTGTCGAGGTGCCGCAGATGAGG 1140 	σ Δ
Qy Dp	1141	TTGCGGTCGGCCATCACTGGCCTGGTGAAAGGTCCTGGCTCTGTCCAGCGGCTCC 1200	O A
Q.y Db	1201	AGAAAGGCCAGTGGGGGGGGTGATGTGGTCAATCTGGTGTCCGTGGACGTGCAGGGCTG 1260	α Δ
Oy Db	1261 1279	ACCGAGAGCGTCCTCTACCTCAACGGCTGTGGCTGCTCTCGTCTGGATCGTGGTCTGC 1320	σ Δ
Qy Db	1321	TTGGTCTATCTGGGAGCTCCTGGGGCCCTCCGCCCTGCCATCGCTGTCTTCTG 1380	O Δ

1500 1518 2175 1440 1560 1578 1620 1638 1677 1698 1737 1758 1797 1818 1857 1878 1917 1935 1977 1995 2037 2055 2097 2115 2157 2217 2235 2277 2295 2337 2355 2397 2415 2457 2475 AGCCTCCTCCTCTGAATTTCTTCATCTCCAAGAAAGGAACCACCATCAGGAGGAGCAA ATCAAGTTCCATGGCTGGGAGGGAGCCTTTCTGGACAGAGTCCTGGGCATCCGAGGCCAG CGTCTGGTCACCTTCCTCTGCCTGGAAGAAGTTGACCCTGGTGTCGTAGACTCCAAGTTCC CAGGAAAGCCCTCCCTGCCTCCACAGAATAAACCTCACGGTGCCCCAGGGCTGTCTGCTG GAGCTGGGCGCCTTGCGGACCTCCGGCCTCCTTCTCTGTGTCGCTGGTGTCCTTCCAA TCTGGAAGCGCTGCCGGGAAGGATTGCATCACCATACACAGTGCCACCTTCGCCTGGTCC GAGGGAATCCACACTTCAATTGGGGAGCAGGCATGAATCTCTCCGGAGGCCAGAAGCAG CGGCTGAGCCTGGCCCGGGCTGTATACAGAAAGGCAGCTGTGTACCTGCTGGATGACCCC CTGGCGCCCTGGATGCCCACGTTGGCCAGCATGTCTTCAACCAGGTCATTGGGCCTGGT ATGAGGCAGAAGGACTCACGGGCACGGCTCACCAGCTCTATCCTCAGGAACTCGAAGACC CCCTGGCTGGAGAGAGTACTAGAAGCCTGTGCCCTGCAGCCAGATGTGGACAGCTTCCCT 1699 1879 1399 1519 1561 1579 1639 1738 1819 1918 2116 1441 1459 1501 1678 1759 1798 1858 1936 1978 1996 2056 2176 2278 1621 2038 2098 2158 2218 2236 2296 2338 2356 2398 2416 δy q δ do yo q Qγ qq ολ Dβ δ Db ò g Qy g φ g φ Ω δ Q οy g QΥ g οy g Q ŏ q ò Q g δ ò

us-09-647-140a-7.rng

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4213 4252 4273 4312 4312 432 4432 4453 4453 50LT 13 516236 AAD16	3133 CGCACACCAGTCGGGAACCTGCTGTTTTTTTTTTTTTTT
4312 4333 4372 4393	CTGGTGGTGGCAGTGGCTACCCCACTGTGGCCATCTGCCACTGTTTCTCCTC
4252	GACATICCAGACAAACICCGGICCCIGCIGAIGIACGCCITIGGACICCIGGAGGICAGC
4192	CGGACACCCATTGGTCACCTGCTAAACCGCTTCTCCAAGGAGACAGAC
4132	3052 AGGITGCICITCCAGAGGCICCIGIGGGAIGIGGTGCGAICTCCCAICAGCITCITIGAG 3111 
4072	2992 CAAGCCATTGGGCTGTTTGCCTCCATGGCTGCTGCTCCTAGGTGGGGCCCGGGCATCC 3051
4012	2932 GGTGGGCAGCAGAGCAGCCCTGCGTGCGGGATCTTCGGGCTCCTCGGCTGTCTC 2991 
3952	2872 CAAGTGGCCTCCTTCTGCCGGGCCTACTGGCTGAGCCTGTGGGCGGACCCTGCAGTA 2931 
Qy 3892 GTTGGCAGGACCGC	2812 TACCTGCGTGGGCACCCCCTCTGCCTCTAGGCACTCTTCCTCTCTCT
Qy 3832 CTCCGGCTGGCTG1 	2752 TGGCCAGCAGGAAGGACAGCATCCAATACGGCAGGGGTGAAGGCCACAGTGCACTGGCC 2811 
3772	2692 GACCGTACCACTTCAGAAGCCCAGAGGTTCCTCTGGATGACCTGACAGGGCAGGA 2751 
3712	2638 GGCAGGAGGCCCGAGCTTAGACGCGAGAGGTCCATCAAGTCAGTCCCTGAGAAG 2691 
3652	2578 AGAGGAGAAAGGAGAACCTGGGACCAGCACCAGGACCCCAGAGGCACCTCTGCA 2637 
3592 3613	2518 CTTCTGCAGAGGGGGCCCTCGTGTGTCTTCTGGATCAAGCCAGACAGCGAGAGT 2577 
3553	2458 GCTGATTGGATCATAGTGCTGGCAAATGGGGCCATCGCAGAGATGGGTTCCTACCAGGAG 2517 

3651 3672 3711 3732 4131 4212 4272 4332 4392 4452 FIGCAGGGCGTGTCCTTCAAGATCCACGCAGGAGAAAGGTGGGCATC 3891 3951 GGATCTGGATCGACGGGTCCCCATTGCCCACGTGGGGCTGCACACA 4011 4071 4251 4311 4431 4491 CCTTGGTGGCCAGCCTGCCGGCCAGCTGCAGTACAAGTGTGCTGAC 4191 4371 GGGCAGGGAAGTCCTCCCTGGCCAGTGGGCTGCTGCGGCTCCAGGAG STGGGCTTCTCTGTCTGCTGCCCTCCAGGTGACCCCAGACACTGCAG **AACTGGACAGACCTAGAAAAAGAACAGCATGGTCAGTGGAGCGGATGCAG** ATCAGCATCATCCCCCAGGACCCCATCCTGTTCCCTGGCTCTCTGCGG PERRECETGGCCAGARACAGCTCCTGTGTCTGGCACGTGCCCTTCTC TIGCTGCAGGACACTCGGACGAGGCTATCTGGGCAGCCCTGGAGACG GCTTCGTGACCAGCCTGCCTGCCAGCTGCAGTATGAGTGCTCAGGC CCGTGATGGACTGTGCCCGGGTTCTGGTCATGGACAAGGGGCAGGTG GCCCGGCCCAGCTGCCCCAGAAGGGCCTGTTTTACAGACTGGCC CCATGCTCGGGAGCTGGTTTGCACAGTGCACTGTGCTGCCCATTGCC CDNA; 4980 BP. | | | | TAGCC 4530 TGGTC 4509

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The invention relates to methods and compositions for diagnosing and treating Pseudoxanthoma elasticum (PXE) and PXE associated physiological dysfunctions. The invention is useful for screening for the presence of a PXE mutation. Mutations associated with PXE maps to the ATP-binding cassette transporter ABCC6 (MRP6-Multidrug Resistance associated consent of protein located in the plasma membrane containing 17 membrane. The protein located in the plasma membrane containing 17 membrane. The spanning helices grouped into three transmembrane domains. PXE is inherited as an autosomal recessive phenotype or appears as a sporadic phenotype. PXE is a heritable disorder characterised by mineralisation of elastic fibers in skin, arteries and the retina, that result in dermal lessons with associated laxity and loss of elasticity, arterial insufficiency, cardiovascular disease and retinal haemorrhages leading to macular degeneration. The method is useful for screening a population of individuals in order to identify individuals with one or more PXE associated MRP6 alleles who are then provided with appropriate genetic counselling in view of the PXE status. The methods are useful for identifying homozygotes, compound heterozygotes or carriers and thus are useful in the area of genetic testing, carrier detection and prenatal diagnosis. The present cDNA sequence encodes mouse APP-binding cassette (ABC) transporter, ABCC6 (MRP6) protein belonging to sub-family "C". Since ABCC6 protein is involved in drug-resistance it is also called
                                                                                                 Mouse; prenatal diagnosis; dermal lesion; cardiovascular disease; MRP6; Multidrug Resistance-associated protein 6; macular degeneration; ABCC6; ATP-binding cassette transporter; arterial insufficiency; chromosome 16; Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Screening presence of Pseudoxanthoma elasticum mutation useful for identifying homozygotes, compound heterozygotes or carriers involves determining presence of mutation in MRP6 (ABCC6) nucleic acid
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                                                                                                                                                                                                                                                                                                                              "Mouse ABCC6 (MRP6) protein"
                                                           cassette transporter ABCC6 (MRP6)
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                                                         ATP-binding
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DB 22; Length 4980;
66.7%; Score 3007.2;
80.1%; Pred. No. 0;
ive 0; Mismatches
                Similarity
   Query Match
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Gaps

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Conservative

Matches 3617;

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2342 2282 2402 2337 2397 2457 2462 2522 2575 2747 2517 2577 2637 2627 2691 2687 2751 2811 2807 2871 2867 2927 3047 3111 3167 3231 3287 2931 2991 3051 3107 3171 3227 3291 TACGCTGGGTTTCAGAGCCTGTATGTGGTTAGCTCATGCCAGCTGAGACGCTTGGAGTCA 3351 2223 GCAGGAGTTCACACCCCAATAGGGGAGCAGGGCATGAATCTTTCTGGGGGCCAGAGCAG TACCTGCGTGCCGTGGGCACCCCCTCTGCCTCTACGCACTCTTCCTCTTCCTTGCCAG 2868 CAAGIGGCATCCTTCTCCCAAGGCTACIGGCTGAGCCTTTGGGCCGATGACCCGGTTGTG 2988 CAAGCCATGGGACTGTTTGCCTCCATGGCTGCGGTGTTCCTGGGTGGAGCCCGGGCCTCA CTGGCGGCCCTGGATGCCCACGTTGGCCAGCATGTCTTCAACCAGGTCATTGGGCCTGGT AGAGGAGAAGGAGAAACATGGGACCAGCACCAAGGACCCCAGAGGCACCTCTGCA GGCAGGAGGCCCGAGCTTAGACGCGA-----GAGGTCCATCAAGTCAGTCCCTGAGAAG GACCGTACCACTTCAGAAGCCCAGACAGAGGTTCCTCTGGATGACCCTGACAGGGCAGGA TGGCCAGCAGGAAAGGACAGCATCCAATACGGCAGGGTGAAGGCCACACAGTGCACCTGGCC CAAGTGGCCTCCTTCTGCCGGGGCTACTGGCTGAGCCTGTGGGGCGGACGACCTGCAGTA AGGTTGCTCCTTCCAGAGGCTCCTGTGGGATGTGGTGCGATCTCCCATCAGCTTCTTTGAG CGGCTGAGCCTGGGCCTGTATACAGAAAGGCAGCTGTGTACCTGCTGGATGACCCC CAAGCCATTGGGCTGTTTGCCTCCATGGCTGCGGGCTTCCTAGGTGGGGCCCGGGCATCC GGTGGGCAGCAGCCAGCCCTGCGTGGCGGGATCTTCGGGCTCCTCGGCTGTCTC CTGGTGGTGGCAGTGGCTACCCCACTGGCCACTGTGGCCATCCTGCCACTGTTTCTCCTC GACATTCCAGACAAACTCCGGTCCCTGATGTACGCCTTTGGACTCCTGGAGGTCAGC 2338 2343 2398 2463 2578 2576 2628 2692 2748 2992 3052 3048 3112 3108 2403 2458 2688 2752 2812 2808 2872 2932 3172 3232 3292 2638 2928 3168 3228 QΥ qq Qγ Db οy Db οý qq δy qq QY Db Oy Db Db Qy g QY Db οy qq QY Db δ Ω οy Db δy qq Ωÿ Q δy QQ δ

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The present sequence is that of human ATP binding cassette
subfamily C protein ABCC1 cDNA. The cDNA was identified using a
differential display method in which monocytes from peripheral
blood were subjected to macrophage differentiation and cholesterol
coding with acetylated low density lipoproteins and subsequent
deloading with high density lipoprotein (HDL3) to identify
cholesterol sensitive genes. The gene maps to chromosome 16q13.12
and is also termed MRP1 (multidrug resistance associated protein).
The invention provides cholesterol-sensitive ABC genes (see
AA294734-63). These genes, and polypeptides encoded by them,
can be used for diagnostic and therapeutic applications, and for
biochemical or cell-based assays to screen for pharmacologically
cative modulator compounds useful for the treatment of lipid
disorders, atherosclerosis or other inflammatory diseases such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Adenosine triphosphate binding proteins useful for identifying agents for treating atherosclerosis and other inflammatory disorders \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96 GAGAACAGCAGGGGTCTGGGTACCCCCCATGTACCTCTGGGTCCTTGGTCCCATCTACCT 155
                                             4428 GCAGAAAGTGGCAATCCTGCTCAGCTGCTGCCCCAGAAAGGCCTGTTTTACAGGCTAGCC
GCAGAGAGCGGCAGCCGGCCCAGCTGCTGGCCCAGAAGGGCCTGTTTACAGACTGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABCC1; ATP binding cassette; human; cholesterol; lipid disorder; atherosclerosis; lipid disorder; dyalipidemia; psoriasis; lupus erythematosus; diagnosis; gene therapy; MRP1; multidrug resistance associated protein; chromosome 16q13.12; ss
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0; Mismatches 1933;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATP binding cassette ABCC1 (MRP1) cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             standard; cDNA;
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Matches 2539; Conserv
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	CCTCTTCATCCACCACGAGGGGGGGGACTCCGGATGTCCCCACTCTTCAAAGCCAA 	GATGGTGCTTGGATTCGCCCTCATAGTCCTGTGTACCTCCAGCGTGGCTGTCGCTCTTTG	GAAAATCCAACAGGGAACGCCTGAGGCCCCAGAATTCCTCATTCAT	CACCACGATGAGCTTCGCAGTGTTCTGAGTCCGAGAGAAAAAGGAGTCCAGTC 	ATCIGGAGIGCIGTIIGGTIACIGGCIICICIGCIITGICIIGCAGCIACCAACGCIGC 	CCAGCAGGCCTCCGGAGCGGCTTCCAGAGCGACCCTGTCCGCCACCTGTC	CACCTACCTATGCTGTGTGTGTGGTGCCACAGTTTGTGCTGTCTGCCTGGCGGATCA	acccccttcttcctgaagaccccagcagtctaacccctgtccagagactggggagc 	CTTCCCCTCCAAAGCCACGTTCTGGTGGTTTCTGGCCTGGTCTGGAGGGGATACAGGG 	GCCACTGAGACCAAAAGACCTCTGGTCGCTTGGGAGAGAAACTCCTCAGAAGAACTTGT 	TTCCCGGCTTGAAAAGAGTGGATGAGGAACCGCAGTGCAGCCCGGAGGCACAACA 	aggcaatagcytttaaaaggaagaggggagtggcatgaaggctcca	GAGACCGAGCCCTTCCTACGGCAAGAGGGAGCCAGTGGCGCCCACTGCT	GAAGGCCATCTGGCAGGTGTTCCATTCTACCTTCCTCTGGGGACCCTCAGCCTCATCAT 	CAGTGATGTCTTCAGGTTCACTGTCCCCAAGCTGCTCAGCCTTTTCCTGGAGTTTATTGG	TGATCCCAAGCCTCCAGCCTGGAAGGCCTACCTCCTCGCCGTGCTGATGTTCCTCTCAGC 	CTGCCTGCAAACGCTGTTTGAGCAGCAGAACATGTACAGGCTCAAGGTGCCGCAGATGAG 	AAGGTCCTGGCTCTGTCCA
	CCATGGCCGGGGCTACCTC                 ACATGACCGAGGCTACATI	CGCCCTCATAGTCCTGTG1 	aacgcctgaggccccagaa   	CGCAGIGIICCIGAIICAC 	IGGTTACTGGCTTCTCTGC 	-GCCTCCGGAGCGGGCTTC         ACCTTAAAAGAGGATGCC	STCTCTGGTGGTGGCACAG 	rgaagaccccagcagtct 	CACGTTCTGGTGGGTTTCT 	AGACCTCTGGTCGCTTGGG 	ggagtggatgaggaaccgc 	aaaggaaaggcggcagtgg         aaggatcctgcccagccg	CGAGCCCTTCCTACGGCAA 	GTGTTCCATTCTACCTTCCTC	STTCACTGTCCCCAAGCTG	CAGCCIGGAAGGGCIACCIC 	STTTGAGCAGCAGAACATG	GTTGCGGTCGGCCATCACTGGTGTACAGAAAGGTCCTGGCTCTGTCCAGCGGCTC
			GAAAATCCAACAGGG          GGAAAGTCGGGGG	CACCACGATGAGCTTC	ATCTGGAGTGCTGTT	CCAGCAG	CACCTACCTATGCCT             TTCTACGTCTACTT	ACCCCCTTCTTCCC:                       CTCACCCCTGTTCTCC	CTTCCCCTCCAAAGCC	GCCACTGAGACCAAAA               GCCCCTGGAGGGCAGG	TTCCCGGCTTGAAAAC 	AGGCAATAGCATTTAA 	GAGACC         TGAGGAGGTGGAGGCT	GAAGGCCATCTGGCAC             TAAGGTGTTATACAAC	CAGTGATGTCTTCAGG	TGATCCCAAGCCTCCA 	CTGCCTGCAAACGCTG	GTTGCGGTCGGCCATC
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qq	QY	QY	Qy	QY Db	Qy Dp	Oy Dp	Oy Db	Qy Dp	Oy Dp	Q Q	QY Dp	Qy Db	Qy	O.Y	QY Db	Oy Db	OY Db	οy

1259 1497 1379 1617 1439 1559 1679 1796 1378 GATCAAGACCGCTGTCATTGGGGCTGTCTATCGGAAGGCCCTGGTGATCACCAATTCAGC 1437 GACCGAGAGCGTCCTCTACCTCAACGGGCTGTGGCTGCCTCTCGTCTGGATCGTGGTCTG 1319 1440 AATGAGGCAGAAGGACTCACGGCCACGGCTCACCAGCTCTATCCTCAGGAACTCGAAGAC 1499 GGAGCTGGGCGCCTTGCGGACCTCCGGCCTCCTTCTCTGTGTCGCTGGTGTCCTTTCA 1619 1857 CTGCACGCCCTTCTGGTGGCCCTTGTGCACATTGCCGTCTACGTGACCACACAAA 1917 2037 1856 1916 2157 1976 2217 2036 2277 2096 2097 2337 2156 2457 CAGAAAGGCCCAGTGCGGTGATGTGGTCAATCTGGTGTCCGTGGACGTGCAGCGGCT 1320 CTTCGTCTATCTCTGGCAGCTCCTGGGGCCCTCCGCCCTCACTGCCATCGCTGTCTTCCT 1620 AGTGTCTACATTTCTGGTCGCACTGGTGTTTGCTGTCCACACTCTGGTGGCCGAGAA CTCTGGAAGCGCTGCCGGGAAGGATTGCATCACCATACACAGTGCCACCTTCGCCTGGTC GAGCCTCCTCTGAATTTCTTCATCTCCAAGAAAAGGAACCACCATCAGGAGGAGCA 1500 CATCAAGTTCCATGGCTGGGAGGGAGCCTTTCTGGACAGAGTCCTGGGCATCCGAGGCCA 1737 GGCCCAGGCTTTCCTGCCTTCTCCATCCACTCCTCGTCCAGGCCCGGGTGTCCTTTGA CCGTCTGGTCACCTTCCTCTGCAGAAGAAGTTGACCCTGGTGTCGTAGACTCAAGTTC CCAGGAAAGCCCTCCCTGCCTCCACAGAATAAACCTCACGGTGCCCCAGGGCTGTCTGCT CAGGAGCGACCCCCCCACATGGCATCACCTTCTCCATCCCCGAAGGTGCTTTGGT GCCTGTTGTCGGTCCAGTGGGGCAGGGAAGTCCTCCCTGCTGTCCGCCCTCCTTGGGGA GCTGTCAAAGGTGGAGGGTTCGTGAGCATCGAGGGTGCTGTGGCCTACGTGCCCCAGGA GGCCTGGGTGCAGAACACCTCTGTGGTAGAATGTGTGCTTCGGGCAGGAGCTGGACCC ACCCTGGCTGGAGAGAGTACTAGAAGCCTGTGCAGCCAGATGTGGACAGCTTCCC TGAGGGAATCCACACTTCAATTGGGGAGCAGGGCATGAATCTCTCCGGAGGCCAGAAGCA 1260 1380 1200 1858 2218 1678 1560 1798 1797 1857 1917 2158 2278 2338 2217 2038 2098 1977 2037 2097 2157 2398 g ò QQ Qy qq Qy Db. q Qγ g ò Óγ g δ ΩD δ ДQ g QQ ò οy ŏ Db ò g δy ag g οy δ Db QYPp ŏ qq Ω Db

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2277 GCGGCTGAGCCTGGCCCGGGCTGTATACAGAAAGGCAGCTGTGTACCTGCTGGATGACCC   1   1   1   1   1   1   1   1   1	2337 CCTGGCGGCCCTGGATGCCCACGTTGGCCAGCATGTCTTCAACCAGGTCATTGGGCCTGG	2397 TGGGCTACTCCAGGGAACAACACGGATTCTCGTGACGCACGC	2457 GGCTGATTGGATCATAGTGCTGCCAAATGGGGCCATCGCAGAGATGGGTTCCTACCAGGA	2517 GCTTCTGCAGAGGAGGGCCCTCGTGTGTCTTCTGGATCAAGCCAGACAGGAGA   1	2577 TAGAGGAGAAGGAGAACAGAACCTGGGACCAGCACCAAGGACCCCAAAGGACCTTGC   1   1   1   1   1   1   1   1   1	2637 AGGCAGGACCCGAGCTTAGACGCGAGAGGTCCATCAAGTCAGTC	2692		2777 AATACGGCAGGGTGAAGGCCACAGTGCACTGGGCTACCTGCGTGCG	2837 TCTGCCTCTACGCACTCTTCCTCTGCCAGCAAGTGGCCTCCTTCTGCGGGGCT	2897 ACTGGCTGAGCCTGTGGGCGGACGACCCTGCAGTAGGTGGGCAGCAGCAGCGAGCCCCCCCC	2957 IGCGIGGGGGAICTICGGGCICCTCGGCIGTCTCCAAGCCATIGGCCIGTITGCCTCCA	3017 TGGCTGCGGTGCTCCTAGGTGGGGCCCGGCATCCAGGTTGCTCTTCCAGAGGTTCCTGT	3077 GGGATGTGGTGCGATCTCCCATCAGCTTCTTTGAGCGGACACCCATTGGTCACTGCTAA 	3137 ACCGCTTCTCCAAGGAGACAGGCTTGACGTGGACATTCCAGACAAACTCCGGTCCC	3197 IGCIGAIGTACGCCTTIGGACTCCTGGAGGTCAGCCTGGTGGTGGCAGTGGCTACCCCAC	3257 TGGCCACTGTGGCCATCCTGCTGTTTCTCCTCTACGCTGGGTTTCAGAGCTGTATG
QY	Qy	Qy Dp	Qy Db	Qy Db	Qy Db	Q Db	oy B	QY Db	Qy Db	Qy	Qy	Qy Db	oy Op	Qy Db	Qy Db	Qy Db	OY Db

3796 4436 4216 4616 3376 3656 3436 3496 3776 3556 3836 3616 3676 3956 3736 4016 4076 3916 4196 3976 4256 4036 4316 4096 4376 4156 4496 4276 4556 4336 4396 4676 ATTTCAACGAGACCTTGCTGGGGGTCAGCGTCATTCGAGCCTTCGAGGAGCAGGAGCGCT TCATCCACCAGAGTGACCTGAAGGTGGACGAGAACCAGAAGGCCTATTACCCCAGCATCG TCTCTGCTGCCCTCCAGGTGACCCAGACACTGCAGTGGGTTGTTCGCAACTGGACAGACC AGTTCCGGGACTTTGGGCTAAGATGCCGACCTGAGCTCCCGCTGTGCAGGGCGTGT ACTCGGACGAGGCTATCTGGGCAGCCCTGGAGACGGTGCAGCTCAAAGCCTTGGTGGCCAA AGAAACAGCTCCTGTGTCTGGCACGTGCCCTTCTCCGGAAGACCCAGATCCTCATCCTGG CCGCCACGTGTGCTGTGCTGAGCAAAGCCCACCTCAGTGCTGGCCTCGTGGGCTTCTCTCT CCCAGGACCCCATCCTGTTCCCTGGCTCTCTGCGGATGAACCTCGACCTGCTGCAGGAGC GCCTGCCCGGCCAGCTGCAGTACAAGTGTGCTGACCGAGGCGAGGACCTGAGCGTGGGCC ACATGGCTGAGACGTTCCAGGGCAGCACAGTGGTCCGGGCATTCCGAACCCAGGCCCCCT TTGTGGCTCAGAACAATGCTCGCGTAGATGAAAGCCAGAGGATCAGTTTCCCGGGACTGG TGCTGACAGGTGGCTTGCGGCCCAATGTGGAGCTCCTGGGGAATGGCCTGGTGTTTGCAG CTGCCCTGTTTGCGGTGATCTCCAGGCACAGCCTCAGTGCTGGCTTGGTGGGCCTCTCAG CCTTCAAGATCCACGCAGGAGAAGGTGGGCATCGTTGGCAGGACCGGGGCAGGGAAGT CCTCCCTGGCCAGTGGGCTGCTGCGGCTCCAGGAGGCAGCTGAGGGTGGGATCTGGATCG ACGGGGTCCCCATTGCCCACGTGGGGCTGCACACTGCGCTCCAGGATCAGCATCATCC CCCTTCCTGACAAGCTAGACCATGAATGTGCAGAAGCCGGGGAGAACCTCAGTGTCGGGC ACGAGGCTACTGCTGCCGTGGACCCTGGCACGGAGCTGCAGATGCAGGCCATGCTCGGGA GCTGGTTTGCACAGTGCACTGTGCTGCCCATGCCCACCGCCTGCGCTCCGTGATGGACT 4617 CACAGTTCGAGGACTGCACCGTCCTCACCATCGCCCACGGCTCAACACACATCATGGACT 4017 4197 4377 4437 3717 4077 4557 3657 3557 3837 3617 3977 4257 4097 4157 4497 4277 4337 3317 3597 3377 3437 3497 3897 3677 3957 3737 3797 3857 3917 4037 4317 4217 Ωp Οy Dp ò g QΫ́ QQ δy QΩ δλ g ΟŸ qq δý g ōλ Db Qγ DP Qγ qq Qγ pp Óγ οg δy qq δ Op Qγ QQ ŏλ Db δ Ωp

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GTGCCCGGGTTCTGGTCATGGACAAGGGGCAGGTGGCAGAGAGCGGCCCGGCCCAGC

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Gaps

Length 5011; 80;

Score 1229.2; DB 24; Lengtl Pred. No. 1.7e-263; 0; Mismatches 1933; Indels

27.3%; 55.8%;

Best Local Similarity 55.8 Matches 2539; Conservative

Query Match

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GCTCTGGGACTGGAATGTCACGTGGAATACCAGCAACCCCGACTTCACCAAGTGCTTTCA GAGAACAGCAGGGTCTGGGTACCCCCCATGTACCTCTGGGTCCTTGGTCCCATCTACCT 

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GGTCTGGAACCAGACAGAGCCTGAACCTGCCGCCACCAGCCTGCTGAGCCTGTGCTTCCT

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Detecting a prostate cancer-associated transcript in a cell in a patient, useful for diagnosing prostate cancer (PC) or screening modulators of PC, by determining if prostate cancer-associated genes are expressed in a prostate tissue
                                                                                                                                                           prostate tumour tissue; human; mammal; cytostatic;
                                  TGCTGGCCCAGAAGGGCCTGTTTTACAGACTGGCCCCAGGAGTCAGGCCTGGT
                                                                                                                                                                                                                                                                                                                                                                          Hevezi P;
                                                                                                                                         Prostate cancer-associated DNA sequence #11.
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2000US-0733742.
2001US-263957P.
2001US-276791P.
2001US-276888P.
                                                                                    ABK92125 standard; DNA; 5011
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2001US-0847046.
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P-PSDB; ABG61810.
                                                                                                                                                           Prostate cancer;
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16-MAR-2001;
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216 GATGGTGCTTGGATTCGCCCTCATAGTCCTGTGTACCTCCAGCGTGGCTGTCGCTCTTTG

CCTCTTCATCCACCACCATGCCGGGGCTACCTCCGGATGTCCCCACTCTTCAAAGCCAA

396 ATCTGGAGTGCTGTTTGGTTACTGGCTTCTCTGCTTTGTCTTGCCAGCTACCAACGCTGC CCAGCAG------GCCTCCGGAGCGGCTTCCAGAGCGACCTGTCCGCCACCTGTC

CACCACGATGAGCTTCGCAGTGTTCCTGATTCACACCGAGAGAAAAAGGGAGTCCAGTC

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276 478 455

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558 ATCCAAAATTATGACAGCCTTAAAAGAGGATGCCCAGGTGGACCTGTTTCGTGACATCAC 717 

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718 TITCTACGICTACTITICCCICITACTCATICAGCICGICITGICCIGITICICAGAICG 777

567 ACCCCCTTCTTCCCTGAAGACCCCCAGCAGTCTAACCCCTGTCCAGAGACTGGGGGCAGC

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CAGIGAIGITTCAGGITCACTGICCCCAAGCIGCICAGCCTTTTCCTGGAGITTAITGG 1019
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CTCACCCCTGTTCTCGGAAACCATCCACGACCTAATCCCTGCCCAGAGTCCAGCGCTTC 837
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                                           CTTCCCCTCCAAAGCCACGTTCTGGTGGGTTTCTGGCCTGGTCTGGAGGGGATACAGGAG 686
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cancer-associated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with prostate cancer-associated polynucleotides (designated PC genes) that selectively hybridise to a sequence that is at least 80% identical to them. The prostate cancer-associated bolynucleotide sequences are differentially expressed in prostate tumour tissue or in prostate cancer and are derived from the tissues of various

The present invention relates to methods of detecting a prostate

organisms such as humans or other mammals (e.g. mice, sheep and dogs). The methods of the invention are useful for diagnosing and treating prostate cancer in mammals. The prostate cancer-associated genes are useful for diagnosing or treating prostate cancer, as well as for

useful for diagnosing or treating prostate cancer, as well as for identifying modulators of prostate cancer or agents that inhibit prostate cancer. The nucleic acid sequences are particularly useful in gene therapy, as a vaccine or in antisense applications.

ABK92115-ABK92263 represent prostate cancer-associated polynucleotide

sednences

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TGATCCCAAGCCTCCAGCCTGGAAGGGCTACCTCCTCGCCGTGCTGATGTTCCTCTCAGG 	CTGCCTGCAACGCTGTTTGAGCAGCAGAACATGTACAGGCTCAAGGTGCCGCAGATGAG	GTTGCGGTCGGCCATCACTGGCCTGGTGTACAGAAAGGTCCTGGCTCTGTCCAGCGGCTCTCTCT	CAGAAAGGCCAGTGCGGTGGGTGGTGCTCAATCTGGTGTCCGTGGACGTGCAGCGGCT 	GACCGAGAGCGTCCTCTACCTCAACGGGCTGTGGCTGCTCGTCTGGATCGTGGTCTG	CTTCGTCTAPCTCTGGCGGCCTCCGCCCTCACTGCCATCGCTGTCTTCCT	GAGCCTCCTCCTCTGAATTTCTTCATCTCCAAGAAAGGAACCACCATCAGGAGGAGCACACACCATCAGGAGGAGCACAAGGACCACCATCATCAGAGCCAAGACCAAGACGTATCAGGGCGATGAATGGCGATGAAGACCAAGACGTATCAGGGCCCA	AATGAGGCAGAAAGGACTCACGGCTCACCAGCTCTATCCTCAGGAACTCGAAGAC 	CATCAAGTTCCATGGCTGGGAGCCTTTCTGGACAGAGTCCTGGGCATCCGAGGCCA 	GGAGCTGGGGCCTTGCGGCCTCCTCTTCTCTGTGCCTGGTGTCCTTCCA	AGGGCCACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	TGCTATGAATGCAGAGAAAGCCTTTGTGACTCTCACAGTTCTCAACATCCTCAACAA	GGCCCAGGCTTTCTGCATCCACTCCTCGTCCAGGCCGGGGTGTCTTTGA	CCGTCTGGTCACCTTCCTCTGCTGGAAGAAGTTGACCCTGGTGTCGTAGACTCAAGTTC 	CTCTGGAAGCGCTGCCGGGAAGGATTGCATCACCATACACAGTGCCACCTTGGCCTGGTC	CCAGGAAAGCCCTCCCTGCCTCCACAAAACCTCACGGTGCCCCAGGGCTGTCTGCT 	GGCIGTIGTCGGTCCAGTGGGGGGGGAGGTCCTCCTGCTGTCGCCCTCCTTGGGA 	GCTGTCAAAGGTGGAGGGTTCGTGAGCATCGAGGGTGCTGTGGCCTACGTGCCCCAGGA 	
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2276 2636 2876 2457 2517 2336 2577 2396 2637 2456 2516 2757 2816 2691 2776 3056 2836 3116 2896 3176 3016 3296 3076 3356 GCTTCTGCAGAGGAAGGGGGCCCTCGTGTGTCTTGGATCAAGCCAGACAGCCAGGAGA 2576 2937 TCAGCAGCTCCTCCTCTATAGTGGGGACATCAGCAGGCACCACAACAGCACCGCAGAAC 2996 3357 ACAGCATCCTGCGGTCACCCATGAGCTTCTTTGAGCGGACCCCCAGTGGGAACCTGGTGA 3416 ACCGCTTCTCCAAGGAGACAGACACGCTTGACGTGGACATTCCAGACAAACTCCGGTCCC 3196 2577 TAGAGGAGAAAGAAACAGAACCTGGGACCAGCACCAAGGACCCCAGAGGCACCTCTGC 2877 ACCAAATGGAGAATGGCATGCTGGTGACGGACAGTGCAGGGAAGCAACTGCAGAGCAGGC TGCGTGGCGGGGTCTTCGGGCTCCTCGGCTGTCTCCAAGCCATTGGGCTGTTTGCCTCCA ACCCTGGCTGGAGAGATACTAGAAGCCTGTGCCCTGCAGCCAGATGTGGACAGCTTCCC TGAGGGAATCCACACTTCAATTGGGGAGCAGGGCATGAATCTCTCCGGAGGCCAGAAGCA | GCGCTGAGCCTGCCCCGGCTGTATACAGAAAGGCAGCTGTGTACCTGCTGGTGATGACCC CCTGGCGGCCCTGGATGCCCACGTTGGCCAGCATGTCTTCAACCAGGTCATTGGGCCTGG GCCTGATTGGATCATAGTGCTGGCAAATGGGGCCATCGCAGAGATGGGTTCCTACCAGGA GGGAIGTGGTGCGATCTCCCATCAGCTTCTTTGAGCGGACACCCATTGGTCACCTGCTAA ------GACCGTACCACTTCAGAAGCCCAGA--2717 CAGAGGTTCCTCTGGATGACCCTGACAGGGCAGGATGGCCAGCAGGAAAGGACAGCATCC 2997 TGCAGAAAGCTGAGGCCAAGAAGGAGGAGCTGGAAGCTGATGGAGGCTGACAAGGCGC AATACGGCAGGGTGAAGGCCACAGTGCACCTGGCCTACCTGCGTGCCGTGGGCACCCCCC TCTGCCTCTACGCACTCTTCCTCTTCCTGCCAGCAAGTGGCCTCCTTCTGCCGGGGCT 3017 TGGCTGCGGTGCTCCTAGGTGGGGCCCGGGCATCCAGGTTGCTCTTCCAGAGGCTCCTGT 2398 2458 2518 2457 2698 2517 2758 2157 2897 2338 2217 2337 2637 2692 2777 3057 3177 2837 2957 3237 3297 3137 Ω qq Ω q Qγ Ob δ Db òγ Ω QY g Qγ q οy QQ ΩŸ Op ŏ qq Qγ qq QY Ω οy Op Óγ Q οy qq ōλ q ōλ g

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                 TGCTGATGTACGCCTTTGGACTCCTGGAGGTCAGCCTGGTGGTGGCGAGTGGCTACCCCAC 3256
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                                                            TCATCCACCAGAGTGACCTGAAGGTGGACGAGAAGGCCTATTACCCCAGGATGG
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	1.1 Homo so Sequence	AF410948 Macaca mu AX410727 Sequence U49248 Human canal AF227274 Mus muscu
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Score		713 713 713 711.6
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## ALIGNMENTS

RESULT 1 AF168791	
rocus	AF168791 4509 bp mRNA linear PRI 25-AUG-1999
DEFINITION	Homo sapiens multi-specific organic anion tranporter-E mRNA,
	partial cds.
ACCESSION	ĀF168791
VERSION	AF168791.1 GI:5764414
KEYWORDS	
SOURCE	Homo sapiens.
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 4509)
AUTHORS	Belinsky, M.G. and Kruh, G.D.
TITLE	MOAT-E (ARA) is a full length MRP/cMOAT subfamily transporter

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/map="16p13"
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expressed in kidney and liver
Br. J. Cancer (1999) In press
2 (bases 1 to 4509)
Belinsky,M.G. and Kruh,G.D.
Direct Submission
Submitted (13-JUL-1999) Medical
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Page 3

o d	1381	AGCCTCCTCCTCTGAATTTCTTCATCTCCAAGAAAGGAACCACCATCAGGAGGAGCAA 1440 	
Qy Db	1441	ATGAGGCAGAAGGACTCACGGGCACGGCTCACCAGCTCTATCCTCAGGAACTCGAAGACC 1500 	
Qy Dp	1501	ATCAAGTTCCATGGCTGGGAGGGAGGCCTTTCTGGACAGAGTCCTGGGCATCCGAGGCCAG 1560	
Qy Dp	1561	GAGCTGGGCGCTTGCGGACCTCCGCCTCTTCTCTGTGTCGCTGTCCTTCCAA 1620	
Qy	1621	GIGICIACATITCIGGICGCACIGGIGITIGCIGICCACACICIGGIGGCCGAGAAI 1680 	
oy Db	1681 1681	GCTATGAATGCAGAGAAAGCCTTTGTGACTCTCACAGTTCTCAACATCCTCAACAAGGCC 1740 	
Oy .	1741	CAGGCTTTCCTGCCCTTCTCCATCCACTCCTCGTCCAGGCCCGGGTGTCCTTTGACCGT 1800	
Qy Db	1801	CIGGICACCTICCTCTGCCTGGAAGATGACCTGGTGTCGTAGACTCAAGTTCCTCT 1860 	
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Qy Dp	1981 1981	GTTGTCGGTCCAGTGGGGGCAGGAAGTCCTCCTGCTGCTCCCCCTCCTTGGGGAGCTG 2040	
O.Y	2041	TCAAAGGTGGAGGGTTCGTGAGCATCGAGGGTGCTGTGGCCTACGTGCCCCCAGGAGGCC 2100	
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Qy Db	2281	CTGAGCCTGGCCCGGCTGTATACAGAAAGGCAGCTGTACCTGCTGGATGACCCCTG 2340	
Qy	2341	GCGGCCCTGGATGCCCACGTTGCCCACATGTCTTCAACCAGGTCATTGGGCCTGGTGGG 2400	
oy B	2401	CTACTCCAGGGAACAACACGGATTCTCGTGACGCACGCAC	
δy	46	TTGGATCATAGTGCTGGCAAATGGGGCCATCGCAGAGATGGGTTCCTACCAGGAGCTT 252	

2520 2580 2580 2640 2640 2700 2700 2760 2760 2820 2820 2880 2880 2940 2940 3000 3000 3060 3060 3120 3120 3180 3180 3240 3240 3300 3300 3360 3420 3420 3480 3480 3540 3540 3600 TCCTTCTGCCGGGGCTACTGGCTGAGCCTGTGGGCGGACGACGCCTGCAGTAGGTGGGCCAG TCGTCTGTCTGCTCCCACATGGCTGAGACGTTCCAGGGCAGCACAGTGGTCCGGGCATTC GGAGAAGGAGAAACAGAACCTGGGACCAGCACCAAGGACCCCAGAGGCACCTCTGCAGGC GGCCTGGTGTTTGCAGCCGCCACGTGTGCTGAGCAAAGCCCACCTCAGTGCTGGC GCCGTGGGCACCCCCCTCTGCCTCTACGCACTCTTCCTCTTCCTCTGCCAGCAAGTGGCC CAGACGCAGGCCCTGCGTGGCGGGATCTTCGGGCTCCTCGGCTGTCTCCAAGCCATT **ACTTCAGAAGCCCAGACAGAGGTTCCTCTGGATGACCCTGACAGGGCAGGATGGCCAGCA** GGAAAGGACAGCATCCAATACGGCAGGGTGAAGGCCACAGTGCACCTGGCCTACCTGCGT GCCGTGGGCACCCCCTCTGCCTCTACGCACTCTTCCTCTTCCTCTGCCAGCAAGTGGCC GACAAACTCCGGTCCCTGCTGATGTACGCCTTTGGACTCCTGGAGGTCAGCCTGGTGGTG GCAGTGGCTACCCCACTGGCCACTGTGGCCATCCTGCCACTGTTTCTCCTCTACGCTGGG AGTITCCCGCGACTGGTGGCTGACAGGTGGCTTGCGGCCAATGTGGAGCTCCTGGGGAAT 2941 3241 3541 2521 2521 2581 2581 2641 2641 2701 2761 2821 2821 2881 2881 2941 3001 3061 3061 3121 3181 3181 3241 3301 3361 3361 3421 3481 3481 2461 2701 2761 3001 3121 3301 3421 g g pp qq Db qq οp qq qq Op g g g qq g g qq ογ Qγ Óγ óλ QY ò Q ŏ Qγ δy δ δ Dp δ δ ŏ δλ ôγ Óγ

KEYWORDS . SOURCE human. ORGANISM HOMO SA ORGANISM HOMO SA MANMALI REFERENCE 1 AUTHORS BOYD, C. TITLE MEthods clastic JOURNAL PATENTY FEATURES SOURCE	CDS				BASE COUNT 8 ORIGIN	Query Match Best Local Simila Matches 4503; Co	Qy 1 ATGGCGGG                     Db 1 ATGGCGGG	0y 61 CCTGCCGCC 	0y 121 CCCATGTAC                     Db 121 CCCATGTAC	Oy 181 GGCTACCTC
3541 GGCCTGGTGTTTGCAGCCGCCACGTGTGCTGAGCAAAGCCCACCTCAGTGCTGGC 3600 3601 CTCGTGGGCTTCTGTTGCTGCTGCCTCCAGGTGACCCAGACACTGCAGTGGTTTT 360 111111111111111111111111111111111111	3781 CAGGGCGGCAGATCCAGGACTTTGGGCTAAGATGCCGACCTGAGCTCCGGCTG	3901 3901 3961 3961	4021 AGGATCAGCATCATCCCCAGGACCCCATCCTGTTCCTGGGCTCTTGGGGATGAACCTC 4080	4141 AAAGCCTTGGTGGCCAGCCTGCCGGCTACAAGTGTGCTGACCGGGCGAG 4200	4261 CAGATCCTCATCCTGGACGAGGCTACTGCTGCACCCTGGCAGCGGAGCTGCAGTG 4320 	4321 CAGGCCATGCTCGGCAGCTGGTTTGCACAGTGCACTGTGCCCATTGCCCACCGCCTG 4380	4381 CGCTCCGTGATGGACTGTGCCCGGGTTCTGGTCATGGACAAGGGGCAGGTGGCAGAGAGC 4440 	4441 GGCAGCCGGCCCAGCTGCTGGCCCAGAAGGCCTGTTTTACAGACTGGCCCAGGAGTCA 4500 	4501 GGCTGGTC 4509 	AX282510 AX282510 LOCUS AX282510 DEFINITION Sequence 2 from Patent W00162977. ACCESSION AX282510 VERSION AX282510.1 GI:16609640
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Kool,M., van der Linden,M., de Haas,M., Baas,F. and Borst,P.
Expression of human MRP6, a homologue of the multidrug resistance
protein gene MRP1, in tissues and cancer cells
Cancer Res. 59 (1), 175-182 (1999)
                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                      Direct Submission
Submitted (05-JUL-1998) Molecular Biology, The Netherlands Cand
Institute, Plesmanlaan 121, Amsterdam 1066 CX, The Netherlands
Location/Qualifiers
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/organism="Homo sapiens"
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/map="16p13"
1. .4535
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/db_xref="G1:3928849"
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24. .4535
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/note="similar to m
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         GCCCCAGAATTCCTCATTCATCCTACTGTGTGGCTCACCACGATGAGCTTCGCAGTGTTC
                                                                                                                                             324 GCCCCAGAATTCCTCATTCATCCTACTGTGTGCCTCACCACGATGAGCTTCGCAGTGTTC
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1201   AGANAGGCCAGTGGGTCATGTGGTCATCGTGTCCTGGACCTGCACCGCGTG   126		0 8	· .		0 8	0 6	0 m	0 m		O m	O m	O m	ο ε	· 6		0 E	0 E	3	ο Δλ
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2604 GGAGAAAGGAGAAACAGAACCTGGGACCAGGACCCAAAGACCCCAGAGGACCTCTGCAGGC ACTICAGAAGCCCAGACAGAGGTTCCTCTGGATGACCCTGACAGGGCAGGATGGCCAGCA GGAAAGGACAGCATCCAATACGGCAGGGTGAAGGCCACAGTGCACCTGGCCTACCTGCGG GCGCCCTGGATGCCCACGTTGGCCAGCATGTCTTCAACCAGGTCATTGGGCCTGGTGGG CTGCAGAGGAAGGGGCCCTCGTGTCTTCTGGATCAAGCCAGACAGCCAGGAGATAGA GGAGAAGGAGAAACAGAACCTGGGACCAGCACCAAGGACCCCAGAGGCACCTCTGCAGGC CAGACGCAGGCAGCCCTGCGTGGCGGGATCTTCGGGCTCCTCGGCTGTCTCCCAAGCCATT TTCCAGAGGCTCCTGTGGGATGTGGTGCGATCTCCCATCAGCTTCTTTGAGCGGACACCC ATTGGTCACCTGCTAAACCGCTTCTCCAAGGAGACAGGACACGGTTGACGTGGACATTCCA GCAGTGGCTACCCCACTGGCCACTGTGGCCATCCTGCCACTGTTTCTCCTCTACGCTGGG TCGTCTGTCTGCTCCCACATGGCTGAGACGTTCCAGGGCAGCACAGTGGTCCGGGCCATTC 

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        283 CTTCTCTACACCTTCAACGCGGCCGTGCCTCTCTGGAGGATCCACCGGGGCATGCCCCAG 342
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80.3%; Pred. No. 0;
Live 0; Mismatches 850; Indels 39;
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                                                                                                                                                                                                                                                                                     Location/Qualifiers
1. 5728
//organism="Rattus norvegicus"
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/note="EMBL/GenBank Accession No. AB010466"
a 1676 c 1663 g 1297 t
                                                                                                                                                                                                                         Mendrick,D., Porter,M.W., Johnson,K.R., Castle,A.L. Elashoff,M.R.
Molecular toxicology modeling
Patent: WO 0210453-A 479 07-FEB-2002;
                                                                                        linear
                                                                                        DNA
                                                                                Sequence 479 from Patent W00210453. AX400803.1 GI:21336983
                                                                                                                                                                                                                                                                             Gene Logic, Inc. (US)
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Matches 3629; Conservative
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	721 AGAGAA.         763 AGAGAA.	agagaaactcctcagaagaacttctttccggcttgaaaaggagtggatgaggaaccgc 780 	
	781 AGTGCA(      823 AGTGAG	AGTGCAGCCCGGAGGCAACAAGGCAATAGCATTTAAAAGGAAAGGCGGCAGTGGCATG 840 	
~ ~	841 AAGGCT( 	AAGGCTCCAGAGACCGAGCCCTTCCTACGGCAAGAAGGAGCCAGTGGCGCCCCACTGCTG 900	
2. 3.	901 AAGGCCI 	AAGGCCATCTGGCAGGTGTTCCATTCTACCTTCTGGGGACCCTCAGCCTCATCATC 960	
J. J.	961 AGTGATO          979 AGCGATO	AGGATGTCTTCAGGTTCACTGTCCCCAAGCTGCTCAGCCTTTTCCTGGAGTTTATTGGT 1020 	Q. 8
ਜੋ ਜੋ	021 GATCCC          039 GACCTC	GATCCCAAGCCTCCAGCCTGGAAGGGCTACCTCGCCGTGCTGATGTTCCTCTCAGCC 1080	0 8
A A	081 TGCCTG        099 TGCCTA	GCCIGCAAACGCTGTTTGAGCACAGAACATGTACAGGCTCAAGGTGCCGCAGATGAGG 1140 	
ਜ ਜ	141 TTGCGG             159 CTGCGA	TTGCGGTCGCCATCACTGGCCTGGTGTACAGAAAGTCCTGGCTCTGTCCAGCGGCTCC 1200 	0 8
ਜ ਜ	201 AGAAAG        219 AGAAAG	GAAAGGCCAGTGCGGTGGGTGAGTGGGTCAATCTGGTGTCCGTGGACGTGCAGGGGTG 1260 	
7 7	261 ACCGAG           279 GTCGAG	GAGAGCGTCCTCTACCTCAACGGGCTGTGGCTGCCTCTCGTCTGGATCGTGGTCTGC 1320 	0 8
ਜ ਜ	321 TTCGTC:             339 TTTGTC:	TIGICIAICTATCTGGCAGCTCCTGGGCCCTCCACTGCCATGGCTGTCTTCTG 1380	
a. a	381 AGCCTCC 	CTCCTCCCTCTGATTTCTTCATCTCCAAGAAAAGGAACCACCATCAGGAGGAGGAA 1440 	
1, 1,	441 ATGAGGG          459 ATGAGGG	ATGAGGCAGAAGGACTCACGGGCACGGCTCACCAGCTCTATCCTCAGGAACTCGAAGACC 1500	
# #	501 ATCAAG         519 ATCAAG	CAGTICCATGGCTGGGAGGGAGCTTTCTGGACAGAGTCCTGGGCATCCGAGGCCAG 1560	
i ii	561 GAGCTGC               579 GAGCTAC	CTGGGCGCGTTGCGGACCTCCGGCCTCTTCTCTGTGTCGCTGGTGTCCTTCCAA 1620 	
16	621 GTGTCT	GTCTACATTTCTGGTCGCACTGGTGGTGTTGCTGTCCACTCTGGTGGCGGAG 1677	

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oy Ob	Qy Dp	Qy	Qy Dp	Oy Db	ογ Op	Oy Op	Qy	Qy Dp	Q _Y	Oy Db.	Qy Db	Oy Op	Qy Db	Qy Dp	QY	Qy	Qy

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Rattus norvegicus mRNA for multidrug resistance-associated protein (MRP)-like protein-1 (MLP-1), complete cds.
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Hirohashi,T., Suzuki,H., Ito,K., Ogawa,K., Kume,K., Shimizu,T. and
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multidrug resistance-associated protein (MRP)-like protein-1
(MLP-1).
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Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                            3892 GTTGGCAGGACCGGGCAGGGAAGTCCTCCCTGGCCAGTGGGCTGCTGCGGCTCCAGGAG
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Hirohashi,T.
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GWPQAPELLIHPTVWLTTMSFATFLIHMERKKGVRASGLLFGYWLLCCLVPAIDTVQQ
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IQMQAALERWFAQCTVLLIAHRLRSVMNCARVLVWDEGQVAESGSPAQLLAQKGLFYR
                       Pharmaceutical
Direct Submission
Submitted (14-JAN-1998) Tomoko Hirohashi, Faculty of Pharmaceut
Sciences, Tokyo University, Department of Pharmaceutics; Hongo
7-3-1, Bunkyo-ku, Tokyo 113, Japan
(E-mail:hirohasi@seizai.f.u-tokyo.ac.jp, Tel:81-3-5802-2045,
Fax:81-3-5800-6949)
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/protein_id="BAA28954.1"
/db_xref="G1:3242458"
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                                                                     CTGATTCACACCGAGAGGAAAAAGGGAGTCCAGTCATCTGGAGTGCTGTTTGGTTACTGG
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qq	Db 1339 TTTGTCTACCTGTGGCAGCTCCTTGGGCCCTCT	GCCCTCACAGCCGTTGCTGTCTTCCTG	1398
Oy Db	1381 AGCCTCCTCCTGAATTTCTTCATCTCCAA	AGAAAAGGAACCACCATCAGGAGAGGAA 	1440
Qy	1441 ATGAGGCAGAAGGACTCACGGGCACGGCTCAC	CTATCCTCAGGAACTCGA	150
ΩĐ	1459		$\vdash$
Qy Dp	1501 ATCAAGTTCCATGGCTGGGAGGGAGCCTTTCTC	GAGTCCTGGG          GACTCCTGCA	9 2
Qy	1561 GAGCTGGGCCCTTGCGGACCTCCGGCCTCCTC	TTCTCTGTGTCT	1620
QY	1621 GTGTCTACATTTCTGGTCGCACTGGTGGTGTT	SCTGTCCACACTCTGGTGGCCGAG	7
qq	Db 1639 GTGTCTACATTCTGGTGGCGCTGGTTTTTTTTTTTTTTT		σ
Qy Db	1678 AATGCTATGAATGCAGAGAAAGCCTTTGTGACT 	TCACAGTTCTCAACAT 	1737 1758
٥ و	1738 GCCCAGGCTTTCCTGCCCTTCTC	CTCGTCCAGGCCCGGGTG	6 -
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QY	1858 TCTGGAAGCGCTGCCGGAAGGATTGCATCACALCACACACACACACACACACACACACACACACA	TACACAGIGC	1917
Qy Dp	1918 CAGGAAAGCCTCCCTGCCTC	CCCAGGGCTGTCTGCT	0 0
Qy Db	1978 GCTGTTGTCGGTCCAGTGGGG 	CCTGCTGTCCGCCCTCCTTGG	03
Qy Db	2038 CTGTCAAAGGTGGAGGGG                    2056 CTGTTGAAGGTAGAAGGG	TGCTGTGGCCTACGTGCCCCAG	, O
oy Dp	2098 GCCTGGGTGCAGAACACCTCTGTGGTAGAGAAT 	GTGCT1         GTGCT1	2157
Oy Dp	2158 CCCTGGCTGGAGAGTACTAGAAGCCTGTGCC 	CTGCAGCAGATGTGGACAGCTTC 	2217 2235
0y Db	2218 GAGGGAATCCACACTTCAATTGGGGAGCAGGGC 	TCTCCGGAGGCCAGAA                               !TTTCTGGGGGCCAGAA	2277 2295
Qy Db	2278 CGGCTGAGCCTGGCCCGGGCTGTATACAGAAAG 	CAGCTGTGTACCTGCTG	2337 2355
Oy Dp	2338 CIGGGGCCCIGGAIGCCCAGGITGGCCAGCAI 	STCTTCAACCAGGTCATTGGGCCTGGT 	2397 2415
Qy	2398 GGGCTACTCCAGGGAACAACAGGGATTCTCG5 	ACGCACTCCACATCTGCCCCAG 	45

2577 2595 2655 2715 2892 3012 2637 2691 2751 2772 2811 2871 2931 GGTGGGCAGCAGCCAGCCCTGCGTGGCGGGATCTTCGGGCTCCTCGGCTGTCTC 2991 2832 CAAGCCATTGGGCTGTTTGCCTCCATGGCTGCGGTGCTCCTAGGTGGGGCCCGGGCATCC 3051 3072 3111 3231 3252 3312 3171 3192 3291 3351 3372 3432 3471 GCCAGCTACTCGTCTGTCTGCTCCCACATGGCTGAGACGTTCCAGGGCAGCACAGTGGTC 3411 CTICTGCAGAGGAAGGGGCCCTCGTGTCTTCTGGATCAAGCCAGACAGCAGAGAT GAAGGAGAAGGAGCACCAGCGAGCCACCAGTAGAAGCTTTTTTTGGA GGCAGGAGCCCGAGCTTAGACGCGAGAGG-----TCCATCAAGTCCGTGAGAAG CTGACAGCAGGAGAGACAGTGTGCAGTATGGCCGGTGAAGAGCGCCACATACCTGAGC 3013 CAAGCCATGGGACTGTTTGCCTCCATGGCTGCTGCTGCTGCTGGGTGTACA 3292 TACGCTGGGTTTCAGAGCCTGTATGTGGTTAGCTCATGCCAGCTGAGACGCTTGGAGTCA AGAGGAGAAGGAGAAACAGGACCTGGGACCAGCACCAAGGACCCCAGAGGCACCTCTGCA GACCGTACCACTTCAGAAGCCCAGACAGATTCCTCTGGATGACCCTGACAGGGCAGGA TACCTGCGTGCCGTGGGCACCCCCTCTGCCTCTACGCACTCTTCCTCTTCCTCTGCCAG CAAGTIGGCCTCCTTCTGCCGGGGCTACTGGCTGAGCCTGTGGGGCGGACGACCCTGCAGTA 3193 GACATCCCAGACAAGAGGGCCCTGCTGCTATGGCTTTGGACTCCTGGAGGTTGGC CTGGTGGTGGCAGTGGCTACCCCACTGGCCACTGTGGCCATCCTGCTGTTTCTCCTC TGGCCAGCAGGAAAGGACAACCAATACGGCAGGGTGAAGGCCACAGTGCACCTGGCC GACATTCCAGACAAACTCCGGTCCCTGCTGATGTACGCCTTTGGACTCCTGGAGGTCAGC 3412 CGGGCATTCCGAACCCAGGCCCCTTTGTGCTCAGAACAATGCTCGCGTAGATGAAAGC 2536 2692 2716 2773 3172 2518 2578 2596 2638 2656 2752 2812 2833 2872 2893 2932 2992 3112 3133 3232 3313 3352 QQ QQ ద qq qq QΥ QY QΥ Óγ δý g Ωy Pp QΥ Ω ÓΥ QQ δy Op Óγ qq QY Dp Óγ QQ  $\Omega$ q δy QQ οy qq a q Qγ  $\delta \lambda$ 

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CTGGGGAATGGCCTGGTGTTTGCAGCCGCCACGTGTGCTGTGCTGAGCCAAAGCCCACCTC 3591
             CTGGGGAATGGCCTGGTGTTGTGGCCGCTACATGTGCTGTGCTGAGCAAGGCTCACCTG
                                                  AGTGCTGGCCTCGTGGCGTTCTCTGTCTCTGCCTCCAGGTGACCCAGACACTGCAG
                                                                                                                 CTCTGGCCCTGTGGGGGGACAGATTGAGTTCCGAGACTTTGGGCTCAGACACCGACCAGAG
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                                                                           AGTGCTGGCCTCGCGGGCTTCTGGTTTCTGCTGCCTCCAGGTAACACAGACTCTGCAG
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RNU73038 5775 bp mRNA linear ROD 05-FEB-1999 Rattus norvegicus liver multidrug resistance-associated protein 6

LOCUS DEFINITION

RESULT 6 RNU73038

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FVTLTVLSIINKAQAFIPFSVHCLVQARVŠFDRLAAFICLEEVDPNGMVLSPSRCSSK
DRISHHQGTFAMSQESPPCLHGINLTVPQGCLLAVVGPVGAGKSSLLGALLGELLKVE
GSVSIEGSVAYVPQEAWVONTSVVENVCFRQELDLPWLQEVLEACALGSDVASFPAGV
HTPVGEQGMILJSGGKRLSLARAVYRRAAYYLMDDPLAALDAHVSQEYFROYIGPSG
LLQGTTRILVTHTLHVLPQADQILVLANGTIAEMGSYQDLLHRNGALVGLLDGARQPA
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KAMFWWASGLLWKGYRKLLGPKDLWSLERENSSEELVSQLEREWRNFSELPGHKGHS
GWGTPETEAFLQPERSQRGPLLRAIWRVFRSTFLLGTLSLVISDAFRFAVPKLLSLFL
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AODHALMBORRISFPRLADRMILAMBLLIGAGUPVPAATCAVLSKHRISAGLAGFS
VSAALQYTOTLOWWYSSWTDLENSWAYNFRODYNHPREAPWRLPSSAAQPIMPCGG
OIEFRDFGLRHRPELPMAVOCVSLKIHAGEKVCIVGRTGAGKSSLTWGLLRLÖEATEG
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IQMQAALERWFAQCTVLLIAHRLRSVMNCARVLVMDEGQVAESGSPAQLLAQKGLFYR
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VPPMYLWVLGPIYLLYIHRHGCCYLRMSRLFKIKMVLGFALILLYTFNAAVPLWRIHR
GWPQAPELLIHPTVWLTTMSFATFLIHMERKKGVRASGLLFGYWLLCCLVPAIDTVQQ
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VLSSGSRKSSAAGDVVNLVSVDVQRLVESILHLNGLWLLFLMIIVCFVYLWQLLGPSA
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LERLLHIRGQELGALKTSAFLFSVSLVSFQVSTFLVALVVFAVHTLVAEDNAMDAEKA
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TGLTAGEDSVQYGRVKSATYLSYLRAVGTPLCTYTLFLFLCQQVASFCQGYWLSLWAD
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                                                                                                                                                                              Euteleostomi;
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Switzerland
                                                                                                                                                                                                                                                                                                                               a novel
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/protein_id="AAAD12747.1"
/db_xref="GI:4225852"
                                                                                                                                                                                                                                                                                             Madon, J., Hagenbuch, B., Stieger, B. and Meier, P.J. cellular localization and functional characterization of rat liver multidrug resistance-associated protein (mrp6) Unpublished
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                                                                                                                                                                           Chordata; Craniata; Vertebrata;
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Madon, J., Hagenbuch, B., Stieger, B. and Meier, P.J.
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Submitted (05-FEB-1999) Internal Medicine,
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/organism="Rattus norvegicus"
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Madon,J., Hagenbuch,B.,
Direct Submission
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      mRNA, complete
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	יה ל מ מ	AGAAC AGAAC	77GG	CCATG	S - S	AACGC      CATGC	CGCAG      CGCCA	TGGTT     } CGGGT	AGCGG      AGGGA	GGTGG         GGTGG	CCAGC         CAAGC	GTGGG       GTGGG	GTCGC        GTCAC	GAGGA        GAGGA	CAGTG        CAGTG	CCCAC        CCCGC	CCTCA      CCTGG	GAGTTTA        GAGTTCA	CCTCT       CTTGT
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8 CCCTGGCTGGAGAGTACTAGAAGCCTGTGCCCTGCAGCCAGATGTGGACAGCTTCCCT	B GAGGGAATCCACACTTCAATTGGGGACAGGCATGAATCTCTCCGGAGGCCAGAACAG   111   1   1   1   1   1   1   1   1	8 CGGCTGAGCCTGGGCCGGGGCTGTATACAGAAAGGGAGCTGTGTACCTGCTGGATGACCCC	8 CTGGCGGCCCTGGATGCCCACGTTGGCCAGCATGTCTTCAACCAGGTCATTGGGCCTGGT	B GGGCTACTCCAGGGAACAACACGGATTCTCGTGACGCACCTCCACATCCTGCCCCAGIIIIIIIIII	B GCTGATTGGATCATAGTGCTGGCAAATGGGGCCATCGCAGAGAGTGGGTTCCTACCAGGAG 	B CTTCTGCAGAGGAGAGGGCCCTCGTGTGTCTTCTGGATCAAGCCAGACAGCCAGGAGAT	B AGAGGAGAAGGAGAAACCTGGGACCAGCACCAAGGACCCCAGAGGCACCTCTGCA	GGCAGGAGGCCCGAGCTTAGACGCGAGAGGTCCATCAAGTCCGTCAGAGG	2 GACCGTACCACTTCAGAAGCCCAGACAGAGGTTCCTCTGGATGACCCTGACAGGGCAGGA	2 TGGCCAGCAGGAAAGGACAGCATCCAATACGGCAGGGTGAAGGCCACAGTGCACCTGGCC	2 TACCTGCGTGCGTGGGCACCCCCTCTGCCTCTACGCACTCTTCCTCTTCCTCTGCCAG	2 CAAGTGGCCTCCTTCTGCCGGGGCTACTGGCTGAGCCTGTGGGGGGACGACGACCTGCAGTA	2 GGTGGGCAGCAGAGCAGCCCTGCGTGGCGGATCTTCGGGCTCCTCGGCTGTCTC	2 CAAGCCATTGGGCTGTTTGCCTCCATGGCTGGGGTGCTCCTAGGTGGGGCCCGGGCATCC	2 AGGITGCICITCCAGAGGCICCIGIGGGAIGIGGIGCGAICICCCAICAGCIICIIIIIIII	2 CGGACACCCATTGGTCACCTGCTAAACCGCTTCTCCAAGGAGACAGAC	2 GACATTCCAGACAAACTCCGGTCCCTGCTGATGTACGCCTTTGGACTCCTGGAGGTCAGC	2 CTGGTGGTGGCAGTGGCTACCCCACTGGCCACTGTGGCCATCCTGCCACTGTTTCTCCTC
215	221	2278	233	2391	245(	2511	2578	2638	2692 2763	2752	2813	2873	3000	3060	3052	3112	3172	3232
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treating pseudoxanthoma
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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elasticum and related conditions
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Pxe international Inc. (US); UNIVERSITY OF
Location/Qualifiers
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/organism="Mus musculus"
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Score 3007.2; Pred. No. 0;

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Query Match Best Local Similarity

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Manmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musinae; Manmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 4980)

Mus musculus mRNA for multidrug resistance-associated protein 6 (MRP6); complete cds

MRP6; complete cds

MRP7; complete cds

MRP7; complete cds

MRP8; Superial on the same (1999)

Morikawa, A.; Suzuki, H., Hirohashi, T. and Sugiyama, Y.

Direct Submission

Morikawa, A.; Suzuki, H., Hirohashi, T. and Sugiyama, Y.

Submitted (03-JUN-1999) Akiko Morikawa, University of Tokyo, Graduate School of Pharmaceutical Sciences; 7-3-1 Hongo, Bunkyo-ku, Tokyo 113-0033, Japan (E-mail:morikawa@seizai.f.u-tokyo.ac.jp, Tel:81-3-5802-2045, Fax:81-3-5800-6949)
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ASAGNIKOPELHHLATYLCLSIVVARIVLSGLVDOPPFFSEDSOPLNPCPEAEASFPS
SVAAFWWASGLLMFGYKLLGFYDLMSLGNENSSEELVSGLEREWRSCNGLPGHKGHS
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EWGDRNSSAWTGWLLAVLAFAAGLLQTLESTGTLSLVISDAFFFAVFLLSLFL
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LITAVAVELSLLPINFFTKKRGFHOEDOMROKASRARLTSSMLRTVRTTKSHGWEHA
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FVTLTLSILMKAOAFLPFSVSLVSFQVSTFLVALVVFAVHTLVAEDNAMDAEKA
BVITTVLSILMKAOAFLPFSVSLVSFQVSTFLVALVGFVGAGKSSLLGELKVF
GSVSIEGSVATVPQEAWVQNTSVAENVCFVGDELLAVGCAGGSSLLGSLLGGELKVF
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/product="multidrug resistance-associated protein-6"
/protein_id="BAR83820.1"
/db.csin_id="E31:821430"
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VPPMYLWVLGPIYLLYIHRHGRCYLRWSHLFKTKMVLGLALILLYTFNVAVPLWRIHQ
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LLQGTYRILLVUTHLHVLPQADRILVLANGTIRBARSYODLLGRRAALVGCLLDGRAQPA
GLQGTYRILLAYDEPGGREPTCREDRERFTEAAPVKGRSTSEVQMEASLDDPEATGLI
AEEDSVRYGRVKITIYLSYLRAVGTPLCTYTLFLFLCQQVASFSQGYMLSLWADDPVV
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                                                   CACCGCCTGCGCTCCGTGATGGACTGTGCCCGGGTTCTGGTCATGGACAAGGGGCAGGTG
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MRP6; multidrug resistance-associated protein-6.
Mus musculus (strain:ddY) male liver cDNA to mRNA.
Mus musculus
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/sex="male"
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Mus musculus MRP6 mRN
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TITLE
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RDFGLARHFEBLLAVGGVSLKIHAGERVGIVGRTGAGKSSLANGLLRLQEAABENIWI
DGVPITHVGLHTLRSRITIPQDPVLFPGSLRMNLDLLQEHTDBGINAALETVQLKAF
VTSLPGGLQYECAGGODDLSYGHKQLLCLARRLLKRYQILILDBATASVDFGTEMQWA
AALERWFTQCTLLLIAHRLRSVMDCARVLVMDEGQVAESGNPAQLLAQKGLFYRLAHE
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Qy	y 1978 GCTGTTGTCGGTCCAGTGGGGCAGGGAAGTCCTCCCTGCTGT 	AAGTCCTCCTGCTGTCGCCCTCCTTGGGGAG	2037
Qy	2038 CTGTCAAAGGTGGAGGGGTTCGT 	GAGCATCGAGGGTGCTGTGGCCTACGTGCCCCAGGAG	2097
QY	2098 GCCTGGGTGCAGAACACCTCT	GTGGTAGAGAATGTGTGCTTCGGGCAGGAGCTGGACCA 	2157 2162
Qy Db	2158 CCCTGGCTGGAGAGAGTACTAGAAG	CCTGTGCCCTGCAGCCAGATGTGGACAGCTTCCCT	2217 2222
Qy Db	y 2218 GAGGGAATCCACACTTCAATTGGGGAGCAGGGCAT 	CAGGGCAIGAAICTCTCCGGAGGCCAGAAGCAG 	2277 2282
Qy Dp	2278 CGGCTGAGCCTGGCCCGGGCTGTA 	TACAGAAAGGCAGCTGTACCTGGTGGATGACCCC	2337
QY Dp	2338 CTGGCGCCCTGGATGCCCACGTTGG 	CCAGCATGTCTTCAACCAGGTCATTGGGCCTGGT	2397
Qy Db	2398 GGGCT      2403 GGATT	ACTCCAGGGAACAACGGATTCTCGTGACGCACGCACTCCACATCCTGCCCCAG	2457
Oy Db	2458 G 1 2463 G	CTGATTGGATCATAGTGCTGGCAAATGGGGCCATCGCAGAGATGGGTTCCTACCAGGG 	2517 2522
Qy Dp	y 2518 CTTCTGCAGAGGAGGGGCCCTCGTGTGTCTTCT 	TGTCTTCTGGATCAAGCCAGACAGCCAGGAGAT	2577
Oy Dp	2578 AGAGGAGA	AGGAGAAACAGAACCTGGGACCAGCACCAAGGACCCCAGAGCACCTCTGCA 	2637 2627
Qy Db	2638 GGCAGGAG           2628 GGTGGGAG	GAGGTCCATCAAGTCCGTCGTGAGAG 	2691 2687
Qy Db	2692 GACCGTACCACTTCAGAAGCCCAGACAGAGGTTCCTV 	GAGGTTCCTCTGGATGACCCTGACAGGGCAGGA	2751
Qy	2752 TG 1 2748 TT	GCCAGCAGGAAAGGACAGCATCCAATACGGCAGGGTGAAGGCCACAGTGCACCTGGCC 	2811 2807
Qy	# 2812 TACCTGCGTGCGTGGCACCCCCTCTGCCTCTACGCACTCTTCCTCTTCTTTCT	TGCCTCTACGCACTCTTCCTCTTCCTCTGCCAG	2871 2867
Oy Dp	2872 CAAGT             2868 CAAGT	GGCCTCCTTCTGCCGGGGCTACTGGCTGAGCCTGTGGGGGGGACGACGCTGCAGTA 	2931 2927
Qy	y 2932 GGTGGCAGCAGACGCAGGCAGCCCTGCGT 	CGTGGCGGGATCTTCGGGCTCCTCGGCTGTCTC	2991 2987
Oy Db	2992 CAAGC         2988 CAAGC	CATTGGGCTGTTTGCCTCCATGGCTGCGGTGCTCCTAGGTGGGGCCCGGGCATCC	3051 3047

AGGTTGCTCTTCCAGAGGCTCCTGTGGGATGTGGTGCGATCTCCCATCAGCTTCTTTGAG 3111 3648 TGGGTGGTCCGCAGCTGGACAGATCTGGAGAACAGCATGGTAGCCGTGGAGCGCGTGCAG 3707 4132 GIGCAGCTCAAAGCCTIGGIGGCCAGCCTGCCGGCCAGCTGCAGTACAAGTGTGCTGAC 4191 TACGCTGGGTTTCAGAGCCTGTATGTGGTTAGCTCATGCCAGCTGAGACGCTTGGAGTCA GCCAGCTACTCGTCTGTCTGCTCCCACATGGCTGAGACGTTCCAGGGCAGCACAGTGGTC CGGGCATTCCGAACCCAGGCCCCCTTTGTGGCTCAGAACAATGCTCGCGTAGATGAAAGC CAGAGGATCAGTTTCCCGCGACTGGTGGCTGACAGGTGGCTTGCGGCCAATGTGGAGCTC CTGGGGAATGGCCTGGTGTTTGCAGCCGCCACGTGTGCTGTGCTGAGCCAAAGCCCACCTC TGGGTTGTTCGCAACTGGACAGACCTAGAGAACAGCATCGTGTCAGTGGAGCGGATGCAG GACTATGCCTGGACGCCCAAGGAGGCTCCCTGGAGGCTGCCCACATGTGCAGCTCAGCCC CCCTGGCCTCAGGGGGGGCAGATCGAGTTCCGGGACTTTGGGCTAAGATGCCGACCTGAG CTCCCGCTGGCTGTGCAGGGCGTGTCCTTCAAGATCCACGCAGGAGAAGGTGGGCATC GTTGGCAGGACCGGGCAGGAAGTCCTCCCTGGCCAGTGGGCTGCTGCGGCTCCAGGAG GCAGCTGAGGGTGGGATCTGGACGGGGTCCCCATTGCCCACGTGGGGCTGCACACA qq ò g Qy Db Oy Dp q 07 05 QY Db QQ Oy Oy qq Oy Db Oy Db òγ Ω Qγ ద οy qq Qγ g Qγ qq δ

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Human multidrug resistance-associated protein (MRP) mRNA, complete
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Cole.S.P., Bhardwaj,G., Gerlach,J.H., Mackie,J.E., Grant,C.E.,
Almquist,K.C., Stewart,A.J., Kurz,E.U., Duncan,A.M. and Deeley,R.G.
Overexpression of a transporter gene in a multidrug-resistant human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 5011)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Structure and expression of the messenger RNA encoding the murine multidrug resistance protein, an ATP-binding cassette transporter Mol. Pharmacol. 49 (6), 962-971 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Valdimarsson, G., Gerlach, J.H., Wilson, G.M., Cole, S.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (30-JAN-1997) Cancer Research Labs, Queen's University, Kingston, ON K7L 3N6, Canada On Feb 10, 1997 this sequence version replaced gi:292332.

Location/Qualifiers
                                                                                                                                                    4307
                                                                                                                                                                                                                   4308 ATGCAGATGCAGGCGGCCCTGGAGCGCTGTTACACACAGTGTACCTTACTGCTTATCGCT 4367
                                                                                                                                                                                                                                                                                                                                     4428 GCAGAAAAGTGGCAATCCTGCTCCAGCTGCTGGAAAGGCCTGTTTTACAGGCTAGCC 4487
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Multidrug resistance-associated protein: sequence correction
Science 260 (5110), 879 (1993)
4128 GTGCAGCTCAAGGCCTTCGTGACCAGCCTGCCAGCTGCAATATGAGTGTGCAGGC
                                                                   CGGAAGACCCAGATCCTCATCCTGGACGAGGCTACTGCTGCCGTGGACCCTGGCACGGAG
                                                                                                                                   4368 CACCGCCTGCGCTGATGGACTGTGCCAGAGTCCTAGTCATGAGGGGCAGGTG
                                                   CGAGGCGAGGACCTGAGCGTGGGCCAGAACAGCTCCTGTGTCTGGCACGTGCCCTTCTC
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L05628.1 GI:1835658
multidrug resistance-associated protein; transporter
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Science 258 (5088), 1650-1654 (1992)
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/db_xref="taxon:9606"
1. .5011
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and Deeley, R.G.
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APVFLVSPTLLGITTLLATFLIQLERRKGVOSSGIMLTFWLVALVCALAILRSKIMTA
LKEDAQVDFRENDITFVYFSLLLIQULSCESDRSPLFSEFILBPWCPESSASFLSR
ITFWAITGLIVRGYROPLEGSIMSLANKEDTSBQVVPVLKNWKKECAKTRKOPVKVU
YSSKDPAQPKESSKVDANEEVBALIVKSPQKEWNPSLFKVLIKTFGPYFLMSFFFKAI
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VILALYLLWLNLGSPSYLAGVAVAVANTAMTVATAMATATAMT
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RLKEYSETEREAPMOIQETAPPSSMPOVGRYDERRNYCLRYREDLDFVLRHINYTINGS
EKVGIVGRTGAGKSSLTLGLFRINSSAGEJIIDGINIAKIGLHDLRFKITIIPODPV
LFSGSLEMNUDPFSQYSDEEWWTSLELAHLKDFVSALPDKLDHECAEGGENLSVGGRO
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                                                                                                                                                                                                                                  /translation="malkgFcSabgSDPLwDwnvTwnTsNpDFTkCFgNTvLvwvPCF
YLWACFPFYFLYLSRHDRGYIQMTPLNKTKTALGFLLwIvCwADLFYSFWERSKGIFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="multidrug resistance-associated protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36 GGTCTGGAACCAGACAGAGCCTGAACCTGCCGCCAGCCTGCTGAGCCTGTGCTTCCT
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                                                              /note="putative"
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/gene="MRP"
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οy		TCCTGCCTGGCGGATCA	266
QQ	718	TCCTGTTTCTCAGATCG	
ζζ Gp	A ACCCCCTTCTTCCCTGAAGACCCCCAGCAGTCTAACCCCTGTCCAGAGACTGGGGCAGC  1	CCAGAGACTGGGGCAGC	626 837
ž a	9Y 627 CTTCCCCTCCAAAGCCACGTTCTGGTGGGTTTCTGGCCTGGTCTGGAGGGGATACAGGG 	TGGAGGGATACAGGAG            GTCCGGGGTACCGCCA	686 897
λ G	OY 687 GCCACTGAGACCAAAAGACCTCTGGTCGCTTGGGAGAAAACTCCTCAGAAGAACTTGT 11 11 11 11 11 11 11 11 11 11 11 11 11	TCCTCAGAAGAACTTGT 	746 957
λ Q	747 TTCCCGGCTTGAAAAGGAGTGGATGAGGAACCGC 	-agtgcagcccgaggcacaaca 	802 1017
ž g	803 AGGCAATAGCATTTAAAAGGAAAGGCGGCAGTGGCATGAAGGCTCCA	TCCATCCATCCAAGTGGATGCGAA	849
දු දු	2Y 850GAGACCGAGCCCTTCCTACGGCAAGAGGAGCCAGTGGCGCCCACTGCT	CAGTGGCGCCCACTGCT 	899 1137
λ G	900	ACCCTCAGCCTCATCAT	959 1197
දු පු	960	TTCCTGGAGTTTATTGG               CTCATCAAGTTCGTGAA	1019 1257
ž g	1020 IGAICCCAAGCCICCAGCCIGGAAGGCIACCICCICGCCGIGCIGAI 	CTGATGTTCCTCTCAGC	1079 1317
ž g	2y 1080 CTGCCTGCAAACGCTGTTTGAGCAGCAGAACATGTACAGGCTCAAGGTGCCGCAGATGAG	AAGGTGCCGCAGATGAG 	1139 1377
λ G	2y 1140 GTTGCGGTCGGCCATCACTGGCCTGGTGTACAGAAAGGTCCTGGCTCTGTCCAGCGGCTCTCGTCTCGCTGTCATCGGAAAGGTCCTGGTCGTCATTCAGCOD 1378 GATCAAGACCGCTGTCATTGGGGCTGTCTATCGGAAGGCCCTGGTGATCAGCG	GCTCTGTCCAGCGGCTC 	1199
Zy Op	2y 1200 CAGAAAGGCCAGTGCGGTGATGTGGTCAATCTGGTGTCCGTGGACGTGCAGCGGCTTCTGTTGTTGTTGTTGTTGTTGTGTGTG	GTGGACGTGCAGCGGCT 	1259
2 <u>y</u>	2Y 1260 GACCGAGAGCGTCTCTACCTCAACGGGCTGTGGCTGCCTCTCGTCTGGATCGTGGTCTG	GTCTGGATCGTGGTCTG 	1319 1557
λ S	1320	GCCATCGCTGTCTTCCT	1379 1617
ž a	2Y 1380 GAGCCTCCTCTGAATTTCTTCATCTCCAAGAAAGGAACCACCATCAGGAGGAGGAGACACACA 1111	CACCATCAGGAGGAGCA 	1439 1677
ž a	2) 1440 AATGAGGCAGAAGGACTCACGGCACGGCTCACCAGCTCTATCCTCAGGAACTCGAAGAC	CTCAGGAACTCGAAGAC       CTCAATGGGATCAAAGT	1499
λ Op	0y 1500 CATCAAGTTCCATGGCTGGGAGCGCCTTTCTGGACAGAGTCCTGGGCATCCGAGGCCA 		1559 1797

1679 2036 2096 2396 1856 1916 2217 2277 2156 2216 2456 GGAGCTGGGCCCTTGCGGACCTCCGGCCTCCTCTTCTCTGTGTCGCTGGTGTCCTTCCA 1619 TGCTA---TGAATGCAGAGAAAGCCTTTGTGACTCTCACAGTTCTCAACATCCTCAACAA 1736 2097 2157 1976 2337 2397 2457 2276 2517 2336 2577 2637 2516 2757 2816 2636 GCTTCTGCAGAGGAAGGGGGCCCTCGTGTGTTCTGGATCAAGCCAGACAGCCAGGAGA 2576 CTGCACGCCCTTTCTGGTGGCCTTGTGCACATTTGCCGTCTACGTGACCATTGACGAGAA CAACATCCTGGATGCCCAGACAGCCTTCGTGTTTTGGCCTTGTTCAACATCCTCGGTT 2518 GGGGTGAGCCTGGCCGGGCCGTGTACTCCAACGCTGACATTACCTCTTCGATGATCC AGTGTCTACATTTCTGGTCGCACTGGTGGTGTTTGCTGTCCACACTCTGGTGGCCGAGAA GGCCCAGGCTTTCCTGCCCTTCTCCATCCACTCCTCGTCCAGGCCCGGGTGTCCTTTGA CCGTCTGGTCACCTTCCTCTGCCTGGAAGAAGTTGACCCTGGTGTCGTAGACTCAAGTTC 2038 ACGCCTGAGGATCTTTCTCCCATGAGGAGCTGGAACCTGACATGAGGACGGCC 2098 TGTCAAAGACGGCGGGGCACGAACACATCACCGTGAGGAATGCCACATTCACCTGGGC CCAGGAAAGCCCTCCCTGCCTCCACAGAATAAACCTCACGGTGCCCCAGGGCTGTCTGCT GGCTGTTGTCGGTCCAGTGGGGGGAAGTCCTCCCTGCTGTCCGCCCTCCTTGGGGA GCTGTCAAAGGTGGAGGGGTTCGTGAGCATCGAGGGTGCTGTGGCCTACGTGCCCCAGGA GCCCTGGGTGCAGAACACCTCTGTGGTAGAGAATGTGTGCTTCGGGCAGGAGCTGGACCC ACCCTGGCTGGAGAGTACTAGAAGCCTGTGCCCTGCAGCCAGTGTGGACAGCTTCCC ACCATATTACAGGTCCGTGATACAGGCCTGTGCCCTCCTCCCAGACCTGGAAATCCTGCC CCTGGCGGCCCTGGATGCCCACGTTGGCCAGCATGTCTTCAACCAGGTCATTGGGCCTGG GGCTGATTGGATCATAGTGCTGGCAAATGGGGCCATCGCAGAGATGGGTTCCTACCAGGA 2577 TAGAGGAGAAGGAGAAACAGGAACCTGGGACCAGCACCAAGGACCCCAGAGGCACCTCTGC GCGGCTGAGCCTGGCCCGGGCTGTATACAGAAAGGCAGCTGTGTACCTGCTGGATGACCC 1620 1798 1680 1918 1917 2218 2338 2458 2578 1560 1858 1797 1857 2037 2278 2097 2217 2397 2698 1737 1978 1977 2157 2398 2277 2337 2457 2517 Dp Op Op g qq qq QΩ g g qq Db δ QΥ g Qγ g δ ò Óγ Qγ ò δ ò Ω δ δ Οy οy ŏ Ω qq ò g ·δ g

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3957 3737 4017	OY 3/9/ AGTTY DD 4077 AATTC	4137	4197	4257	4317	4377	415/	4497	4277	4537	4397	UY 445/ TGCTC Db 4737 TCCTC		DEFINITION SEC ACCESSION ARK VERYWORDS	Σ	;	SOULCE BASE COUNT
	2717 CAGAGGITCCTCTGGATGACCCTGACAGGGCAGGATGGCCAGCAGCAGGAAAGGACAGCATCC 2776 2997 TGCAGAAAGCTGAGGCCAAGAAGGAGGAGGAGCTGGAAGGAGGCTGACAAGGCGC 3056	2777 AATACGGCAGGTGAAGGCCACAGTGCACCTGGCTACCTGCGTGCG	2837 TCTGCCTCTACGCACTCTTCCTCTTCCTCTGCCACAAGTGGCCTCCTTCTGCGGGGCT 2896 11	2897 ACTGGCTGAGCCTGTGGGCGGACGACCCTGCAGTGGGCGGCGGGCG	2957 IGGGIGGGGGATCTTCGGGCTCCTCGGGTGTCTCCAAGCCATTGGGCTGTTTGCCTCCA 3016 1	3017 TGGCTGCGGTCCTAGGTGGGCCCGGCATCCAGGTTGCTCTTCCAGAGGCTCCTGT 3076 1	3077 GGGAFGTGGTGCGATCTCCCATCAGCTTCTTTGAGCGGACACCCATTGGTCACCTGCTAA 3136 1	3137 ACCGCTTCTCCAAGGAGACACGGTTCACGTGGACATTCCAGAAACTCCGGTCCC 3196	3197 IGCTGATGTACGCCTTTGGACTCCTGGAGGTCAGCCTGGTGGCAGTGGCTACCCCAC 3256  3477 ICATGGGCTCCCTGTTCAACGTCATGGTGCTGCTGGTGGCTGGC	3257 IGGCCACTGTGCCATCCTGCACTGTTTCTCCTCTGCGGGTTTCACAGCCTGTATG 3316	3317 IGGTIAGCICAIGCCAGCIGAGACCCTIGGAGTCAGCCAGCTACTCGTCTGCTCCC 3376 11	3377 ACATGGCTGAGAGCATCCAGGCAGCACAGTGGTCCGGGCATTCCGAACCCAGGCCCCCT 3436	3437 TTGTGGCTCAGAACATGCTCGCGTAGATGAAGCCAGAGGATCAGTTTCCCGCGACTGG 3496 1	3497 TGGCTGACAGGTGCGCCAATGTGGAGCTCCTGGGGAATGCCTGGTTTGCAG 3556	3557 CCGCCACGTGTGCTGAGCAAAGCCCACCTCAGTGCTGGCCTCGTGGGCCTTCTCTG 3616	3617 TCTCTGCTGCCTCCAGGTGACCCAGACACTGGGTTGTTCGCAACTGGACAGACC 3676 1	3677 TAGAGAACAGCATCGTGTCAGTGGAGCGGATGCAGGACTATGCCTGGACGCCCAAGGAGG 3736 
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inclassified.
1 (bases 1 to 5011)
Deeley, R.G. and Cole, S.P.C.
Methods for conferring multidrug resistance on a cell
Patent: US 5891724-A 3 06-APR-1999;
Location/Qualifiers
1. .5011
..."unknown"
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Squence 3 from patent US 5891724.
R070199 GI:7221087
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Deeley, R.G. and Cole, S.P.C.
Methods for identifying chemosensitizers
Patent: US 6001563-A 3 14-DEC-1999;
Location, Qualifiers
1. 5011
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AR093440.1 GI:10020189
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Matches 2538; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 5867)
Zaman, G.J. R., Flens, M.J., van Leusden, M.R., de Haas, M., Muelder, H.S., Lankelma, J., Pinedo, H.M., Scheper, R.J., Baas, F., The buman multidrug resistance-associated protein MRP is a plasma membrane drug-efflux pump

REFERENCE AUTHORS

TITLE

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Direct Submission
Submitted (22-MAR-1994) G. Zaman, Division of Molecular Biology,
Netherlands Cancer Institute, Plesmanlaan 121, 1066 CX Amsterdam,
NETHERLANDS
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ilarity 55.8%; Pred. No. 2.8e-221;
Conservative 0; Mismatches 1934;
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/db_xref="taxon:9606"
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/gene="MRP"
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7 ACCTIGGTGGAGAGAGTACAAGCCTGTGCCCTGCAGCCAGATGTGGACAGCTTCCC	7 TGAGGGAATCCACACTTCAATTGGGGAGCAGGCATGAATCTCTCCGGAGGCCAGAAGCA 	7 GCGGCTGAGCCTGGCCCGGGCTGTATACAGAAAGGCAGCTGTGTACCTGCTGGTGATGACCCCTTTTT	CCTGCGGCCCTGGATGCCCACGTTGGCCAGCATGTCTTCAACCAGGTCATTGGGCCTGG	TGGGCTACTCCAGGGAACAACACGGATTCTCGTGACGCACGC	' GGCTGATTGGATCATAGTGCTGGCAAATGGGGCCATCGCAGAGATGGGTTCCTACCAGGA 	GCTTCTGCAGAGGAAGGGGCCCTCGTGTGTCTTCTGGATCAAGCCAGACAGCCGGAGA III II III III III III III III III	'TAGAGGAGAAAGGAGAACCIGGGACCAGCACCAAGGACCCCAGAGGCACCTCTGC	** AGGCAGGAGCCCGAGCTTAGACGCGAGAGGTCCATCAAGTCAGTC		CAGAGGTTCCTCTGGATGACCCTGACAGGGCAGGATGGCCAGGAAAGGACAGCATCC	AATACGGCAGGGTGAAGGCCACAGGCCTGGCCTACCTGCGTGCG	TCTGCCTCTACGCACTCTTCCTCTTGCCAGCAAGTGGCCTCCTTCTGCGGGGCT			TGCTGCGGTGCTCCTAGGTGGGCCCGGGCATCCAGGTTGCTCTTCCAGAGGCTCCTGT	GGGATGTGGTGCGATCTCCATCAGCTTCTTTGAGCGGACACCCATTGGTCACCTGCTAA	ACCGCTTCTCCAAGGAGACAGGGTTGACGTGGACATTCCAGACAAACTCCGGTCCC
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3316 3595 3436 3496 3556 3557 CCGCCACGTGTGTGTGTGTGAGCAAAGCCCACCTCAGTGCTGGCCTTCGTGGGCTTCTCTG 3616 3617 TCTCTGCTGCCCTCCAGGTGACCCAGACACTGCAGTGGGTTGTTCGCAACTGGACAGACC 3676 4255 4315 4375 TGCTGATGTACGCCTTTGGACTCCTGGAGGTCAGCCTGGTGGTGGCAGTGGCTACCCCAC 3256 3916 ACGGGGTCCCCATTGCCCACGTGGGCTGCACACACTGCGCTCCAGGATCAGCATCATCC 4036 CCCAGGACCCCATCCTGTGCCTGTGTGTGTGAACCTCGACTGCTGCAGGAGC 4096 4156 AATICCGGAACTACTGCCTGCGCTACCGAGAGGACCTGGACTTCGTTCTCAGGCACATCA 4135 4195 3917 CCTCCCTGGCCAGTGGGCTGCTGCGGCTCCAGAGGCAGTGAGGGTGGGATCTGGATCG 3976 4435 4216 4495 4276 4555 AGTICCGGGACTITGGGCTAAGAIGCCGACCTGAGCTCCCGCTGGCTGTGCAGGGCGTGT 3856 ACGAGGCTACTGCTGCCGTGGACCCTGGCACGGAGCTGCAGATGCAGGCCATGCTCGGGA 4336 TGGCCACTGTGGCCATCCTGCCACTGTTTCTCCTCTACGCTGGGTTTCAGAGCCTGTATG 3377 ACATGGCTGAGACGTTCCAGGGCAGCACAGGGGTCCGGGCATTCCGAACCCAGGCCCCCT 3497 TGGCTGACAGGTGGCTTGCGGCCAATGTGGAGCTCCTGGGGAATGGCCTGGTGTTTGCAG 3437 ITGIGGCICAGAACAAIGCICGCGIAGAIGAAAGCCAGAGGAICAGIITCCCGCGACIGG **ACTCGGACGAGGCTATCTGGGCAGCCCTGGAGACGGTGCAGCTCAAAGCCTTGGTGGCCA** GCCTGCCCGGCCAGCTGCAGTACAAGTGTGCTGACCGAGGCGAGGACCTGAGCGTGGGCC CCTTCAAGATCCACGCAGGAGAAGGTGGGCATCGTTGGCAGGACCGGGGCAGGAAGT 3257 3197 3737 3797 4076 3857 4136 4256 4316 4376 3977 4037 4097 4157 4277 . අු å qq οy g οy δy q Qy Db qq δy qq δ δy QQ οy QQ οy В δy g Qy Db 9 6 δŻ Dp οy g qq Ω ò

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4337 GCTGGTTTGCACAGTGCACTGTGCTGCCCATTGCCCACCGCCTGCGCTCCGTGATGGACT
                                                        CACAGITGGAGGACTGCACCGTCACCATCGCCCACCGGCTCAACACCATCATGGACT
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Pred. No. 2.3e-220;
0; Mismatches 1937; Indels 80;
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Deeley,R.G. and Cole,S.P.C.
Methods for identifying chemosensitizers
Patent: US 6001563-A 1 14-DEC-1999;
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Sequence 1 from patent US 6001563.
AR093439 GI:10020188
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55.7%;
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Best Local Similarity 55.7
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